SIMEHOLON

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(without alignments)
3772.184 Million cell updates/sec
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                                                                                                                 October 27, 2003, 10:19:13 ; Search time 59.995 Seconds
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GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
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                                                                                                                                                                                                                                                                                                                                    830525 seqs, 258052604 residues
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Maximum Match 100%
Listing first 45 summaries
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Gapop 10.0 , Gapext 0.5
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	Description	Q911y2 hordeum vul	Q9lyf8 arabidopsis	022444 arabidopsis	Q8vwv9 pinus pinas	09zp26 arabidopsis	0987v7 arabidopsis	Ogave3 physcomitre	Q91gc6 oryza sativ	O9lec9 solanum tub	Q9zp04 tropaeolum	091zt7 arabidopsis	073626 coturnix co	Q9uv08 emericella	O8bqi6 mus musculu	O91245 mus musculu	Q9mym4 bos taurus
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	Query Natch Length DB	879	902	902	910	907	915	916	929	928	935	855	932	992	953	953	937
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ALIGNMENTS

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STRAINECT TOTAL AND TAXES.

MEDLINE-20267959; PubMed-10806244;

MEDLINE-20267959; PubMed-10806244;

MEDLINE-20267959; PubMed-10806244;

MEDLINE-20267959; PubMed-10806244;

Thank proselectric-point alpha-glucosidase from barley malt.";

A high-isoelectric-point alpha-glucosidase from barley malt.";

Plant Physiol. 123.275-286(2000).

R EMBL; AR18226; AAF76254.1;

R EMBL; AR18226; AAF76254.1;

R InterPro; IPR000327; Glyco hydro_31.

R PROSITE; PS00129; GLYCOSYL HYDROL_F31_1; 1.

R PROSITE; PS00129; GLYCOSYL HYDROL_F31_2; 1.

R PROSITE; PS00092; NG MTASE; 11

R PROSITE; PS00092; NG MTAS
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Spermatophyta, Magnoliophyta, Liliopsida, Poales, Poacee, Pooideae,
Triticeae, Hordeum.
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Last annotation update)
                                                           879 AA
                                                                                                                                                                                          Created)
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AGL97.
Hordeum vulgare (Barley).
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STGDVQRLAVYASLETDSRLRVRITDADHPRWEVPQDIIPRPAPGDVLHDAPPASSAPLQ
                   AQKYVLILDPGIRVDPIDATYGTFVRGMQQDIFLKRNGTNFVGNVWPGDVYFPDFMHPAA
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Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
eurosids II; Brassicales; Brassicaceae; Arabidopsis.
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01-0CT-2000 (TrEMBLrel. 15, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
Alpha-glucosidase 1 (ATSg11720/T22P22_110).
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[1] = SEQUENCE FROM N.A.

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DVQRLAVYASLETDSRLRVRITDADHPRWEVPQDIIPRPAPGDVLHDAPPASSAPLQG-- 116
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EMBL, ALIG3814; CAB87690.1; ---
EMBL; BT002222; AAN72233.1; ---
Bevan M., Hilbert H., Braun M., Holzer E., Brandt A., Duesterhoeft Bancroft I., Mewes H.W., Rudd S., Lemcke K., Mayer K.F.X., Submitted (APR-2000) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A. Shinn P., Cheuk R., Kim C.J., Koesema E., Meyers M.C., Bann P., Chen H., Cheuk R., Kim C.J., Koesema E., Meyers M.C., Banh J., Bowser L., Carninci P., Dale J.M., Goldsmith A.D., Hayashizaki Y., Ishida J., Jiang P.X., Jones T., Kamiya A., Karlin-Neumann G., Kawai J., Lam B., Lee J.M., Lin J., Liu S.X., Miranda M., Narusaka M., Nguyen M., Onodera C.S., Palm C.J., Pham P.K., Quach H.L., Sakurai T., Satou M., Seki M., Southwick A. Toriumi M., Yamada K., Yamamura Y., Yu G., Yu S., Shinozaki K., Davis R.M., Theologis A., Ecker J.R.;
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Matches 471; Conservative 136; Mismatches 191; Indels
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Pfam; PF01055; Glyco_hydro_31, 1.
PROSITE; PS00129; GLYCOSXL_HYDROL_F31_1; 1.
PROSITE; PS010707; GLYCOSXL_HYDROL_F31_2; 1.
SEQUENCE 902 AA; 101118 WW; DB56817DAA000B3B CRC64;
                                                                                                                                                                                                   EU Arabidopsis sequencing project;
Submitted (APR-2000) to the EMBL/GenBank/DDBJ databases.
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            TSALPAGRASLYGLGEHTKSSFRLRHNDSFTLWNADIGASYVDVNLYGSHPFYMDVRA-- 222
                                  FTAAELRPFVDRLHRNAQKYVLILDPGIRVDPIDATYGTFVRGMQQDIFLKRNGTNFVGN 398
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Sanchez M., Gianzo C., Sampedro J., Revilla G., Zarra I.;
"Changes in alpha-xylosidase expression during intact and auxin-
induced growth of pine hypocotyls.";
Submitted (NOV-2001) to the EMBL/GenBank/DDBJ databases.
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Pinus pinaster (Maritime pine).
Bukaryota; Viridiplantae; Streptophyta; Embryophyta; 'Spermatophyta; Coniferopsida; Coniferales; Pinaceae; 'Col_TaxID=71647;
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Last annotation update)
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PPYKINNSGDKRPINNKTVPATSIHFGNISEYDAHNLYGLLEAKATHQAVVDITGKRPFI
                                                                       CGRWIQLGAFYPFSRDHSAIFTVRRELYLMPSVAASGRKALGLRYQLLFYFYTLMYEARM
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                                                 LSRSTFVGSGRYTAYWTGDNAATWGDLRYSINTMLSFGLFGMPMIGADICGFNGNTTEEL
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Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magmoliophyta, eudicotyledons, core eudicots, Rosidae,
eurosids II, Brassicales, Brassicaceae, Arabidopsis.
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C STRAIN=Landsberg;
MEDLINE=98045620; PubMed=9411456;
MEDLINE=98045620; PubMed=9411456;
MADINTOG J.D., Hall B.D., Gough C.M., Stephen A.L.;
T Nucleotide sequence of an alpha-glucosidase gene (Accession No. T AF014806) from Arabidopsis thaliana (PGR97-141).";
Plant Physiol. 115:863-863 [1997).
R EMBL, AF014806; AAB02656.1; -.
R InterPro; IPR000322; Glyco_hydro_31.
R PROSITE; PS00129; GLYCOSYL_HYDROL_F31_1; 1.
R PROSITE; PS00170; GLYCOSYL_HYDROL_F31_2; 1.
Glycosidase; Hydrolase.
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Best Local Similarity 55.0%; Pred. No. 2.2e-175;
Matches 470; Conservative 136; Mismatches 192;
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|PDFLNPKTVNFWADEISHFHQMVPVDGLWIDMNEISNFCSGKCSIPTNRSCPGTGFPWE
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                                                                                                            DVQRLAVYASLETDSRLRVRITDADHPRWEVPQDIIPR-PAPGDVLHDAPPASSAPLQGR
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                                                                                            Gaps
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                                                                           DB 10; Length 910;
                                                                                                                                                                                                                                                                                                             FPOFMHPAAAEFWAREISLFRRTIPVDGLWIDMNEISNFYNPE---PMN
                                                                          Query Match 47.4%; Score 2193.5; DB 10; Lengt Best Local Similarity 49.9%; Pred. No. 2.4e-156; Matches 430; Conservative 144; Mismatches 223; Indels
EMBL; AF448201; AAL40352.1; -.
InterPro; IPR001032; Glyco hydro_31.
InterPro; IPR001092; HLH_basic.
Ffam; PF01055; Glyco hydro_31; 1.
PROSITE; PS00129; GLYCOSYL_HYDROL_F31_1; 1.
PROSITE; PS00070; GLYCOSYL_HYDROL_F31_2; 1.
SEQUENCE 910 AA; 100609 MW; C4B75C7306CC16F9 CRC64;
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                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
SEQUENCE FROM N.A.
STRAILNE-V. Columbia; TISSUB=Seedling hypocotyl;
MEDLINE=21295581; PubMed=11402218;
Sampedro J., Siełro C., Revilla G., Gonzalez-Villa T., Zarra I.;
Sampedro J., Siełro C., Revilla G., Gonzalez-Villa T., Zarra I.;
Sampedro J., Siełro C., Revilla G., Gonzalez-Villa T., Zarra I.;
Cloning and Expression Pattern of a Gene Encoding an alpha-Xylosidase
Active against Xyloglucan Oligosaccharides from Arabidopsis.";
Plant Physiol. 126:910-920 (2001)
ENBL, FA0044813, AADOS539.1;
InterPro; IPR000322; Glyco hydro_31.
PROSITE; PS00129; GLYCOSYL_HYDROL_F31_1; 1.
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                                                                                                                                                                                   Arabidopsis thaliana (Mouse-ear cress).
Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, eudicotyledons; core eudicots, Rosidae;
eurosids II, Brassicales; Brassicaceae; Arabidopsis.
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                                                 01-MAY-1999 (TrEMBLrel. 10, Created)
01-MAY-1999 (TrEMBLrel. 10, Last Bequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
Alpha-xylosidase precursor (Fragment).
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116 907 ALPHA-XYLOSIDASE.
907 AA; 101647 MW; 58ABBD235366C588</pre>
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45.4%; Score 2100; DB 10;
Best Local Similarity 46.6%; Pred. No. 2.7e-149;
Matches 431; Conservative 145; Mismatches 267;
     PRT;
PRELIMINARY;
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NCBI_TaxID=3702;
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Bowser L., Carninci P., Dale J.M., Goldsmith A.D., Hayashizaki Y.,
Ishida J., Jiang P.X., Jones T., Kamiya A., Karlin-Neumann G.,
Kawai J., Lam B., Lee J.M., Lin J., Liu S.X., Miranda M., Narusaka M.,
Nguyen M., Onodera C.S., Pahn C.J., Phan P.K., Quach H.L., Sakurai T.,
Satou M., Seki M., Southwick A., Tang C.C., Toriumi M., Yamada K.,
Yamamura Y., Yu G., Yu S., Shinozaki K., Davis R.W., Theologis A.,
                                                                                                                           GVLRDTGRRPFVLSRSTFVGSGRYTAYWTGDNAATWGDLRYSINTMLSFGLFGMPMIGAD
              PYFYTLMYEAHMTGAPIARPLFFSYPHDVATYGVDRQFLLGRGVLVSPVLEPGPTTVDAY
                                                                                                                                                                FPAGRWYRLYDYSLAVATRTGKHVRLPAPADTVNVHLTGGTILPLQQSALTTSRARRTAF
                                                                                                                                                                              300 NSYAQSRTLVISKVVLMGHRSPAAPKKLTVHVN--SAEVEASSSAGT-----RYQNAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Arabidopsis thaliana (Mouse-ear cress).

Bukaryota, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magmoliophyta; eudicotyledons; core eudicots; Rosidae;
eurosids 11; Brassicales; Brassicaceae; Arabidopsis.

NCBI_TaxID=3702;
                                                      ICGFNGNTTEELCGRWIQLGAFYPFSRDHSAIFTVRRELYLWPSVAASGRKALGLRYQLL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SECURINCE FROM N.A.
SECURINCE FROM N.A.
SECURINCE FROM N.A.
VYSOLSKAIA V.S., Schwartz J.R., Yu G., Toriumi M., Lenz C., Liu S.,
Liee J.M., Li J., Gonzalez A., Liu A., Liu K., Vaysberg M., Sakano H.,
Choi E., Chiou J., Altafi H., Araujo R., Barooks S.,
Buehler E., Chao Q., Conn L., Conway A.B., Dunn P., Hansen N.,
Howng B., Huizar L., Khan S., Kim C., Palm C., Rowley D., Shinn P.,
Walker M., Davis R.W., Ecker J.R., Federspiel N.A., Theologis A.;
"The sequence of BAC F2455 from Arabidopsis thaliana chromosome 1.";
Submitted (AUG-1999) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             [1] SEQUENCE FROM N.A.
SEQUENCE FROM N.A.
STRAIN=cv. Columbia;
Sampedro J., Steiro C., Villa T.G., Revilla G., Zarra I.;
Sampedro J., Steiro C., Villa T.G., Revilla G., Zarra I.;
"Cloning and expression pattern of an alpha-xylosidase gene from "Arabidopeia thaliana.";
Arabidopeia thaliana.";
Submitted (APR-1999) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Ecker J.R.;
"Arabidopsis cDNA clones.";
Submitted (SEP-2001) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
Alpha-xylosidase precursor (ATIG68560/F2445_10)
XYLI OR F24J5.20.
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                                                                                                                                                                                                                                                                                                                                 851 GLGGVAHIGGLSLVVGEEFELKVAM 875
                                                                                                                                                                                                                                                                                                                                                         883 VM---VEVRGLEMLVGKDFNMSWKM 904
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SLYGLGEHTKSS-FRLRHNDSFTLWNADIGASYVDVNLYGSHPFYMDVRAPG---TAHGV 229
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          -----PMNALDDPPYRINNDGTGRPINNKTVRPLAVHYGGVTBYEEHNLFGLLEARATGR 503
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        473 DCKNITKTRWDDPPYKINATGVVAPVGFKTIATSATHYNGVRBYDAHSIYGFSETIATHK 532
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SEQUENCE FROM N.A.

Chang C.H., Cheuk R., Shinn P., Bowser L., Carninci P., Chan M., Chang C.H., Dale J.M., Hayashizaki Y., Hsuan V.W., Chan M.M., Chang C.H., Dale J.M., Hayashizaki Y., Hsuan V.W., Chan M.M., Chang C.H., Ramiya A., Karlin-Neumann G., Kawai J., Lam B., Ishida J., Jones T., Kamiya M., Narusaka M., Nguyen M., Onodera C.S., Palm C.J., Chart H.L., Sakurai T., Satou M., Seki M., Southwick A., Tang C.C., Toriuni M., Wong C., Wu H.C., Yamada K., Yu G., Yuan S., Ashinozaki K., Davis R.W., Theologis A., Ecker J.R.;

"Arabidopsis ORF clones";

"Arabidopsis ORF clones";

"Arabidopsis ORF clones";

"BRBL, ARAD37831; ---

"BRBL, AROB3781; ---

"BRBL, ANOS7482; AAL09716.1; ---

"BRBL, ANOS7482; AAL09716.1; ---

"BRBL, ANOS7482; AAL09716.1; ---

"BRBL, ANOS755; Glyco-hydro_31.

"Brant, PF01055; Glyco-hydro_31.

"BROMER PROSITE; PS00129; GLYCOSYL_HYDROL_F31_1; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RSSTGDVQRLAVYASLETDSRLRVRITDADHPRWEVPQDIIPRPAPGDVLHDAPPASSAP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LLLCLCLCLFAP------RLCSSKEEGPLAARTVLAVAVTMEGAL--RAEAATGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LLLALILC-FSPTQSYKTIGKGYRLVSI-EESP------DGGFIGYLQVKQKN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LOGRVLSPAGSDLVLTVHASPFRFTVSRRSTGDTLFDTAPGLVFRDKYLBVTSALPAGRA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LLLSSNGMDVLYGGSYVTYKVIGGVLDFYFFAGPNPLAVVDQYTQLIARPAPMPYWSFGF
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    45.4%; Score 2100; DB 10; Length 915; 46.6%; Pred. No. 2.7e-149;
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124 915 ALPHA-XYLOSIDASE.
915 AA; 102398 MW; 28F9610D8D7EA657 CRC64;
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825 FAERSLHSGSL--VSRVIAGNYALEQGLVLQSIRFLGVSGPVS----DVIVNGERIVSAE 878
   350 TFDPVRYDENTVREFVKELHANGQQYIVILDPGISVG--YKNYSTLBRGLKDDIFLKNEF 407
                                 GTNFVGNVWPGDVYFPDFMHPAAAEFWARBISLFRRTIPVDGLWIDMNEISNF----- 444
                                                  : | | | | | : | | : | | 468 FDTLTLGMGKNDSDNDRCLLHCVNGTSRFDDPPYKINHVGTYDNLGVKTIAMTVKHYNGV 527
                                                                                                                                                             485 TEYEEHNLFGLLEARATGRGVLRD-TGRRPFVLSRSTFVGSGRYTAYWTGDNAATWGDLR 543
                                                                                                                                                                              TILPLOOSALTISRARRIAFHILVALAED -- GTASGYLFLDDGDSPEYGRRSDWS-MVRF 780
                                                                                                                                                                                                                                                                                                                                                                                                                                        765 QILPMQEARLTSAEVKKTPFTLVVVFSADASASASGKLFVDSGVDIBMGIQDGSSTFVQF 824
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    781 NYKIPUNKGAIKVKSEVVHNSYAQSRTLVISKVVLMGHRSPAAPKKLTVHVNSAEVEASS 840
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                                                                                               -----YNPEPMALDDPPYRINNDGTGRPINNKTVRPLAVHYGGV
                                                                                                                                                                                                                          544 YSINTMLSFGLFGMPMIGADICGFNGNTTEELCGRWIQLGAFYPFSRDHSAIFTVRRELY
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Oryza sativa (Rice),
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Ouery Match 44.3%; Score 2049.5; DB 10; Length 929; Best Local Similarity 45.9%; Pred. No. 1.8e-145; Matches 424; Conservative 144; Mismatches 277; Indels 79;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-0cT-2000 (TrEMBLrel. 15, Created)
01-0cT-2000 (TrEMBLrel. 15, Last sequence update)
01-0cT-2002 (TrEMBLrel. 22, Last annotation update)
EST AU092739(C53221) corresponds to a region of the predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PAC
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Sasaki T., Matsumoto T., Yamamoto K.;
*Oryza sativa nipponbare(GA3) genomic DNA, chromosome 1,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     clone:P0504H10.";
Submitted (JUN-2000) to the EMBL/GenBank/DDBJ databases.
EMBL; AP002526; BAA99366.1; -
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InterPro; IPRO0022; Glyco_hydro_31.
Pfam; PF0105; Glyco hydro_31; 1.
PROSITE; PS00129; GLYCOSYL_HYDROL_F31_1; 1.
SEQUENCE 929 AA; 102550 MW; 536ElD0B9D7F97BF CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  841 --SAGTRYQNAGGLGGVAHIGGLSLVVGEEFELKVAM 875
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    332
                                                            713 FPPGSWYHMFDMTQAVVSKNGKRVTLPAPLNFVNVHLYQNTILPTQQGGLISKDARTTPF 772
                                                                                                                TLDRVNFTAAELRPFVDRLHRNAQKYVLILDPGIRVDPIDATYGTFVRGMQQDIFLKRN- 391
653 PFLYTLNYEAHMTGAPIARPLFFSFPEYTECYGNSRQFLLGSSFMISPVLEQGKTEVEAL 712
                               FPAGRWYRLYDYSLAVATRIGKHVRLPAPADTVNVHLTGGTILPLQQSALITSRARTAF 743
                                                                                              744 HLLVAL --- AEDGTASGYLFLDDGDSPEYGRRSDWS-MVRFNYKIPNNKGAIKVKSEVVH 799
                                                                                                                                                            300 NSYAQSRTLVISKVVLMGHRSPAAPKKLTVHVN--SAEVEASSSAGT------RYQNAG 850
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                                                                                                                                                                                                                                                                                                                                                                                                                                                 Physcomitrella patens subsp. patens.
Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Bryophyta,
Bryopsida, Funariidae, Funariales, Funariaceae, Physcomitrella.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   moss.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Hwatashi Y., Nishiyama T., Hasebe M.;
Hwatashi Y., Nishiyama T., Hasebe M.;
"Establishment of gene- and enhancer-trap systems of the mo Physcomitreal patens.",
Submitted (MAR-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; AB057452; BAB39467.1;
InterPro; IPR001032; Glyco-hydro-31.
InterPro; IPR001032; Glyco-hydro-31.
PROSITE; PS00125; Glyco-hydro-31.
PROSITE; PS00129; GLYCOSYL-HYDROL F31.1;
PROSITE; PS00129; GLYCOSYL-HYDROL F31.1;
PROSITE; PS00129; GLYCOSYL-HYDROL F31.2; 1.
SEQUENCE 916 AA; 102282 WW; AĀCEZĀCGE440D863 CRC64;
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Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                       Created)
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                                                                                                                                                                                                                                                                                                                                                                    01-JUN-2001 (TrEMBLrel. 17,
                                                                                                                                                                                                                                                                                                                                                                                                                   Putative alpha-glucosidase
                                                                                                                                                                                                                                                                                                                                       PRELIMINARY;
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Best Local S:
Matches 422
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SEQUENCE FROM N.A.
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Best Local &
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                                                     LSPA---GSDLVLTVHASPFRFTVSRRSTGDTLFDTAPG-LVFRDKYLEVTSALPAGRAS
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15 CIPLCLLFLTLASS - - NGVFAAAPPKVGSGYKLVSLVEHPEGGALVGYLQVKQRTSTYGP
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MEDLINE=2158; PubMed=11469591;
Taylor M.A.; Ross H.A., McRae D., Wright F., Viola R., Davies H.V.;
"Copy-DNA cloning and characterisation of a potato alpha-glucosidase: expression in Escherichia coli and effects of down-regulation in Planta 213:258-264(2001).
BMBL, AJ27744; CABS6677.1; -
BMBL, AJ27744; CABS6677.1; -
PROSITE; PRO1055; Glyco hydro-31; ThrerPro; IPR000322; Glyco hydro-31; ThrerPro; IPR000322; Glyco hydro-31; ThrerPro; Typuco Hydro-31; ThrerPro; Threr
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Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Asteridae; lamiids; Solanales; Solanaceae; Solanum.
WCBI_TaxID=90692;
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725 KTEVKALPPPGTWYSLLDMTETVDSKKGQYYTLDAPLHVVNVHLYQNTILPMQQGGLLSK 784
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                                       ------PMNALDDPPYRINNDGTGRPINNKTVRPLAVHYGGVTEYEBHNLFGLL 496
                                                                               557 MPMIGADICGFNGNTTEELCGRWIQLGAFYPFSRDHSAIFTVRRELYLWPSVAASGRKAL 616
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Arabidopsis thaliana (Mouse-ear cress).
Bukaryota, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
eurosids II; Brassicales; Brassicaceae; Arabidopsis.
NCBI_TaxID=3702;
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Jordan N., Bangert S., Wiedelmann R., Vobs H., Unseld M.,
Fudd S., Lemcke K., Mayer K.F.X., Quetier F., Salanoubat
Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EU Arabidopsis sequencing project;
Submitted (APR-2000) to the EMBL/GenBank/DDBJ databases.
EMBL, AL162459; CAB82018.1;
Interpro; IRR00132; Glyco hydro_31.
Pfam; PF01055; Glyco hydro_31; 1.
PROSITE; PS00129; GLYCOSYL_HYDROL_F31_1; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-OCT-2000 (TrEMBLrel. 15, Created)
01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-UNN-2002 (TrEMBLrel. 21, Last annotation update)
Hypothetical 95.9 kDa protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              895 EQIFVGKLDAEESKPESLMVEVKGLDIPVGKNFVMSWKM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Matches 404; Conservative 144; Mismatches 245;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      845 RYQNAGGLGG-----VAHIGGLSLVVGEEFELKVAM
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SEQUENCE FROM N.A.
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                                       449
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         --TAHGVLLLSSNGMDVLYGGSYVTYKVIGGVLDFYFFAGPNPLAVVDQYTQLIARPAPM 282
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PYWSFGFHOCRYGYLNVSDLERVVARYAKARIPLEVMWTDIDYMDGFKDPTLDRVNFTAA 342
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ELRPFVDRLHRNAQKYVLILDPGIRVDPIDATYGTFVRGMQQDIFLKRNGTNFVGNVWPG 402
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  425 AVNFPDFLNPKTVDWWGDEVRRFHELVPVDGLWIDMNBDLEFLFWEMANPQGKQCPTGEG 484
   KSEVVHNSYAQSRTLVISKVVLMGHRSPAAPKKLTVHVNSAEVEASSSAGTRYQNAGGL- 852
                                                                                                                                          SEQUENCE FROM N.A.
STRAIN=cv. tall climbing mixed; TISSUE=Cotyledon;
Crombine H.J., Chengappa S., Jarman C., Sidebottom C., Reid G.;
Crombine H.J., Chengappa S., Jarman C., Sidebottom C., Reid G.;
"Molecular characterisation of a xyloglucan oligosaccharide-acting alpha-D-xylogidase from the cotyledons of nasturtium (Tropaeolum majus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      403 DVYFPDFWHPAAAEFWAREISLFRRTIPVDGLWIDMNEISNF----YNPE----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Alpha D-xylosidase precursor.
Tropaeolum majus (Common nasturtium).
Eukaryota, Viridiplantae, Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
eurosids II; Brassicales; Tropaeolaceae; Tropaeolum.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   42.1%; Score 1950.5; DB 10; Length 935;
.larity 45.6%; Pred. No. 5.2e-138;
Conservative 134; Mismatches 263; Indels 81;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 L) seeds.";
Submitted (AUG-1999) to the EMBL/GenBank/DDBJ databases.
EMBL, Al131520; CAA10382.2;
InterPro: IFR00322; Glyco.hydro_31.
Pfoul055; Glyco.hydro_11; 1.
PROSITE; PS00129; GLYCOSYL_HYDROL_F31_1; 1.
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25 935 ALPHA-D-XYLOSIDASE.
935 AA; 104937 MW; 22DE6901E9CE19BD CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-MAY-1999 (TrEMBLrel. 10, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
                                                                                                                                                                                                                             ----GG-----VAHIGGLSLVVGEEFELKVAMSY 877
                                                                                                                                                                                                                                                                 895 KLEEGGHKKSMMLDIKGLELPIGKNP----AMSW 924
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401; Conser
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NCBI_TaxID=4020;
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SIGNAL
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Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 415 AEFWAREISLFRRTIPVDGLWIDMNEISNFYNPE----PWNALDDPPYR---INNDGTGR 467
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maltase
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                                                                                                                                                                                                                                                                                                                                                                                                                               88;
                                                                                                    cDNA of Japanese
its mRNA in acid
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                                                                                                                                                                                                                   databases
                                                                                                                                                                                                                                                                                                                             SMART; SM00018; PD; 1.
PROSTIE; PS00129; GLYCOSYL HYDROL F31 1; 1.
PROSTIE; PS00707; GLYCOSYL HYDROL F31 2; 1.
SEQUENCE 932 AA; 104689 MW; BGZE18ZP03DE3F61 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 33.0%; Score 1529; DB 13; Best Local Similarity 40.0%; Pred. No. 3.1e-106; Matches 334; Conservative 136; Mismatches 278;
                                                                                                                                                                                              "Genomic sequences of ggaal and ggaal.";
Submitted (MAR-2002) to the EMBL/GenBank/DDBJ
EMBL, AB000067; BAA25884.1; -.
HSSP; P04155; 1PS2.
                                                        MEDLINE = 98201735; PubMed = 9540858; Kunita R., Nakabayashi O., Wu U.Y., Hagiwara Famnybacker M., Chen Y T., Kikuchi T., Molecular cloning of acid alpha-glucosidase (coturnix cotunix japonica) and the lack of Heichient qualis ". Biophys. Acta 1362:269-278(1997).
                                                                                                                                                                                                                                                                     Interpro; IPR000122; Glyco hydro 31. Interpro; IPR0000129; P. trefoil. Pfam; PF01055; Glyco hydro 31; 1. Pfam; PF00088; trefoil; 1.
                                                                                                                                                                       SEQUENCE FROM N.A.
                                FROM N.A
    WCBI_TaxID=93934;
                                                                                                                                                                                       Nakabayashi O.;
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01-AUG-1998 (TrEMBLrel. 07, Last sequence update)
01-MAC-2003 (TrEMBLrel. 23, Last annotation update)
Acid alpha glucosidase.
GAAI OR GAAI.
Coturnix coturnix japonica (Japanese quail).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
                                                                                                                    -APGTAHGVLLLSSNGMDVLYGGSYVTYKVIGGVLDFYFFAGFNPLAVVDQYTQLIARPA
                                                                                                                                                                       224 SGKAYAHSVLLINSHGMDVFYRGDSLTYKVIGGVFDFYFFAGPSPLAVVDQYTSLIGRPA
                                                                                                                                                                                                                                   284 PMPYWS------LVVVXD---VVDNYQKAKIPLDVIWNDADYMDGYKDFTLDLVNFP
                                                                                                                                                                                                                                                                                       489 FVGSGQYAAHWTGDNQGTWQSLQVSISTMLNPGIFGVPWVGSDICGFFPPTPEELCNRWI
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                                                            TSALPAGRASLYGLGEHTKSS-FRLRHNDSFTLWNADIGASYVDVNLYGSHPFYMDVR--
                                                                                                                                                                                                                  PMPYWSFGFHQCRYGYLNVSDLERVVARYAKARIPLEVMWTDIDYMDGFKDFTLDRVNFT
                                                                                                                                                                                                                                                                       AAELRPFVDRLHRNAQKYVLILDPGIRVDPIDATYGTFVRGMQQDIFLKRNGTNFVGNVW
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NNDGTGRPINNKTVRPLAVHYGGVTEYEEHNLFGLLEARATGRGVLRDTGRRPFVLSRST
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ATKKAMRIRYALLPYFYTLMHDAHTTGSTVLRALAMEPPDPSLAAIDNQFLVGPSILVT 806
     447 DVFLKNPDGSLYIGAVWPGYTVFPDWHHPDAADFWANELVTWYEKVKFDGVWYDMSEVSS 506
                                                                                                          507 FCVGSCGSRNRTLNPVHPPFRLPGBPGNVDYBYPEGFELSNATEAASAASSSQAATTA 566
                                                                                                                                                                ------LDDPPYRINNDGTGRPINNKTVRPLAVHYGGVTEYEEHN 491
                                                                                                                                                                                                 567 TETTISTSSYLRISPTPGVRNVNYPPYVINHVQTGHDLAVHAVSPNATHVDGYHEYDVHS 626
                                                                                                                                                                                                                                                               LFGLLEARATGRGVLRDTGR-RPFVLSRSTFVGSGRYTAYWTGDNAATWGDLRYSINTML 550
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MEDLINE-22354683; PubMed=12466851;
The FANTOM Consortium,
The RIKEN Genome Exploration Research Group Phase I & II Team;
The RIKEN Genome Exploration Research Group Phase I & II Team;
"Analysis of the mouse transcriptome based on functional annotation 60,770 full-length CDNAs.";
Nature 420:553-573(2002).
BABLI AKO52211; BAC348811; -.
EMBL; AKO88481; BAC40382.1; -.
SEQUENCE 953 AA; 106247 MW; 956B89685FB5FF81 CRC64;
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(1-MAR-2003 (TrEMBLrel. 23, Last annotation update)

Glucosidase.

Mus musculus (Mouse).

Bukaryota: Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Muscl_TaxIb=10090;
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(TrEMBLrel. 23, Last sequence update)
(TrEMBLrel. 23, Last annotation update)
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Best Local Similarity 38.6%; Pred. No. 2e-99;
Matches 331; Conservative 124; Mismatches 317;
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                                                                                                                                     837
                                                                                                                                                                                                                    GFKDFTLDRVNFTAAELRPFVDRLHRNAQKYVLILDPGIRV-DPIDA--TYGTFVRGMQQ 384
                                                                                                                                                                                      LFLDDGDSPEYGRRSDWSMVRFNYKIPNNKGAIK--VKSEVVHNSYAQSRTLVISKVVLM 816
SVNSSGEMLKLSAPLDHLNLHLREGSILPTQKPGITSKATRGNPLHLIVALSTRATAWGD
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                                                                                                                                                                                                                                                                                                                      GVQEP--PSKVL-----LDGQEKPFSYLDNQ-----VLTVSGLGLVLSQGFSLQ 930
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota; Fungi, Ascomycota; Pezizomycotina; Eurotiomycetes;
Eurotiales; Trichocomaceae; Emericella.
NCBI_TaxID=162425;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Boase N.A., Murphy R.M., Kelly J.M.;
Boase N.A., Murphy R.M., Kelly J.M.;
"An amylase cluster in Aspergillus nidulans.";
Submitted (NOV-1999) to the EMBL/GenBank/DDBJ databases.
BMBL; AF208225; AAF17102.1; -..
InterPro; IPR001064; Crystallin.
InterPro; IPR001064; Crystallin.
PROSITE; PS00225; CRYSTALLIN BETAGAMA; 1.
PROSITE; PS00129; GLYCOSYL HYDROL F31_1; 1.
PROSITE; PS00129; GLYCOSYL HYDROL F31_2; 1.
SPROSITE; PS00107; GLYCOSYL HYDROL F31_2; 1.
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01-MAY-2000 (TrEMBLrel. 13, La
01-MAR-2003 (TrEMBLrel. 23, La
Alpha-glucosidase AgdA.
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                               PFRFTVSRRSTGDTLFDT - - APGLVFRDKYLRVTSALPAGRASLYGLGEHTKSSFRLRHN
                                                                            DSFTLWNADIGASYVDVNLYGSHPFYMDVRAPGTAHGVLLLSSNGMDVLYGGS-YVTYKV
                                                                                                                        251 IGGVLDFYFFAGPNPLAVVDQYTQLIARPAPMPYWSFGFHQCRYGYLNVSDLERVVARYA
                                                                                                                                   333 TGGILDVYVFLGPEPKSVVQQYLDVVGYPPMPPYWGLGFHLGRWGYSSTAIVRQVVENWT
                                                                                                                                                                 311 KARIPLEVMWTDIDYMDGFKDFTLDRVNFTAAELRPFVDRLHRNAQKYVLILDPGIRVDP
                                                                                                                                                                               568 HYNLANLYGLTEAIASSRALVKTRCTRPFVISRSTFSGHGRYAGHWTGDVRSSWEHLAYS
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                                              371 IDATYGTFVRGMQQDIFL-KRNGTNFVGNVWPGDVYFPDFMHPAAAEFWAREISLFRRTI
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[1] SEQUENCE FROM N.A. SEQUENCE FROM N.A. Strausberg R.; Strausberg R.; Submitted (JUL-2001) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Q91245 PRELIMINARY; PRT; 953 AA.
Q91245;
Q1-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
Similar to glucosidase, alpha, acid.
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                                                                                                                                                                                                                                                                                                                                                                                                                            96;
                                                                                                                                                                                                                                                                                                                                                          Query Match 31.1%; Score 1438; DB 11; Length Best Local Similarity 38.6%; Pred. No. 2.4e-99; Matches 331; Conservative 123; Mismatches 318; Indels
MGD; MGI:95609; Gaa.
InterPro; IPR000322; Glyco hydro_31.
InterPro; IPR000322; Glyco hydro_31.
InterPro; IPR00039; Ptrefoil.
Pfam; PP01085; Glyco hydro_31; 1.
Ffam; PP01088; trefoil; 1.
SMART; SM00018; PD; 1.
PROSITE; PS001079; GLYCOSYL HYDROL_F31 1; 1.
PROSITE; PS0000707; GLYCOSYL HYDROL_F31 2; 1.
SROWINE: PS000025; PTREFOIL; 1.
SEQUENCE 953 AA; 106157 MW; 32086D7354A5FP91 CRC64;
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817 G-----HRSPAAPKKL 827

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Search completed: October 27, 2003, 10:30:52 Job time: 69.995 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

October 27, 2003, 10:19:13 ; Search time 12.1941 Seconds (without alignments) 3382.161 Million cell updates/sec Run on:

US-10-043-418-1 4630 1 MATVGVLLCLCLCLCLFAPRL.....IGGLSLVVGEEFELKVAMSY 877 Title: Perfect score: Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

127863 seqs, 47026705 residues Searched:

127863 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match Of Maximum Match 100* Listing first 45 summaries

SwissProt_41:* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

STIMMINE

	ption	hordeum vul	spinacia ol	beta vulgar	mucor javan	aspergillus	homo sapien	mus musculu	schizosacch	oryctolagus	candida alb	asper		homo	schizosacch	debaryomyce	rattus norv	suncus muri	candida tsu					-	_			torpedo cal		-			candida rug	
	Description	043763	004893	004931	092442	P56526	P10253	P70699	Q9c0y4	P07768	074254	012558	P14410	043451	006600	P22861	P23739	062653	P29064	906000	Q9£234	P38138	059645	666d6D	P31434	P32138	001336	P19965	P08236	029441	P39045	008017	94	P48692
SUMMARIES	ΙD	AGLU HORVU	AGLU_SPIOL	AGLU_BETVU	AGLU_MUCJA	AGLU_ASPNG	LYAG HUMAN	LYAG_MOUSE	AGLU_SCHPO	SUIS_RABIT	AMYG CANAL	AGLU_ASPOR	SUIS_HUMAN	MGA HUMAN	YAJI SCHPO	AMYG_DEBOC	SUIS_RAT	SUIS SUNMU	AGLU_CANTS	AGLU TETPY	AGL2_BACTQ	YB79_YEAST	AGLU_SULSO	XXLS_SULSO	YICI_ECOLI	YIHQ_ECOLI	YCR2_ERWHE	SP15_TORCA	BGLR HUMAN	Y817_ARCFU	DAC_ACTSP	PBUA PSESP	LIP2_CANRU	RBL_CHRHI
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ď	Query Match	100.0	52.3	51.2	31.7	30.5			29.6	29.5	29.5	29.1	28.7	28.3	27.7	27.6	27.6	27.3	24.7	21.2	20.3	16.5	14.7	10.4	٠				2.6	•		•	2.4	4.2
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CYAA BORPE PGDS XENLA	PC16_HUMAN PTPN_HUMAN	RBL_PORAE M122_DROME CAPP_COREF	IGA4 HAEIN BGLR CERAE PTPN BOVIN
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tive 0; Mismatches
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STANDARD;

AGLU SPIOL ID AGLU SPIOL AC 004893;

(Rel. 36, Created) (Rel. 36, Last sequence update)

15-JUL-1998 15-JUL-1998

CA EE

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        glucosidase from spinach.";
Plant Mol. Biol. 33:765-768(1997).
-! FUNCTION: ALPHA-GLUCOSIDASE I AND II HAVE HIGH ACTIVITY TOWARDS
-!- EUNCLICOSACCHARIDES AND STARCH, WHILE FORM III AND IV HAVE HIGH
ACTIVITY TOWARDS MALTO-OLIGOSACCHARIDES BUT LOW ACTIVITY TOWARD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                10 LGILLVFLLQYLVAG--ISTSENDP---EGVIGYGYGYKVK-SVKVDSGT-RRSLTALPQLV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     non-reducing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        -!- CATALYTIC ACTIVITY: Hydrolysis of terminal, non-reducing linked D-glucose residues with release of D-glucose.-!- PTM: FOUR DIPPERENT FORMS (I-IV) MAY BE PRODUCED BY POST-
                                                                              Spinacia oleracea (Spinach).
Makaryota Viridiplantae; Streptophyta; Embryophyta; Tracheo
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Caryophyllidae, Caryophyllales; Chenopodiaceae; Spinacia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TRANSLATIONAL MODIFICATION.
-!- SIMILARITY: BELONGS TO FAMILY 31 OF GLYCOSYL HYDROLASES.
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ALPHA-GLUCOSIDASE.

BY SIMILARITY.

N-LINKED (GLCNAC. . . ) (POTEN N-LINKED M-LINKED M-LIN
                                           Alpha-glucosidase precursor (EC 3.2.1.20) (Maltase)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         of a cDNA
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InterPro; IPR00322; Glyco hydro 31.
Pfam; PP01055; Glyco hydro 31; 1.
PROSITE; PS00129; GLYCOSYL, HYDROL, F31 1; 1.
PROSITE; PS00707; GLYCOSYL, HYDROL, F31 2; 1.
Hydrolase; Glycosidase; Glycoprotein; Signal.
.5-JUL-1998 (Rel. 36, Last annotation update)
                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A., AND PARTIAL SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sugimoto M., Furui S., Suzuki Y.;
"Molecular cloning and characterization
                                                                                                                                                                                                                                                                                                                                                                          STRAIN=cv. Dash;
MEDLINE=97238484; PubMed=9132069;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EMBL; D86624; BAA19924.1; -.
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its mee by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     154 ---GLVFRDKYLEVTSALPAGRASLYGLGEHTKSSFRLRHNDSFTLWNADIGASYVDVNL 210
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               site
                            sugar beet alpha-glucosidase.";
Biosci. Biotechnol. Biochem. 59:459-463(1995).
-!- FUNCTION: HIGH ACTIVITY FOR ALPHA-GLUCAN.
-!- CATALYTIC ACTIVITY: Hydrolysis of terminal, non-reducing linked D-glucose residues with release of D-glucose.
-!- PTM: THE N-TERMINUS IS BLOCKED.
-!- SIMILARITY: BELONGS TO FAMILY 31 OF GLYCOSYL HYDROLASES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 51.2*; Score 2370; DB 1; Length 913; Best Local Similarity 51.2*; Pred. No. 1.1e-162; Matches 466; Conservative 147; Mismatches 235; Indels 6;
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         modification and amino acid sequence
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InterPro; JRS00322; Glyco hydro_31.

PROSITE; PS00129; GLYCOSYL_HYDROL_F31_1; 1.

PROSITE; PS00707; GLYCOSYL_HYDROL_F31_2; 1.

PROSITE; PS00707; GLYCOSYL_HYDROL_F31_2; 1.

PROSITE; PS00707; GLYCOSYL_HYDROL_F31_2; 1.

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PGOSITE; PS00707; GLYCOSYL_HYDROL_F31_1; Signal.
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15-JUL-1998 (Rel. 36, Last sequence update)
30-MAY-2000 (Rel. 39, Last annotation update)
Alpha-glucosidase preursor (EC 3.2.1.20) (Maltase).
Beta vulgaris (Sugar beet).
Beta vulgaris (Sugar beet).
Spermatophyta; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Caryophylidae; Caryophylales; Chenopodiaceae; Beta.
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MEDLINE=95252592; PubMed=7766184;
Iwanami S., Matsui H., Kimura A., Ito H., Mori H., Honma Chiba S.;
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218 MDVRAPGTAHGVLLESSNGMDVLYGGSYVTYKVIGGVLDFYFFA----GPNPLAVVDQYT 273
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   334 LDRVNPTAAELRPFVDRLHRNAQKYVLILDPGIRVDPIDATYGTFVRGMQQDIFLKR-NG 392
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N-LINKED (GLCNAC. .) (POTENTIAL).

W, CFAB4759DC431403 CRC64;
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31.7%; Score 1470; DB 1; Length 864;
Best Local Similarity 36.9%; Pred. No. 6.3e-98;
Matches 328; Conservative 158; Mismatches 281; Indels 122;
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    APTPGSTLDNPPYKINNSGGRVPINSKTIPATAMHYGNVTEYNAHNLYGFLESQATREAL 539
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                                                                     LRDTGRRPFVLSRSTFVGSGRYTAYWTGDNAATWGDLRYSINTMLSFGLFGMPMIGADIC
                                                                                                                                   GFNGNTTEELCGRWIQLGAFYPPSRDHSAIFTVRRELYLWPSVAASGRKALGLRYQLLPY
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01-NOV-1997 (Rel. 35, Created)
11-NOV-1997 (Rel. 35, Last sequence update)
15-SEP-2003 (Rel. 42, Last annotation update)
Alpha-glucosidase precursor (EC 3.2.1.20) (Maltase).
Mucor javanicus.
Eukaryota; Fungi; Zygomycota; Zygomycetes; Mucorales; Mucoraceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               -!- CATALYTIC ACTIVITY: Hydrolysis of terminal, non-reducing 1,4-linked D-glucose residues with release of D-glucose.
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MEDLINE=96271012; PubMed=8830045;
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NCBI_TaxID=51122
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                                                                                                                                                           MEDLINE=97308516; PubMed=9165762;
Nakamura A., Nishimura I., Yokoyama A., Lee D.-G., Hidaka M., Masaki H., Kimura A., Chiba S., Vozumi T.;
"Cloning and sequencing of an alpha-glucosidase gene from Aspergillus niger and its expression in A. nidulans.";
J. Biotechnol. 53:75-84(1997).
                                                                                                                                                                                                                                                Eukaryota, Fungi, Ascomycota, Pezizomycotina, Eurotiomycetes,
Eurotiales, Trichocomaceae, mitosporic Trichocomaceae, Aspergillus.
NCBI_TaxID=5061;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (GLCNAC. .) . (GLCNAC. .) .
                                                15-JUL-1998 (Rel. 36, Created)
15-JUL-1998 (Rel. 36, Last sequence update)
15-SEP-2003 (Rel. 42, Last annotation update)
Alpha-glucosidase precursor (EC 3.2.1.20) (Maltase)
AGLA.
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Pfam; PF01055; Glyco_hydro_31; 1.

PROSITE; PS00129; GLYCOSYL_HYDROL_F31_1; 1.

PROSITE; PS001707; GLYCOSYL_HYDROL_F31_2; 1.

Hydrolase; Glycosidase; Glycoprotein; Signal.

SIGNAL

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ACT SITE

490 490

CARBOHYD

26 386

O-LINKED (POTENTIAL OCARBOHYD

124 124

N-LINKED (GLCNAC.
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                                  985 AA
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                                  PRT;
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                                                                                                                                                                                                                         SEQUENCE OF 26-252 AND 267-985.
                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL; D45356; BAA23616.1; -. GlycoSuiteDB; P56526; -.
                                 STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Aspergillus niger.
                                                                                                                                          SEQUENCE FROM N.A.
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601
601
                                AGLU ASPNG
P56526; 013451;
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DVQRLAVYASLETDSRLRVRI ---- TDADHPRWE - VPQDIIPRPAPGDVLHDAPPASSAP 113
                                                                                                                                                                                                                                                    LOGRVLSPAGSDLVLTVHASP-FRFTVSRRSTGDTLFDT-APGLVFRDKYLEVTSALPAG 171
                                                                                                                                                                                                                                                                                                            -AP------GTAHGVLLLSSNGMDVLYGGSYVTYKVIGGVLDFYFFAGPNPLA 267
                                                                                                                                                                                                                                                                                                                                                                                                                                       VVDQY-TQLIARPAPMPYWSFGFHQCRYGYLNVSDLERVVARYAKARIPLEVMMTDIDYM 326
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 316 VTRQYLTSTVGLPAMQQYNTLGFHQCRWGYNNWSDLADVVANFEKFEIPLEYIWTDIDYM 375
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              QDIFLKR-NGTNFVGNVWPGDVYFPDFMHPAAAEFWARBISLFRRTIPVDGLWIDMNBIS 442
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  491
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          492 LFGLLEARATGRGVLR--DTGRRPFVLSRSTFVGSGRYTAYWTGDNAATWGDLRYSINTM 549
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        699
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DGPKDFTLDRVNFTAAELRPFVDRLHRNAQKYVLILDPGIRV-DPIDAT--YGTFVRGMQ 383
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LSFGLFGMPMIGADICGFNGNTTELCGRWIQLGAFYPFSRDHSAIFTVRRELYLWPSVA 609
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  172 RASLYGLGEHTKSSFRLRHNDSFTLWNADIGASYVDVNLYGSHPFYMDVR-----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ----LDDPPYRINNDGTGRPINNKTVRPLAVHYGGVTEYEEHN
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                                                                                                                                                                                                  Conservative 139; Mismatches 243; Indels 133;
                                                                                                                                                                     30.5%; Score 1410.5; DB 1; Length 985; 37.3%; Pred. No. 1.4e-93;
           LPLOQSALTTSRARRTAFHLLVALAEDGTASGYLPLDDGDS 766
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second allele.";
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SEQUENCE FROM N.A., AND PARTIAL SEQUENCE OF 70-89; 123-145; 204-215; 230-249; 332-345; 349-370; 394-409; 480-513; 520-545; 703-719; 726-731 AND 795-803.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Martiniuk F., Bodkin M., Tzall S., Hirschhorn R., aldentification of the base-pair substitution responsible for a human acid alpha glucosidase allele with lower 'affinity' for glycogen (GAA 22) and transient gene expression in deficient cells.";
Am. J. Hum. Genet. 47:440-445(1990).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             'Human lysosomal alpha-glucosidase. Characterization of the catalytic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Hoefsloot L.H., Hoogeveen Westerveld M., Reuser A.J.J., Oostra B.A., "Characterization of the human lysosomal alpha-glucosidase gene."; Biochem. J. 272:493-497(1990).
               LYAG HUMAN STANDARD; PRT; 952 AA.
P10255; Q14351; Q16302;
01-MAR-1999 (Rel. 10, Created)
01-FBB-1991 (Rel. 17, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Lysosomal alpha-glucosidase precursor (EC 3.2.1.20) (Acid maltase).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Reuser A.J.J., Kroos M.A., Hermans M.M.P., Bijvoet A.G.A., verbeet M.P., van der Ploeg A.T., "Glycogenosis type II (acid maltase deficiency)."; Muscle Nerve 3:661-869 (1995).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WEDLINE-90262651; PubMed=2111708; Martail K., Martail L., Martail K., Martail 
                                                                                                                                                                                                                                                                                                                           TISSUE=Placenta, Testis, and Urine;
MEDLINE=88005058; PubMed=3049972;
Hoefsloot L.H., Hoogeveen-Westerveld M., Kroos M.A., van Beeumen Greuser A.J.J., Oostra B.A.;
"Primary structure and processing of lysosomal alpha-glucosidase;
homology with the intestinal sucrase-isomaltase complex.";
EMBO J. 7:1697-1704(1988).
                                                                                                                                                                                   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE=93168114; PubMed=8435067;
Hermans M.M.P., Wisselaar H.A., Kroos M.A., Oostra B.A.,
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Hermans M.M.P., Kroos M.A., van Beeumen J., Oostra B.A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Submitted (JUN-1990) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Biol. Chem. 266:13507-13512(1991).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
MEDLINE=91097465; PubMed=2268276;
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Biochem. J. 289:681-686(1993).
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                                                                                                                                                                sapiens (Human)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
                                                                                                                                                                                                                            NCBI_TaxID=9606;
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MEDLINE=91379015; PubMed=1898413;
Hermans M.M.P., de Graaff E., Kroos M.A., Wisselaar H.A., Oostra B.A.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE=94004908; PubMed=8401535; Hermans M.M.P., Kroos M.A., de Graaff E., Oostra B.A., Reuser A.J.J.; Hermans M.M.P., Kroos M.A., de Graaff E., Oostra B.A., Reuser A.J.J.; "Two mutations affecting the transport and maturation of lysosomal alpha-glucosidase in an adult case of glycogen storage disease type
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Martiniuk F., Mehler M., Bodkin M., Tzall S., Hirschhorn K., Zhong N.,
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MEDLINE-95072571; PubMed=7981676;
Huie M.L., Chen A.S., Brooks S.S., Grix A., Hirschhorn R.;
"A de novo 13 nt deletion, a newly identified C647W missense mutation and a deletion of exon 18 in infantile onset glycogen storage disease type II (GSDI).";
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE=93168115; PubMed=8094613; Hermans M.M.P., de Graaff E., Kroos M.A., Wisselaar H.A., Willemsen R., Costra B.A., Reuser A.J.J.; The conservative substitution Asp-645-->Glu in lysosomal alphaglucosidase affects transport and phosphorylation of the enzyme in Biochem. J. 289:687-693 (1993).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                "Identification of a point mutation in the human lysosomal alpha-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     glucosidase gene causing infantile glycogenosis type II."
Biochem. Biophys. Res. Commun. 179:919-926(1991).
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VARIANT GSD-II THR-318,
MEDLINE=91353580; PubMed=1652892;
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Hum. Mutat. 4:291-293(1994).
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251 IGGVLDFYFFAGPNPLAVVDQYTQLIARPAPMPYWSFGFHQCRYGYLNVSDLERVVARYA 310
                                                                                                                                                                                    311 KARIPLEVMWIDIDYMDGFKDFILDRVNFTAAELRPFVDRLHRNAOKYVLILDPGIRVDP 370
                                                                                                                                                                                                                                      393 RAHFPLDVQWNDLDYMDSRRDFTFNKDGF--RDFPAMVQELHQGGRRYMMIVDPAISSSG 450
                                                                                                                                                                                                                                                                                           371 IDATYGTFVRGMQQDIFL-KRNGTNFVGNVWPGDVYFPDFMHPAAAEFWAREISLFRRTI 429
                                                                                                                                                                                                                                                                                                                                                                                                                                   568 HYNLHNLYGLTEAIASHRALVKARGTRPPVISRSTFAGHGRYAGHWTGDVWSSWEQLASS 627
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             868 LERGAYIQVIFLARNMIVNE--LVRVISE------GAGLQLQKVIVLG--VATAPQQ 915
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 748 EALLITPVLQAGKAEVTGYFPLGTWYDLQTVPIEALGSLPPPPAAPREPAIHSEGQWVTL 807
                                                                                                              451 PAGSYRPYDEGLRRGVFITNETGQPLIGKVWPGSTAFPDFTNPTALAWEDMVAEFHDQV
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1-NOV-1997 (Rel. 35, Last sequence update)
30-MAY-2000 (Rel. 39, Last annotation update)
Lysosomal alpha-glucosidase precursor (EC 3.2.1.20) (Acid maltase)
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Mammalia, Butheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus.
NCBI_TaxID=10090;
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STRAIN=BALB/c; TISSUB=Liver;
Ding J.H., Yang B.Z., Reuser A.J.J., Roe C.R.;
Submitted (SEP-1996) to the EMBL/GenBank/DDBJ databases.
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MEDLINE=98205825; PubMed=9535769;
Huie M.L., Tsujino S., Brooks S.S., Engel A., Elias E., Bonthron D.T.,
Bessley C., Shanske S., Diamauro S., Goto Y.I., Hirschhorn R.;
"Glycogen storage disease type II: identification of four novel
missense mutations (D645N, 6648S, R672M, R672Q) and two
insertions/deletions in the acid alpha-glucosidase locus of patients
of differing phenotype.";
                                                 VARIANTS GSD-II ARG-299; LYS-903 DEL AND VARIANTS HIS-199; ARG-223 AND
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                                                                                                                                     Plotz P.H., Raben N.; "Leaky splicing mutation in the acid maltase gene is associated with delayed onset of alycogenosis twom TT "."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           "Glycogen storage disease type II: genetic and biochemical analysis of novel mutations in infantile patients from Turkish ancestry."; Hum. Mutat. 11:209-215(1998).
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"Identification of a de novo point mutation resulting in infantile form of Pompe's disease.";
Biochem. Biophys. Res. Commun. 208:886-893(1995).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     HIS-199 AND ARG-223.
MEDLINE=98180719; PubMed=9521422;
Hermans M.M.P., Kroos M.A., Smeitink J.A.M., van der Ploeg A.T.,
Kleijer W.J., Reuser A.J.J.;
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                                                                                                                               R.C., Miller
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"Acid alpha-glucosidase deficiency; identification and expre
a missense mutation (SS29V) in a Japanese adult phenotype.";
Hum. Genet. 97:496-499(1996).
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MEDLINE=95209708; PubMed=7695647;
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Raben N., Lee E., Lee L., Hirschhorn R., Plotz P.H.;
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Boerkoel C.F., Exelbert R., Nicastri C., Nichols
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                                                                                                                                                                                                          delayed onset of glycogenosis type II.";
Am. J. Hum. Genet. 56:887-897(1995).
Mol. Genet. 3:2213-2218(1994)
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PROSITE; PS00129; GIYCOSYL HYDROL F31_1; 1.
PROSITE; PS00170; GIYCOSYL HYDROL F31_2; 1.
Hydrolase; Glycosidase; Glycoprotein; Lysosome; Signal.
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InterPro: IPR000519; P_trefoil.
Pfam; PF01055; Glyco hydro_31; 1.
Pfam; PF00088; trefoil; 1.
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568 HYNLHNLYGLTEALASSRALVKTRGTRPFVISRSTFSGHGRYAGHWTEDVRTSWEHLAYS
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MEDLINE=21195240; Pubmed=11298741; GLU-484 AND ASP-647.
OKUYAMA M., OKUNDO A., Shimizu N., Mori H., Kimura A., Chiba S.;
"Carboxyl group of residue Asp647 as possible proton donor in catalytic reaction of alpha-glucosidase from Schizosaccharomyces pombe.";
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Schizosaccharomycetales, Schizosaccharomycetaceae,
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16-OCT-2001 (Rel. 40, Last sequence update)
16-SEP-2003 (Rel. 42, Last annotation update)
Alpha-gluadadase precursor (EC 3.2.1.20) (Maltase).
AGL OR SPAPB24D3.10C.
Schizosaccharomyces pombe (Fission yeast).
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                           92 DYPLLFLAVTYEEADRVHISIKDANNTQFQFTSRKD------LWDAP-----
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                 al Similarity 34.9%; Pred. No. 1.1e-90; 320; Conservative 166; Mismatches 281; Indels 149;
 Length 969;
   29.6%; Score 1370.5; DB 1;
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                                                                                                                                                                                                                                                                                                                     PRELIMINARY SEQUENCE OF 1-37 AND 1007-1014.

WEDLINE=83105704; PubMed=7152027;
A 5joestroem H., Noren O., Christiansen L.A., Wacker H., Spiess M.,
Bigler-Meier B., Rickli E.E., Semenzad G.;
Bigler-Meier B., Rickli E.E., Semenzad G.;
Bigler-Meier B., Rickli E.E., Semenzad G.;
Insertion of pro-sucrase--isomaltase-rickle biosynthesis and membrane transcripton of pro-sucrase--isomaltase-rickle biosynthesis and membrane an insertion of pro-sucrase--isomaltase-rickle biosynthesis and membrane are insertion of pro-sucrase--isomaltase-rickle biosynthesis and membrane are remained by membrane by an exportive processidase--isomaltase-rickle biosynthesis and maltose by an alpha-b-glucosidase-type action.

-! CAPALYTIC ACTIVITY: Hydrolysis of sucrose and maltose by an alpha-amylase and in isomaltose.

-! CAPALYTIC ACTIVITY: Hydrolysis of sucrose and maltose by an alpha-amylase and in isomaltose.

-! CAPALYTIC ACTIVITY: Hydrolysis of sucrose and maltose by an alpha-amylase and in isomaltose.

-! CAPALYTIC ACTIVITY: Hydrolysis of sucrose and maltose by an alpha-amylase and in isomaltose.

-! CAPALYTIC ACTIVITY: Hydrolysis of sucrose and maltose by an alpha-amylase and in isomaltose.

-! CAPALYTIC ACTIVITY: Hydrolysis of sucrose and maltose by parker by a sucrement by a sucre
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                                                                                                                      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
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InterPro; IPRO00319; P_trefoil.
Pfam; PF01008; Glyco hydro_31; 2.
Pfam; PF01008; trefoil; 2.
SMART; SM0018; PD; 2.
PROSITE; PS00129; GIXCOSYL_HYDROL_F31_1; 2.
PROSITE; PS00707; GLYCOSYL_HYDROL_F31_1; 2.
ROSITE; PS00707; GLYCOSYL_HYDROL_F31_2; 2.
Multifunctional enzyme; Transmembrane; Glycoprotein; Hydrolase; Glycosidase; Repeat; Signal-anchor; Sulfation.
INIT_MET 1826 SUCRASE-ISOMALTASE, INTESTINAL.
                                                                                                                                                                                     SEQUENCE FROM N.A.
MEDLINE-86245068; PubMed=3755079;
Hunziker W., Spiess M., Semen G., Lodish H.F.;
"The sucrase-isomaltase complex: primary structure, membrane-orientation, and evolution of a stalked, intrinsic brush border
01-AUG-1988 (Rel. 08, Created)
30-MAY-2000 (Rel. 39, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Sucrase-isomaltase, intestinal [Contains: Sucrase (EC 3.2.1.48)
Isomaltase (EC 3.2.1.10)].
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DUPLICATION.
SIMILARITY: Contains 1 P-type (trefoil) domain.
SIMILARITY: BELONGS TO FAMILY 31 OF GLYCOSYL HYDROLASES.
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ISOMALTASE.
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                                                                                                    Oryctolagus cuniculus (Rabbit)
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Cell 46:227-234(1986).
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81 KLKBATNIYGYDFEYLMLSVEYQSDTRLNVHIEPTDLTDVFVLPEELVVKPKLEGD---- 136
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      187 NTTLPKGH-SITGLGESIHGSL----NEPGVVKTLYANDI-ADPIDGNIYGVHPVYYDQR 240
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KRSFILTRSTFAGSGRHAAHWLGDNTATWEQMEWSITGMLEFGLFGMPLVGADICGFLAE 639
                                         TIEELCGRWIQLGAFYPFSRDHSA-----IFTVRRELYLWPSVAASGRKALGLRYQL 622
                                                                                                                                     SRARRTAFHLLVALAEDGTASGYLFLDDGDSPEYGRRSDWSMVRFNYKIPNNKGAIKVKS 795
                                                                                                                                                                                                                                                                                                      TASRMNPLGLIIALNDDNTAVGDFFWDDGETKOTVQNDNY--ILYTFAVSNN----NLNI 859
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Calderone R.;

"Identification and cloning of GCAI, a gene that encodes a cell
surface glucoamylase from Candida albicans.";
Med. Mycol. 37:357-366(1999).

-!- CATALYTIC ACTIVITY: Hydrolysis of terminal 1,4-linked alpha-D-
glucose residues successively from non-reducing ends of the chains
with release of beta-D-glucose.

-!- SUBCELLULAR LOCATION: CELL WALL ASSOCIATED.

-!- SIMILARITY: BELONGS TO FAMILY 31 OF GLYCOSYL HYDROLASES.
                                                                                                                                                                                                                                                                                                                                                                 EVVHNSYAQSRTLVISKVVLMGHRSPAAPKKLTVHVNSAEVEASSSAGTRYQNAGGLGGV
                                                                                                                 LPYFYTLMYEAHMTGAPIARPLFFSYPHDVATYGVDRQFLLGRGVLVSPVLEPGPTTVDA
                                                            ||||||| ||:||||||||||:|:|
TTEELCRRWMQLGAFYPFSRNHNADGFEHQDPAFFGQDSL-----LVKSSRHYLNIRYTL
                                                                                                                                                                                        YFPAGRWYRLYDYSLAVATRIG-----KHVRLPAPADIVNVHLIGGIILPLQQSALIT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                15-JUL-1999 (Rel. 38, Created)
15-JUL-1999 (Rel. 38, Last sequence update)
15-JUL-1999 (Rel. 38, Last sequence update)
Glucoamylase 1 11, Last annotation update)
Glucoamylase 1 precursor (EC 3.2.1.3) (Glucan 1,4-alpha-glucosidase)
(1,4-alpha-D-glucan glucohydrolase).
GAM1 OR GCM1
Candida albicans (Yeast).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EMBL, AF082188, AAC31968.1, -.
InterPro; IPR000322; Glyco_hydro_31.
InterPro; IPR01055; Glyco_hydro_31, 1.
PROSITE; PS00129; GLYCOSYL_HYDROL_F31_1; 1.
PROSITE; PS00707; GLYCOSYL_HYDROL_F31_2; 1.
Hydrolase; Glycosidase; Polysaccharide degradation; Glycoprotein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
Saccharomycetales; mitosporic Saccharomycetales; Candida.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STRAIN=SC5314;
MEDLINE=99451422; PubMed=10520161;
Sturtevant J., Dixon F., WadSworth E., Latge J.-P., Zhao X.-J.,
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GLUCOAMYLASE 1.
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Length 985;

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          YTLLHESHVTGIPIMRAFNWQFPYSKELAGVDTQFFVGDALLVTPVLEPGVNHTKGIFPG 780
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-----EEALYUDFVA
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                                                                                                              GR--WYRLYDYSLAVATRTGKHVRLPAPADTVNVHLTGGTILPLQQSALTTSRARTAFH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Bukaryota; Pungi; Ascomycota; Pezizomycotina; Eurotiomycetes;
Eurotiales; Trichocomaceae; mitosporic Trichocomaceae; Aspergillus.
NCBI_TaxID=5062;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE=96012211; PubMed=7549103; Minetoki T., Gomi K., Kitamoto K., Kumagai C., Tamura G.; Minetoki T., Gomi K., Kitamoto K., Kumagai C., Tamura G.; Nucleotide sequence and expression of alpha-glucosidase-encoding gene (agdA) from Aspergiallus oryzae.";
Biosci. Biotechnol. Biochem. 59:1516-1521(1995).
-:-FUNCTION: Hydrolyzes malto-olligosaccharides, but has a low activity toward soluble starch.
-:- CATALYTIC ACTIVITY: Hydrolysis of terminal, non-reducing 1,4-lincose residues with release of D-glucose.
-:- INDUCTION: By maltose.
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15-JUL-1998 (Rel. 36, Created)
15-JUL-1998 (Rel. 36, Last sequence update)
15-SEP-2003 (Rel. 42, Last annotation update)
Alpha-glucosidase precursor (EC 3.2.1.20) (Maltase) (AGL).
                                                                                                                                                                                                                                                                                                                                                          -- GAVYLIDLEKFIKEGAFAEEFTLQ 945
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                                                                                                                                                                                                                                                                                                                               DISEASE: Defects in SI are the cause of disaccharide intolerance
                                                                                                                                                                                                                                                                                                  to
                                                                                                                                                                                        MEDLINE=92159963; PubMed=1353958;
Chantret I., Lacasa M., Chevalier G., Ruf J., Islam I., Mantei N.,
Edwards Y., Swallow D., Rousset M.,
"Sequence of the complete cDNA and the 5' structure of the human
sucrase-isomaltase gene. Possible homology with a yeast
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   I [MIM:222900].
MISCELLANEOUS: THERE IS A HIGH DEGREE OF HOMOLOGY BETWEEN THE ISOMALTASE AND SUCRASE PORTIONS (41 % OF AMINO ACID IDENTITY) INDICATING THAT THIS PROTEIN IS EVOLUED BY PARTIAL GENE
                                                                                                                                       Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                                                         "Isolation of a cDNA probe for a human jejunal brush-border hydrolase, sucrase-isomaltase, and assignment of the gene locus
                                                                              01-JAN-1990 (Rel. 13, Created)
30-MAY-2000 (Rel. 39, Last sequence update)
38-FBE-2003 (Rel. 41, Last annotation update)
Sucrase-isomaltase, intestinal [Contains: Sucrase (EC 3.2.1.48)
Isomaltase (EC 3.2.1.10)].
                                                                                                                                                                                                                                                       SEQUENCE OF 1-677 FROM N.A.
MEDLINE=88112852; PubMed=2962903;
Green F., Edwards Y., Hauri H.-P., Povey S., Ho M.W., Pinto M.,
Swallow D.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SIMILARITY: BELONGS TO FAMILY 31 OF GLYCOSYL HYDROLASES. SIMILARITY: Contains 1 P-type (trefoil) domain.
                                                                 PRT; 1826 AA
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                  956 Y---NATSHVLHVGGL 968
       846 YONAGGLGGVAHIGGL 861
                                                                 STANDARD;
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                                                                                                                                 Homo sapiens (Human)
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                                                                                                                                                                                                                                  gluccamylase.
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modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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non-profit institutions as long as its content is in no
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GO; GO:0005794; C:Golgi apparatus; TAS.
InterPro; IPR000322; Glyco_hydro_31.
InterPro; IPR000529; P. trefcoll.
Pfam; PF01055; Glyco_hydro_31; 2.
Pfam; PF00088; trefcoll; 2.
SWART; SW00018; PD; 2.
PROSITE; PS00025; P_TREFOIL; 1.
PROSITE; PS00129; GLYCOSYL_HYDROL_F31_1; 2.
PROSITE; PS00179; GLYCOSYL_HYDROL_F31_2; 1.
Multifunctional enzyme; Transmembrane; Glycoprotein; Hydrolase; Glycosidase; Repeat; Signal-anchor; Sulfation; Disease mutation.
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EMBL; M22616; AAA60551.1; ALT_SEQ.
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209272 MW;
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Genew; HGNC:10856; SI.
MIM; 222900; -.
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Best Local Similarity
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TISSUE=Small intestine;
  QLGAFYPFSRDHSA-----IFTVRRELYLWPSVAASGRKALGLRYQLLPYFYTLMYE 632
LYGLGEHTKSSFRLRHNDSFTLW---NADIGASYVDVNLYGSHPFYMDVR-APGTAHGVL 230
                                              237 IYGIĞEQVHK - RFRHDLSWKTWPIFTRDQLPGDNNNNLYGHQTFFMCIEDTSGKSFGVF 294
                                                               LLSSNGMDV-LYGGSYVTYKVIGGVLDFYFFAGPNPLAVVDQYTQLIARPAPMPYWSFGF 289
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                                                                                                  HOCRYGYLNVSDLERVVARYAKARIPLEVMMTDIDYMDGFKDFTLDRVNFTAAELRPFVD 349
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                                                                                                                                     RLHRNAQKYVLILDPGIRVD--PIDATYGTFVRGMQQDIFLKRN--GINFVGNVWPGDVY 405
                                                                                                                                                                         PPDFWHPAAAEFWAREISLFRRTIPVDGLWIDMNEISNFYNPEP-----MNALDDPPYRIN 461
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   30-MAY-2000 (Rel. 39, Created)
28-FEB-2003 (Rel. 41, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Maltase-glucoamylase, intestinal [Includes: Maltase (EC 3.2.1.20)
(Alpha-glucosidase); Glucoamylase (EC 3.2.1.3) (Glucan 1,4-alpha-glucosidase)].
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1856 AA.
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation-the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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"Tyrosine sulfation, a post-translational modification of microvillar enzymes in the small intestinal enterocyte.";
EMBO J. 6:2891-2896 (1987).
-I- FUNCTION: MAY SERVE AS AN ALTERNATE PATHWAY FOR STARCH DIGESTION WHEN LUMINAL ALPHA-AMYLASE ACTIVITY IS REDUCED BECAUSE OF IMMATURITY OR MALNUTRITION. MAY PLAY A UNIQUE ROLE IN THE DIGESTION OF MALTED DIETARY OLIGOSACCHARIDES USED IN FOOD
                                                                                                                                                                                                                                                                                                                                                                                                                                              TISSUE=Small intestine mucosa;
MEDLINE=89066802; PubMed=3143729;
Naim H.Y., Sterchi E.E., Lentze M.J.;
"Structure, biosynthesis, and glycosylation of human small intestinal
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SIGNAL-ANCHOR (TYPE-II MEMBRANE PROTEIN)
(POTENTIAL).
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-!- PTM: DOES NOT UNDERGO INTRACELLULAR OR EXTRACELLULAR PROTEOLYTIC
                                                                                             Sterchi E.E.;
"Human small intestinal maltase-glucoamylase cDNA cloning. Homology
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SMART; SMOGIUS; DD; 2.

PROSITE; PSO0129; GLYCOSYL HYDROL_F31_1; 2.

PROSITE; PSO0129; PLREFOIL; 1.

Multifunctional enzyme; Transmembrane; Glycoprotein; Hydrolase; Glycopidase; Repeat; Signal-anchor; Sulfation.

INIT MET 0 CYTOPLASMIC (POTENTIAL).

DOMAIN 1 12 CYTOPLASMIC (POTENTIAL).

TEANSMEM 13 33 SIGNAL-ANCHOR (TYPE-II MEMBRANE PI 'POTENTIAL).
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-!- PTM: SULPATED (BY SIMILARITY).
-!- SIMILARITY: BELONGS TO FAMILY 31 OF GLYCOSYL HYDROLASES.
-!- SIMILARITY: BELONGS TO PAMILY 31 OF GLYCOSYL HYDROLASES.
-!- SIMILARITY: Contains 2 P-type (trefoil) domains.
MEDLINE-98112863; PubMed-9446624;
Nichols B.L., Eldering J.A., Avery S.E., Hahn D., Quaroni
Sterchi E.E.;
                                                                                                                                                                                                                                            REVISIONS TO 776; 1049; 1100; 1541; 1612 AND 1811.
Nichols B. B.L., Bldering J.A., Avery S.E., Hahn D., Quaroni
Sterchi E. E.;
Submitted (DEC-2001) to the EMBL/GenBank/DDBJ databases.
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GO; GO:0005983; P:starch catabolism;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     maltage-glucoamylase.";
J. Biol. Chem. 263:19709-19717(1988)
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Interpro; IPR000519; P. trefeil.
Pfam; PF01055; Glyco hydro_31; 2.
Pfam; PF00088; trefeil; 2.
                                                                                                                                                        to sucrase-isomaltase.";
J. Biol. Chem. 273:3076-3081(1998)
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ABOUT NEW LIABARTON BY CONTROLINE M. Lyne M., Lyne R., Stewart A., RADINEZIARRAN PUDNEZIARRAN BY RAJANDER J., Baker S., Basham D., Bowman S., Beroks K., Brown D., Brown S., Chillingworth T., Churcher C.M., Charles C.M., Brown D., Brown S., Chillingworth T., Fraser A., Goble A., Hamlin N., Harris D., Hidalgo J., Hodgson G., A. Horbes D., Horneby T., Howarth S., McDonald S., McLean J., Money P., Moule S., Mungall K., Murphy L., Niblett D., Odell C., A. Diver K., O'Neil S., Pearson D., Gwail M.A., Rabbinowitsch E., A. Oliver K., O'Neil S., Saunders D., Seeger K., Sharp S., Rutherford K., Rutter S., Saunders D., Seeger K., Sharp S., Rutherford K., Taylor R.G., Tivey A., Walsh S.V., Warren T., Whitchead S., Relton J., Volckaert G., Aert R., Robben J., Grymonprez B., Wodward J., Volckaert G., Aert R., Robben J., Grymonprez B., Relton J., Volckaert G., Aert R., Robben J., Grymonprez B., Relton J., Volckaert G., Lehrach H., Menler D., Hilbert H., Rabeling C., Fuchs M., Fritzc C., Holzer E., Moestl D., Hilbert H., Rabeling C., Fuchs M., Fritzc C., Hurt C., Moore K., Hurst S., Roblen C., Klang Z., Hurt C., Moore K., Hurst S., Roller R., Acalibert F., Aves S.J., Xiang Z., Hurt C., Moore K., Hurst S., Mortier S., Calibert F., Aves S.J., Xiang Z., Hurt C., Moore K., Hurst S., Lelaure V., McLose M., Rochet M., Gaillardin C., Tallada V.A., Garzon A., Thode G., Dominguez A., Revuelta J.L., Moreno S., Armstrong J., Forsburg S.L., Revuelte J., Lowe T., McCombie W.R., Paulsen I., Potashkin J., The Shpakovski G.V., Ussery D., Barrell B.G., Nurse P., The Genome sequence of Schizosaccharomyces pombe.";
                                                             899 NEIKILGTEEPS---NUTVKHNGVPSGTSPTV-TYDSNL----KVAIITDIDLLLGGAYT 950
                               FVGSGRYTAYWTGDNAATWGDLRYSINTMLSFGLFGMPMIGADICGFNGNTTEELCGRWI 580
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                                                                                                                                                            LYDYSLAVATRIGKH-VRLPAPADIVNVHLIGGTILPLQQSALTISRARRTAFHLLVALA 750
                                                                                                                                                                                                                                 EAHMIGAPIARPLFFSYPHDVATYGVDRQFLLGRGVLVSPVLBPGPTTVDAYFPAGRWYR 691
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-FEB-1996 (Rel. 33, Created)
01-OCT-1996 (Rel. 34, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Putative family 31 glucosidase C30D11.01c precursor (EC 3.2.1.-).
SPACIOD11.01C OR SPAC56FB 01.
Schizosaccharomyces pombe (Pission yeast).
Bukaryota; Pungi; Ascomycota; Schizosaccharomycetes;
Schizosaccharomycetales; Schizosaccharomycetes;
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NCBI_TaxID=4896;
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              SLGFOMSRWGYKTLSDLINMRSYLNASNIPTEGFWNDIDYMSEFRTFTVNSTAFPPNQTL 396
                                                 PFVDRLHRNAQKYVLILDPG1-RVDP---IDATYGTFVRGMQQD1FLKR-NGTNFVGNVW
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                                                                                                                                                                                                                                                                                                                                                                                                                  697 MVGADVCGYNGNTDEELCARWMALGAFLPFYRNHNSLGSIPQEPFRWASVAEASRSAIEI
                                                                                                                  PGDVYFPDFMHPAAAEFWAREI-----SLFRRTIPVDGLWIDMNEISNF----
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P2286; Q92336;
01-AUG-1991 (Rel. 19, Created)
01-AUG-1991 (Rel. 19, Last sequence update)
16-JUL-1998 (Rel. 36, Last annotation update)
17-JUL-1998 (Rel. 36, Last annotation update)
17-JUL-1998 (Rel. 36, Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Dobmen R.J., Strasser A.W.M., Dahlems U.M., Hollenberg C.P., (Gloning of the Schwanniomyces occidentalis glucoamylase gene (GAMI) and its expression in Saccharomyces cerevisiae.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sukaryota, Pungi, Ascomycota, Saccharomycotina, Saccharomycetes, Saccharomycetales, Saccharomycetacese, Debaryomyces
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STRAIN=ATCC 26076;
MEDLINE=91071592; Pubmed=1979298;
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                                            This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation-the European Bioinformatics Institute. There are no restrictions on its most by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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PIR; T38598; T38598
GeneDB Syombe; SPAC30D11.01c; -.
InterPro; IPR000322; Glyco hydro_31; 1.
PROSITE; PS00129; GLYCOSYL HYDROL F31 1; FALSE NEG.
PROSITE; PS00107; GLYCOSYL HYDROL F31 2; 1.
Hypochetical protein; Hydrol-Bs; Glycosidase; Glycoprotein; Signal. SIGNAL
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              - SIMILARITY: BELONGS TO FAMILY 31 OF GLYCOSYL HYDROLASES
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            70 AAKGYDLVNVTNTPRGLTGILKLKEATNIYGYDFÖYLNLTV--EYQADTRLNVHIEPTDL 127
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        84 HPRWEVPQDIIPRP-APGDVIHDAPPASSAPLOGRVLSPAGSDLVLTVHASPFRFTVSRR 142
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SDVFVLPEHLVVKPLVEGD------AQSYNFD-----NSDLVFEYSNTDFSFEVIRS 173
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STGDTLFDTAPG-LVFRDKYLEVTSALPAGRASLYGLGE-----HTKSSFRLRHNDSFT 195
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         225
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LDFYFFAGPNPLAVVDQYTQLIARPAPMPYWSFGFHQCRYGYLNVSDLERVVARYAKARI 314
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         374 T---YGTFVRGMQQDIFLKR-NGTNFVGNVWPGDVYFPDFMHPAAAEFWAREISLFRRTI 429
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    83
           ancestral gene.";

FEBS Lett. 294:109-112(1991).

-!- FUNCTION: THIS GLUCOAMILASE HAS A SPECIFICITY TOWARD BOTH

-!- FUNCTION: THIS GLUCOAMILASE HAS A SPECIFICITY TOWARD BOTH

ALPHA-1, 4 AND ALPHA-1, 6 LINKAGES.

-!- CATALYTIC ACTIVITY: Hydrolysis of terminal 1,4-linked alpha-D-

glucose residues auccessively from non-reducing ends of the chains

with release of beta-D-glucose.

-!- SIMILARITY: BELONGS TO FAMILY 31 OF GLYCOSYL HYDROLASES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STKEVLESTKGNPLVFSNQFIQFNSSLPRNHV-ITGLGESIHGLVNBPGSVK-----T
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  30 AARTVLAVAVT----MEGALRAEAATGGRSSTGDVQRLAVYASLETDSRLRVRITDAD-
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Schwanniomyces occidentalis glucoamylase are derived from a common
                                                                                                                                                                                                                                                          PIR; JN0102; JN0102.
InterPro; IPR000322; Glyco hydro 31.
InterPro; IPR000322; Glyco hydro 31.
PROSTITE; PS00129; GLYCOSYL HYDROL F31 1; 1.
PROSTITE; PS00707; GLYCOSYL HYDROL F31 2; 1.
Hydrolase; Glycosidase; Polysaccharide degradation; Glycoprotein;
                                                                                                                                                                                                                                                                                                                                                                                                                                       (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ch 27.6%; Score 1279.5; DB 1; Length 958; al Similarity 34.4%; Pred. No. 3.7e-84; 315; Conservative 137; Mismatches 313; Indels 151;
                                                                                                                                                                                                                                                                                                                                                                                                                              (POTENTIAL)
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qa		: : : SRFLSRKHSDMDKVI 455
ò	430PVDGLWIDMNBISNF	NP 447
qq	456 KDMYELTPFDGIWADMNEVSSFCVGSCGTGKYFENPAYPPFTVGSKATSYPVGFDVSNAS	 PPFTVGSKATSYPVGFDVSNAS 515
ò	448BPMVAL	DDPPYRINNDGTGRPINNK 472
qq	516 EWKSIQSSISATAKTSSTSSVSSSSTIDYMYTLAPGKGNINYPPYAIYNMQGDSDLATH	SNINYPPYALYNMQGDSDLATH 575
È	473 TVRPLAVHYGGVTEYEEHNLFGLLEARATGRGVLR-DTGRRPFVLSRSTFVGSGRYTAYW	GRRPFVLSRSTFVGSGRYTAYW 531
qq	576 AVSPNATHADGIVEYDIHNLYGYLQENATYHALLEVFPNKRPPMISRSTFPRAGKWIGHW	NKRPPMISRSTFPRAGKWIGHW 635
ò	532 TGDNAATWGDLRYSINTMLSFGLFGMPMIGADICGFNGNTTEELCGRWIQLGAFYPFSRD	NTTEELCGRWIQLGAFYPFSRD 591
qq	636 GGDNTADWAYAYAYFSIPQAFSWGIAGLPFFGADVCGFNGNSDSELCSRWMQLGSFFFFFRYRN	NSDSELCSRWMQLGSFFPFYRN 695
ò	592 HSAIFTVRRELYLWPSVAASGRKALGLRYQLLPYFYTLMYEAHMTGAPIARPLFFSYPHD	MYEAHMIGAPIARPLFFSYPHD 651
Db	696 HNYLGAIDQEPYVWESVAEATRISMAIRYLLLPYYYTT	LHESHTTGLPILRAFSWQFPND 755
ò	652 VATYGVDRQFLLGRGVLVSPVLEPGPTTVDAYFP-AGRMYRLYDYSLAVATRIGKHVR	WYRLYDY SLAVATRIGKHVR 708
qa	756 RSLSGVDNQFFVGDGLVVTPVLEPGVDKVKGVFPGAGKEEVYYDWYIQREVHFKDGKNET	EBVYYDWYTQREVHFKDGKNET 815
ογ	709 LPAPADIVNVHLTGGTILPLQQSALTISRARRIAFHLLVALAEDGTASGYLFLDDGDSPE	VALAEDGTASGYLFLDDGDSPE 768
ДD	816 LDAPLGHIPLHIRGGNVLPTQEPGYTVAESRQNPFGLIVALDNDGKAQGSLYLDDGESLV	VALDNDGKAQGSLYLDDGESLV 875
ò	769 YGRRSDWSMVRFNYKIPNNKGAIKVKSEVVHNSYAQSRTLVISKVVLMGHRSPAAPKKLT	TLVISKVVLMGHRSPAAPKKLT 828
q	876 VDSSLLVSFSVSDNTLSASPSGDYKADQPLANVTILGVGHK	PLANVTILGVGHKPKS 919
ò	829 VHVNSAEVEASSSAGT 844	
qq	920 VKFENANUDFTYKKST 935	
Search of Job time	Search completed: October 27, 2003, 10:20:20 Job time : 20.1941 secs	

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us-10-043-418-1.rpr

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5.1.6
Compugen Ltd.
GenCore version
Copyright (c) 1993 - 2003
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using sw model - protein search, OM protein October 27, 2003, 10:19:13; Search time 22.9249 Seconds (without alignments) 3678.964 Million cell updates/sec Run on;

US-10-043-418-1

4630

1 MATVGVLLLCLCLCLFAPRL.....IGGLSLVVGEEFELKVAMSY Title: Perfect score: Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

283308 segs, 96168682 residues Searched:

283308 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database

PIR 76:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

		de			Sorting	
	Score	Query Match	Length	DB	ID	Description
	4630	100.0	877	5	865057	alpha-qlucosidase
	2451	52.9	902	~	T48531	alpha-glucosidase
٠.	2422.5	52.3	903	7	T09143	alpha-glucosidase
	2370	51.2	913	~	JC5463	alpha-glucosidase
	2100	45.4	915	~	H96709	hypothetical prote
	1904	41.1	855	~	T47534	
	1470	31.7	864	~	JC4624	alpha-glucosidase
	1396.5	30.2	952	-	A32609	alpha-glucosidase
	1370	29.6	7	Н	A23945	sucrose alpha-gluc
	1348.5	29.1		N	JC4217	alpha-glucosidase
	1329.5	28.7	7	Н	תמאמ	sucrose alpha-qluc
	1302	28.1		7	T50267	probable family 31
	1282.5	27.7	993	7	T38598	probable family 31
	1279.5	27.6		Н	JN0102	-
	1279	27.6	184	7	T10799	sucrose alpha-gluc
	1194.5	25.8		7	JC1200	alpha-glucosidase
	1192.5		174	~	T15893	hypothetical prote
	1142		Н	7	S19686	alpha-glucosidase
	1113.5			7	T16693	hypothetical prote
	1002		856	N	T22575	
	895			~	AE2402	alpha-glucosidase
	853			7	T22050	hypothetical prote
	853			N	T22044	
	826.5	17.9	919	7	T07391	ᆽ
	815	17.6	763	7	AG1460	alpha-glucosidase
	813	17.6	941	7	T32449	hypothetical prote
	801	17.3	763	7	AH1097	alpha-glucosidase
	775.5	16.7	818	~	AC2472	alpha-glucosidase
	762.5	16.5	954	7	S46105	glucan 1,4-alpha-g

alpha-glucosidase	sucrose alpha-gluc	probable glucosida	qlucosidase BH0704	alpha-xylosidase (qlycosyl hydrolase	alpha-xylosidase -	probable glycosyl	hypothetical prote	hypothetical prote	hypothetical 88.1	alpha-glucosidase	hypothetical prote	glycosidase homolo	hypothetical prote	alpha-glucosidase
H90486	S11386	AD0104	H83737	D90483	B87347	A72394	A10968	D91195	E86042	B65167	H97033	T27893	AG1749	A83888	F97177
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14.7		11.9	11.2	10.4	10.0	9.7	4.6	9.2	9.5	9.1	8.7	8.5	4.		8.1

ALIGNMENTS

ò QRLAVYASLETDSRLRVRITDADHPRWEVPQDIIPRPAPGDVLHDAPPASSAPLQGRVLS 120 120 121 PAGSDLVLTVHASPFRFTVSRRSTGDTLFDTAPGLVFRDKYLEVTSALPAGRASLYGLGE 180 180 HTKSSFRLRHNDSFTLWNADIGASYVDVNLYGSHPFYMDVRAPGTAHGVLLLSSNGMDVL 240 240 YGGSYVITYKVIGGVLDFYFFAGPNPLAVVDQYTQLIARPAPMPYWSFGFHQCRYGYLNVS 300 241 YGGSYVTYKVIGGVLDFYFFAGPNPLAVVDQYTQLIARPAPMPYWSFGFHQCRYGYLNVS 300 301 DLERVVARYAKARIPLEVMMTDIDYMDGFKDFTLDRVNFTAAELRPFVDRLHRNAQKYVL 360 9 1 MATYGVILLCLCLCLFAPRICSSKEEGPLAARTVLAVAVTWEGAIRAEAATGGRSSTGDV QRLAVYASLETDSRLRVRITDADHPRWEVPQDIIPRPAPGDVLHDAPPASSAPLQGRVLS PAGSDLVLIVHASPFRFTVSRRSTGDTLFDTAPGLVFRDKYLEVTSALPAGRASLYGLGE 1 MATVGVLLLCLCLCLFAPRLCSSKEEGPLAARTVLAVAVTMEGALRAEAATGGRSSTGDV Gaps .; 0 DB 2; Length 877; 0; Indels Query Match
100.0%; Score 4630;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 877; Conservative 0; Mismatches 241 61 61 181 121 셤 ò qq ò a ò a ò g ઠે a

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alpha-glucosidase (EC 3.2.1.20) - spinach
C:Species: Spinacia oleracea (spinach)
C:Species: Spinacia oleracea (spinach)
C:Species: Spinacia oleracea (spinach)
C:Species: In-Mun-1999 #sequence_revision 11-Jun-1999 #text_change 21-Jul-2000
C;Accession: T09143
R:Sugimoto, M.; Furui, S.; Suzuki, Y.
Plant Mol. Biol. 33, 765-766, 1997.
Plant Mol. Biol. 33, 765-766, 1997
A;Title: Molecular cloning and characterization of a cDNA encoding alpha-glucosidase
A;Reference number: Z16585, MUID:97238484; PMID:9132069
A;Reference number: Z16585, MUID:97238484; PMID:9132069
A;Scatus: preliminary; translated from GB/EMBL/DDBJ
A;Scatus: preliminary; translated from GB/EMBL/DDBJ
A;Scatus: 1-903 acsuga csusus csetences: EMBL:D86624; NID:g2081626; PIDN:BAA19924.1; PID:g2081627
A;Experimental source: strain Dash
C;Superimental Sucrasse/isomaltase homology cSIM>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              838 VTFVGFENVENVK--TYEVRTSERLRSPRISLIKTVSDNDDPRFLS-----VEVSKLS 888
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                     TSALPAGRASLYGLGEHTKSSFRLRHNDSFTLWNADIGASYVDVNLYGSHPFYMDVRA--
                                          ----PGTAHGVLLLSSNGMDVLYGGSYVTYKVIGGVLDFYFFAGPNPLAVVDQYTQLIAR
                                                                                                                     PAPMPYWSFGFHQCRYGYLNVSDLBRVVARYAKARIPLEVMWTDIDYMDGFKDFTLDRVN
                                                                                                                                                                                                       FTAAELRPFVDRLHRNAQKYVLILDPGIRVDPIDATYGTFVRGMQQDIFLKRNGTNFVGN
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Nalternate names: protein T22P22.110
C:Species: Arabidopsis thaliana (mouse-ear cress)
C:Species: Arabidopsis thaliana (mouse-ear cress)
C;Accession: T48531
R;Bevan, M.; Hilbert, H.; Braun, M.; Holzer, E.; Brandt, A.; Duesterhoeft, A.; Bancroft, submitted to the Protein Sequence Database, April 2000
A;Reference number: Z24430
A;Reference number: Z24430
A;Residues: 1-902 abry
A;Molecule type: DNA
A;Residues: 1-902 abry
A;Residues: 1-902 cbry
A;Residues: 1-902 cbry
A;Residues: 1-902 cbry
A;Cross-references: EMBL;Alf3814
A;Experimental source: cultivar Columbia; BAC clone T22P22
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A;Introns: 78(2; 313/1; 390/1; 605/3; 747/1
A;Note: T22P22.110
C;Superfamily: lysosomal alpha-glucosidase; sucrase/isomaltase homology; trefoil homolog
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         13;
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DLERVVARYAKARIPLEVM#TDIDYMDGFKDFTLDRVNFTAAELRPFVDRLHRNAQKYVL
                                                                                    YGGVTEYEEHNLFGLLEARATGRGVLRDTGRRPFVLSRSTFVGSGRYTAYWTGDNAATWG
                                                             ILDPGIRVDPIDATYGTFVRGMQQDIFLKRNGTNFVGNVMPGDVYPPDFMHPAAAEFWAR
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52.9%; Score 2451; DB 2; Length 902;
Best Local Similarity 55.2%; Pred. No. 3e-178;
Matches 471; Conservative 136; Mismatches 191; Indels 5
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                                                                          10 LGILLVFLLQYLVAG--ISTSENDP---EGVIGYGYKVK-SVKVDSGT-RRSLTALPQLV
                                                                                                                ----SAPLQGR---VLSPAGSDLVLT-VHASPFRFTVSRRSTGDTLFDTAPG---
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                                                                                                                                                                                                                                                                                                                     PIPGSTLDNPPYKINNSGVMLPIINKTIPPTAMHYGDIPBYNVHNLFGYLEARVTRAAL
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                                      4 VGVLLLCLCLCLCRAPRLCSSKEEGPLAARTVLAVAVTMEGALRAEAATGGRSSTG----
                     Gaps
   Length 903
Query Match 52.3%; Score 2422.5; DB 2; Length Best Local Similarity 53.6%; Pred. No. 4.4e-176; Matches 486; Conservative 132; Mismatches 234; Indels
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N;Alternate names: alpha-D-glucoside glucohydrolase
C;Species: Beta vulgaris var. altissima (sugar beet)
C;Decies: Beta vulgaris var. altissima (sugar beet)
C;Dacession: UC3463; Resquence_revision 12-Sep-1997 #text_change 20-Jun-2000
C;Accession: UC5463; P64330
R;Matsui, H.; Iwanami, S.; Ito, H.; Mori, H.; Honma, M.; Chiba, S.
Biosci. Biotechnol. Biochem. 61, 875-880, 1997
A;Title: Cloning and sequencing of a cDMs encoding alpha-glucosidase from sugar beet.
A;Reference number: JC5463; MUD:97321863; PMID:9178565
A;Recession: UC5463; MUD:97321863; PMID:9178565
A;Residues: 1-33 *AMIN
A;Residues: 1-33 *AMIN
A;Residues: 1-33 *AMIN
A;Residues: 234-261;1310-365507-541;810-840 *AMIZ>
A;Molecule type: protein
A;Residues: 234-261;1310-365507-541;810-840 *AMIZ>
A;Residues: 234-261;1310-365507-541;810-840 *AMIZ>
A;Residues: 1-313-440;130
A;Molecule type: protein
A;Residues: 1-313-440;130-440;130
A;Molecule type: protein
C;Comment: This enzyme is a exo-glucohydrolase that catalyzes the hydrolysis of alpha-C;Comment: This enzyme is a exo-glucohydrolase; sucrase/isomaltase homology; trefoil homol C;Keywords: glycosidase; hydrolase homology <SIM>
F;149-803/Domain: sucrase/isomaltase homology <SIM>
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Matches 466; Conservative 147; Mismatches 235; Indels
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Best Local 3
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RESULT 4 JC5463 alpha-glucosidase (EC 3.2.1.20) - sugar beet

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hypothetical protein F16L2.150 - Arabidopsis thaliana C; Species: Arabidopsis thaliana (mouse-ear cress) C; Species: Arabidopsis thaliana (mouse-ear cress) C; Sate: 20-Apr-2000 #sequence_revision 20-Apr-2000 #text_change 19-May-2000 C; Accession: T47534 F; Wiedelmann, R.; Voss, H.; Unseld, M.; Mewes, H.W.; Rudd, submitted to the Protein Sequence Database, March 2000
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                                                                                                                                                                       DCKNITKTRWDDPPYKINATGVVAPVGFKTIATSATHYNGVREYDAHSIYGFSETIATHK 532
                                                                                                                                                                                                                          GVLRDTGRRPFVLSRSTFVGSGRYTAYWTGDNAATWGDLRYSINTMLSFGLFGMPM1GAD 563
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                                                                                                                                                                                                                                                                                                                                                                                             PYPYTLMYEAHMTGAPIARPLFFSYPHDVATYGVDROPLLGRGVLVSPVLEPGPTTVDAY
                                                                                                                                               ----PMNALDDPPYRINNDGTGRPINNKTVRPLAVHYGGVTEYBEHNLFGLLEARATGR
                                                                                                                                                                                                                                               ICGFNGNTTEELCGRWIQLGAFYPFSRDHSAIFTVRRELYLWPSVAASGRKALGLRYQLL
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41.1%; Score 1904; DB 2; Length 855;
Best Local Similarity 43.8%; Pred. No. 1.3e-136;
Matches 404; Conservative 144; Mismatches 245; Indels 130;
                                                                MHPAAAEFWAREISLFRRTIPVDGLWIDMNEISNFYN----PE-
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A;Accession: T47534
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-855 <JOR>
A;Cross-references: EMBL:AL162459
C;Genetics:
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A,Introns: 69/3; 291/1; 427/3; 699/1
A,Note: F16L2.150
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C; Species: Arabidopsis thaliana (mouse-ear cress)
C; Date: O.2.Mar-2001 #sequence_revision 02-Mar-2001 #text_change 31-Mar-2001
C; Accession: H96709
R; Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alonso, Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, K.; ansen, N.F.; Hughes, B.; Huizar, L.
Nature 408, 816-820, 2000
A; Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C. C.A.; Li, J.H.; Li, J.H.; Li, Sakano, H.
Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.
A; Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon, Ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Vonter, J.C.; Davis, R.W.
A; Hule: Sequence and analysis of chromosome 1 of the plant Arabidopsis.
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                                                                                                      804
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                                                                                                                                                                                   SRTLVISKVVLMGHRSPAAPKKLTVHVNSAEVEASS-SAGTRYQNAGGLGGVAHIGGLSL 863
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A;Cross_references: GB:AE005173; NID:g5734722; PIDN:AAD49987.1; GSPDB:GN00141
                                               720 RGNWYSLSNYTSSVSVSAGTYVSLSAPPDHINVHIHEGNIVAMQGEAMTIQAARSTPFHL
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                       AGRWYRLYDYSLAVATRIGKHVRLPAPADTVNVHLTGGTILPLQQSALTISRARTAFHL
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                                                                                                                                                                                                                                                                     VVGEEFELKV 873
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LVGQAFKLEL 906
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A; Status: preliminary
A; Molecule type: DNA
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A;Map position: 1
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SAPLQGRVLSPAGSDLVLTVHASPFRFTVSRRSTGDTLFDTAPG-----LVFRDKYLEV
                                                                               222 -APGTAHGVILLSSNGMDVLYGGSYVTYKVIGGVLDFYFFAGPNPLAVVDQYTQLIARPA
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                                                            alpha-glucosidase (EC 3.2.1.20) - Rhizomucor circinelloides f. circinelloides C.Species Rhizomucor circinelloides f. circinelloides C.Species Rhizomucor circinelloides f. circinelloides C.Date: 10-May-1996 #sequence_revision 19-Jul-1996 #text_change 20-Jun-2000 C.Accession: JC4624, Pc4149
R.Sugimoto, M.; Suzuki, Y.
B.Bochem, 119, 500-505, 1996
A.Title: Molecular cloning, sequencing, and expression of a cDNA encoding alpha-glucosid A.Reference number: JC4624, MUID:96271012, PMID:8830045
                                                                                                                                                                                                                                         A,Accession: UC4624
A,Molecule type: mRNA
A,Residues: 1-864 <SUG1>
A,Cross-references: DDBJ:D67034; NID:g1498134; PIDN:BAA11053.1; PID:g1498135
A,Accession: PC4149
A,Molecule type: protein
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A;Residues: 203-214;492-495;612-623;715-731;742-751;769-778 cSUG2>
A;Note: the source is designated as Mucor javanicus IFO4570
C;Coment: This enzyme is an exo-carbohydrase, and catalyzes the splitting of an alphē ccloament: This enzyme is an exo-carbohydrase, and catalyzes the splitting of an alphē velocity as coluble starch.
C;Superfamily: lysosomal alpha-glucosidase; sucrase/isomaltase homology; trefoil homol C;Reywords: glycoptotein; glycosidase, hydrolase
F;122-805/Domain: sucrase/isomaltase homology cSIM>
F;132-805/Domain: sucrase/isomaltase homology cSIM>
F;130,Active site: Asp #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                217
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ----TGGRSSTG-----DVQRLAVYASLETDSRLRVRITDADHPRWEVPQDIIPRPA
                                                                                                                                                                                                                                                                                                                                                                                 1 MATVGVLLLCLCLCLFAPRLCSSKEEGPLAARTVLAVAVT-----MEGALRAEAA---
                                                                                                                                                                                                                                                                           Query March 31.7%; Score 1470; DB 2; Length 864; Best Local Similarity 36.9%; Pred. No. 1.5e-103; Matches 328; Conservative 158; Mismarches 281; Indels 122;
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C;Function:
A;Description: also has EC 3.1.2.3 activity; hydrolyzes alpha 1,4 and alpha 1,6 glycos
A;Description: also has EC 3.1.2.3 activity; hydrolyzes alpha 1,4 and alpha 1,6 glycos
A;Note: deficiency causes glycogen storage disease homology; trefoil homology
C;Superfamily: lysosomal alpha-glucosidase; sucrase/isomaltase homology; trefoil homology ark?
F;82-130/Domain: trefoil homology ark?
F;208-867/Domain: sucrase/isomaltase homology sSIM>
F;508-867/Domain: sucrase/isomaltase homology sSIM>
F;508-867/Domain: sucrase/isomaltase homology sSIM>
F;509-70/Cleavage site: Gln-Ala (unidentified proteinase) #status experimental
F;122-123/Cleavage site: Met-Gly (unidentified proteinase) #status experimental
F;140,233/Binding site: carbohydrate (Asm) (covalent) #status experimental
F;203-204/Cleavage site: Arg-Ala (unidentified proteinase) #status experimental
F;300,470,492,652,882,925/Binding site: carbohydrate (Asm) (covalent) #status predicte
F;518/Active site: Asp #status predicted
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 178 RLHFTIKDPANRRYEVPLE------TOPHVHSRAPSPLYS---VBFSEE 216
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   127 CPFPPSYPSYKLENLSSSEMGYTATLT-----RTTPTFFPKDILTLRLDVMMETEN 177
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    192 DSFTLWNADIGASYVDVNLYGSHPFYMDVRAPGTAHGVLLLSSNGMD-VLYGGSYVTYKV 250
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TGGILDVYIFLGPEPKSVVQQYLDVVGYPFMPPYWGLGFHLCRWGYSSTAITRQVVENMT 392
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CLFAPRICSSKEEGPLAARTVLAVAVTMEGALRARAATGGRSSTGDVQRLAVYASLETDS
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A; Residues: 1-126, VLL', 130-199, 'R', 200-222, 'H', 224-371, 'L', 373-401, 'R', 403-412, 'TSRSTRM A; Residues: 1-126, VLL', 130-199, 'R', 200-222, 'H', 224-371, 'L', 373-401, 'R', 403-412, 'TSRSTRM A; Cross-references: EMBL: Y00839
A; Accession: S18847
A; Molecule type: protein
A; Residues: 70-89;123-126
A; Rin, C.Y.; Shieh, J.J.
B; Connun. 208, 886-893, 1995
A; Title: Identification of a de novo point mutation resulting in infantile form of Pompe A; Reference number: 152309; MUID: 95209708; PMID: 7695647
A; Reference number: 152309
A; Reference number: 152309
A; Reference number: 152309
A; Reference number: 152309; MUID: 95209708; PMID: 7695647
A; Reference number: 152309
A; Reference number: 1523
                                                                                                                                                                     alpha-glucosidase (EC 3.2.1.20) precursor, lysosomal - human
NAIternate names: acid alpha-glucosidase; acid maltase; maitase-glucoamylase
C;Species: Homo sapiens (man)
C;Species: Homo sapiens (man)
C;Date: 21-May-1990 #sequence_revision 05-Apr-1995 #text_change 18-Jun-1999
C;Date: 21-May-1990 #sequence_revision 05-Apr-1995 #text_change 18-Jun-1999
C;Date: 21-May-1990 #sequence_revision 05-Apr-1995 #text_change 18-Jun-1999
R;Arciniuk, F.; Bodkin, M.; Tzall, S.; Hirschhorn, R.
DNA Cell Biol. 10, 283-292, 1991
A;Title: Isolation and partial characterization of the structural gene for human acid al A;Accession: A40577; MUID:91229698; PMID:1674202
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A;Molecule type: mRNA
A;Residues: 1-952 <MA2>
A;Residues: 1-952 <MA2>
A;Residues: 1-952 <MA2>
B;Martsiniuk, F.; Bodkin, M.; Tzall, S.; Hirschhorn, R.
Am. J. Hum. Genet. 47, 440-445, 1990
A;Title: Identification of the base-pair substitution responsible for a human acid alpha
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  includes
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A;Contents: partial sequence of GAA 2 allelic form
A;Accession: A35698
A;Accession: A55698
A;Accession: A5698
A;Status: not compared with conceptual translation
A;Molecule type: mANA
A;Residues: 1-90, NV, 92-129 < MA3>
A;Residues: 1-90, NV, 92-129 < MA3>
B;Residues: 1-90, NV, 92-129 < MA3>
A;Residues: 1-50, NV, 92-109
A;A;Moefsloot, L.H.; Hoogeveen-Westerveld, M.; Kroos, M.A.; van Beeumen, J.; Reuser, A.J.J
ENBO J. 7, 1697-1704, 1988
A;Title: Primary structure and processing of lysosomal alpha-glucosidase; homology with
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A;Map position: 17q23-17q23
A;Introns: 182/3; 231/2; 286/3; 319/1; 359/1; 398/3; 442/3; 479/3; 517/3; 546/1; 585/2;
A;Note: GAA 1, GAA 2, and GAA 4 are common alleles in the normal population
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A;Status: not compared with conceptual translation
A;Molecule type: DNA
A;Residues: 1-952 vmAA
A;Note: order of exons in Figure 2 is incorrect
B;Martiniuk, F.; Mehler, M.; Tzall, S.; Meredith, G.; Hirschhorn, R.
DNA Cell Biol. 9, 85-94, 1990
A;Title: Sequence of the cDNA and S'-flanking region for human acid alpha-glucosidase, s with previous cDNA and amino acid sequences.
A;Reference number: A32609; MUID:9026551; PMID:2111708
A;Accession: A32609
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A, Accession: S63526
A, Molecule type: protein
A, Residues: 68-74, 'X', 76-79, 'X', 81 < FUL>
C; Comment: In common with other lysosomal enzymes, posttranslational processing processing at both amino and carboxyl ends.
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C; Genetics

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Ajintrons: 234/2; 371/2; 428/2
C;Superfamily: Schwanniomyces glucan 1,4-alpha-glucosidase GAM1; sucrase/isomaltase hc
C;Keywords: glycoprotein; glycosidase; hydrolase
F;152-998/Domain: sucrase/isomaltase homology <SIM>
F;152-998/Domain: sucrase/isomaltase homology <SIM>
F;156,145,255,349,444,508,536,539,602,644,661,835,881,929,957/Binding site: carbohydre
F;492/Active site: Asp #status predicted
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                                       | : | | | :: | | | :: | DITGKSFGVFLANSNAMEIFIQPTPIVIYRVIGGILDFYIFLGDTPEQVVQQYQELIGRP 345
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RRPFVLSRSTFVGSGRYTAYWTGDNAATWGDLRYSINTMLSFGLFGMPMIGADICGFNGN 570
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SRARRIAFHLLVALAEDGTASGYLFLDDGDSPEYGRRSDWSMVRFNYKIPNNKGAIKVKS 795
                                                                                                                                    280 APMPYWSFGFHOCRYGYLNVSDLBRVVARYAKARIPLBVMWTDIDYMDGFKDFTLDRVNF 339
                                                                                                                                                                                                                                                                                                         406 NG--LPDFVQDLHDHGQKYVIILDPALSINRRASGEAYESYDRGNAQNVWVNESDGTTP1 463
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               452 ALDDPPYRINNDGTGRPINNKTVRPLAVHYGGVTBYEEHNLFGLLEARATGRGVLR-DTG 510
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               683 YFPAGRWYRLYDYSLAVATRIG------KHVRLPAPADIVNVHLIGGIILPLQQSALIT 735
   -APGTAHGVLLLSSNGMDV-LYGGSYVTYKVIGGVLDFYFFAGPNPLAVVDQYTQLIARP 279
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TASRMNPLGLIIALNDDNTAVGDFFWDDGSTKDTVQNDNY--LLYTFAVSNN----NLNI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     796 EVVHNSYAQSRTLVISKVVLMGHRSPAAPKKLTVHVNSAEVEASSSAGTRYQNAGGLGGV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     861 TCTHELYSEGTTLAFQTIKILGVTETVT--QVTVAENNOSMSTHSNFTYDPSNQ----V
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TIBELCGRWIQLGAFYPFSRDHSA-----IFTVRRELYLWPSVAASGRKALGLRYQL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LPPLYTLPYKAHAFGETVARPVLHEFYEDTNSWVEDREFLWGPALLITPVLTQGAETVSA
                                                                                                                                                                               340 TABELRPFVDRLHRNAQKYVLILDPGIRVD--PIDATYGTFVRGMQQDIFLKRNG--TNF
                                                                                                                                                                                                                                                                                                                                                                                                                                                     VGNVWPGDVYFPDFMHPAAAEFWAREISLFRRTIPVDGLWIDMNEISNFYNPEPM----N
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    856 AHIGGLSLVVGEEFELK 872
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   222
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A, Description: sucrose alpha-glucosidase catalyzes the hydrolysis of the 1,2-alpha-D-glu
A, Description: sucrose alpha-glucosidase catalyzes the hydrolysis of the 1,2-alpha-D-glu
A, Description: sucrose alpha-glucosidase catalyzes the hydrolysis of the 1,2-alpha-D-glu
C, Repwords: carbohydrate digestion; duplication; glycoprotein; glycosidase; hydrolase;
C, Reywords: carbohydrate digestion; duplication; glycoprotein; glycosidase; hydrolase;
F, 13-32/Domain: wenbrane associated #status predicted <TMA>
F, 13-32/Domain: werine/threonine-rich
F, 63-109/Domain: sucrase/isomaltase homology <SIM>
F, 199-84/Domain: sucrase/isomaltase homology <SIM>
F, 1008-1827/Product: sucrose alpha-glucosidase (sucrase chain) #status experimental <SUC
F, 108-1837/Product: sucrase/isomaltase homology <SIM>
F, 108-1838/F, 108-
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**Residues: 1-1827 - «HU»
**R. **Residues: 1-1827 - «HU»
**R. **Sjoestroem, H.; Noren, O.; Christiansen, L.A.; Wacker, H.; Spiess, M.; Bigler-Meier, B
FEBS Lett. 148, 321-325, 1982
**A;Title: N-terminal sequences of pig intestinal sucrase-isomaltase and pro-sucrase-isoma
**A;Title: N-terminal sequences of pig intestinal sucrase-isomaltase and pro-sucrase-isoma
**A;Reference number: A25987; MUID:83105704; PMID:7152027
**A;Reference number: A25987; MUID:83105704; PMID:7152027
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A; Description: oligo-1,6-glucosidase catalyzes the hydrolysis of 1,6-alpha-D-glucosidic A; Pathway: carbohydrate digestion
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A;Molecule type: protein
A;Residues: 2-32, XXX, 36-38,1008, N',1010-1014, E' <5J2>
R;Frank, G; Brunner, J; Jauser, H; Macker, H; Semenza, G;; Zuber, H.
FEBS Lett. 96, 183-188, 1978
A;Title: The hydrophobic anchor of small-intestinal sucrase-isomaltase. N-terminal A;Reference number: A29163; MUID:79086207; PMID:729784
                                                                                                                                                                                                                                         oucrose alpha-glucosidase (EC 3.2.1.48) / oligo-1,6-glucosidase (EC 3.2.1.10) - r
NyAlternate names: small intestinal sucrase/isomaltase (SI)
C;Species: Oryctolagus cuniculus (domestic rabbit)
C;Dates: Oryctolagus cuniculus (domestic rabbit)
C;Dates: O3-Mar-1994 #sequence_revision 03-Mar-1994 #text_change 24-May-1996
C;Accession: A23945; B25987; A239163
R;Hunziker, W.; Spiess, M.; Semenza, G.; Lodish, H.F.
Cell 46, 227-234, 1986
A;Title: The sucrase-isomaltase complex: primary structure, membrane-orientation, A;Reference number: A23945; MUD:86245068; PMID:3755079
A;Accession: A23945
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   ---GAGLQLQKVTVLG--VATAPQQ 915
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                                                                                                                                        947
                                                                                                                                    ----VLSNGVPVSNFTYSPDTKVLDI------CVSLLMGEQF
                                                                       LTVHVNSAEVEASS - - - SAGTRYQNAGGLGGVAHIGGLSLVVGEEF
LERGAYTQVIFLARNNTIVNE--LVRVTSE-
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Cipecies: Homo sapiens (man)
Cipate: 19-Nov-1988 #sequence revision 24-May-1996 #text_change 08-Dec-2000
Cipacession: S36082; A27326; S24329; A61136
A;Reference number: S36082
A;Accession: A;Accession: A27326; MUID:88112852; PMID:2962903
A;Accession: A27326;
'Alternate names: limit dextrinase; small intestinal sucrase/isomaltase (S)
Species: Homo sapiens (man)
Date: 19-Nov-1988 #sequence revision 24-May-1996 #text_change 08-Dec-2000
Accession: S36082; A27326; $24329; A61136
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                                                                                                                      114 LQGRVLSPAGSDLVLTVHASP-FRFTVSRRSTGDTLFDT-APGLVFRDKYLEVTSALPAG
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                                                                                                  DVQRLAVYASLETDSRLRVRIT----DADHPRWEV-PQDIIPRPAPGDVLHDAPPASSAP
                                                            Gaps
                                                                                                                                                                                                                                                     172 RASLYGLGEHTKSSFRLRHNDSFTLWNADIGASYVDVNLYGSHPFYMDVR-----
                      Query Match 29.1%; Score 1348.5; DB 2; Length 985; Best Local Similarity 34.1%; Pred. No. 3.4e-94; Matches 312; Conservative 158; Mismatches 289; Indels 157;
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                                                                                                                                                                                                   A; Residues: 1-661, "F, 663-931 «CHA»
A; Cross-references: EMBL:X63597
A; Cross-references: EMBL:X63597
A; Cross-references: EMBL:X63597
B; Goretto J. P.; Ferrero, A.; Chambraud, L.; Rigal, A.; Bonicel, J.; Maroux, S. Gastroenterology 101, 618-625, 1991
A; Title: Expression of sucrase-isomaltase and dipeptidylpeptidase IV in human shifterence number: A61136; MUID:91317403; PMID:1677636
A; Accession: And Direction A; Residues: 2-14, P', 16-20; 1008-1015, E', 1017-1021, TX', 1024 «GOR»
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A; Molecule type: mRNA
A; Residues: 1-61, X', 63-678 < GRE>
A; Cross-references GB: M22616
A; Chantret, I:, Lacaea, M.; Chevalier, G.; Ruf, J.; Islam, I.; R
Biochem. J. 285, 915-923, 1992
A; Title: Sequence of the complete cDNA and the 5' structure of the A; Reference number: S24329; MUID: 92359963; PMID: 1353958
                                                                                                                                                                                                                                                                                                                                                                                                                                        A;Gene: GDB:SI
A;Cross-references: GDB:120377; OMIM:222900
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swcrose alpha-glucosidase (EC 3.2.1.48) / oligo-1,6-glucosidase (EC 3.2.1.10) [validated

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304; Conservative 153; Mismatches 285; Indels 152;
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;Superfamily: Schwanniomyces glucan 1,4-alpha-glucosidase GAM1; sucrase/isomaltase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Status: preliminary; translated from GB/EMBL/DDBJ
Molecule type: DNA
Residues: 1-95 <HUN>
Gross-references: EMBL:AL133522; PIDN:CAB63549.1; GSPDB:GN00066; SPDB:SPAC922.02c
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238 IYGIGEQVHK--RFRHDLSWKTWPIFTRDQLPGDNNNNLYGHQTFFMCIEDISGKSFGVF 295
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   C;Species: Schizosaccharomyces pombe
C;Date: 09-Jun-2000 #sequence_revision 09-Jun-2000 #text_change 21-Jul-2000
C;Accession: T50267
R;Hunt, C.; Aves, S.; McDougall, R.C.; Rajandream, M.A.; Barrell, B.G.
submitted to the EMBL Data Library, December 1999
A;Reference number: Z25031
                                                                                                                                                                   HOCRYGYLNVSDLERVVARYAKARIPLEVMWTDIDYMDGFKDFTLDRVNFTAAELRPFVD
                                                                               FPDFMHPAAAEFWAREISLFRRTIPVDGLWIDMNEISNFYNPEP-----MNALDDPPYRIN
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                     LLSSNGMDV-LYGGSYVTYKVIGGVLDFYFFAGPNPLAVVDQYTQLIARPAPMPYWSFGF
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                                          LMNSNAMEIFIQPTPIVTYRVTGGILDFYILLGDTPEQVVQQYQQLVGLPAMPAYWNLGF
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                                                                                                                              118 VLSPAGSDLVLTVHASPFRFTVSRRSTGDTLFDT-APGLVFRDKYLEVTSALPAGRASLY
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                                                                                                                                                                                                                           GLGEHTKSSFRLRHNDSFTLWNADIGASYVDVNLYGSHPFYMDVR
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probable family 31 glycosyl hydrolase (alpha glucosidase) precursor - fission yeast C;Species: Schizosaccharomyces pombe C;Decies: Schizosaccharomyces pombe C;Date: 20-Oct-2000 #sequence_revision 20-Oct-2000 #text_change 20-Oct-2000 C;Accession: T38598; S65559; T38911 R;Pearson, D.; Churcher, C.M.; Barrell, B.G.; Rajandream, M.A.; Walsh, S.V. submitted to the EMBL Data Library, November 1995 A;Reference number: Z21801 A;Recession: T38598

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homod

Length 995;

Score 1302; DB 2; Pred. No. 1.2e-90;

28.1%;

Query Match Best Local Similarity

QY 619 RYQLLPYFYLMYEAHWTGAPIARPLFESYPHDVATYGVDRQFLLGRGVLVSPVLEPGPT 678 Db 757 RYSLLPYWYTLMHTASVDCTPMYRPLFFEFPRQISLASVDKQMIGTALLISPALEPNTT 816 CD 757 RYSLLPYWYTLMHTASVDCTPMYRPLFFEFPRQISLASVDKMIGTALLISPALEPNTT 816 QY 679 TVDAYFPAGRWYRLYDYSLAVATRTGHVRLPPRADTVNVHLTGGTILPLQQSALTT 735 I	RESULT 14 JN0102 glucan 1,4-alpha-glucosidase (EC 3.2.1.3) GAM1 precursor - yeast (Schwanniomyces occi N.Alternate names: acid maltase; glucoamylase C;Alternate names: acid maltase; glucoamylase C;Species: Schwanniomyces occidentalis C;Date: 10-Mar-1994 #sequence_revision 05-Apr-1995 #text_change 18-Jun-1999 C;Accession: JN0102 R;Dobmen, R.J.; Strasser, A.W.M.; Dahlems, U.M.; Hollenberg, C.P. Gene 95, 111-121, 1990 A;Title: Gloning of the Schwanniomyces occidentalis glucoamylase gene (GAM1) and its A;Title: Gloning of the Schwanniomyces occidentalis glucoamylase gene (GAM1) and its	A; Mclecule INDIO2: ANDIO2; MOID2; MOID2; MOID2; MOID2; MOID2010;	Gaps 27; TDAD- 83 EPTDL 127 EPTSRR 142	DD 128 SDVEVLPEHLVVKRLVEGDAQSYNEDNSDLVFFSFEVIKS 173 QY 143 STGDTLEDTAPG-LVFRDKYLEVTSALPAGRASLYGLGEHTKSSFRLRHNDSFT 195 174 STKEVLFSTKGNPLVFSNQFIQFNSSLPRGHTV-ITGLGESIHGLVNBPGSVKT 225 DD 174 STKEVLFSTKGNPLVFSNQFIQFNSSLPRGHTV-ITGLGESIHGLVNBPGSVKT 225 QY 196 LWNADIGASYVDVNLYGSHPPFYMDYR-APGTAHGYLLLSSNGMDVLYGGSVYTYKVIGGV 254 DD 226 LFANDVG-DPIDGNIYGYHPVYLDGRYDTETHAVYMTSAIGEVLIGEESITWRALGGV 284 QY 255 LDFYFFAGPNPLAVYDQYTGLIARPAPMPYWFGFHQCRYGYLNVBLERRVARXAKRI 314 DD 285 IDLYFFSGPTPKDAIQQYVKEIGLPAFQPYWSLGYHQCRWGYDTIEKLSEVVENFKKPNI 344 QY 315 PLEVWWTDIDYMDGFKDFTLDRVNFTAAELRPFVDRLHRNAQKYVLILDDFGIRV-DPIDA 373
A; Molecule type: DNA A; Residues: 1-385 <pea> A; Residues: 1-385 <pea> A; Residues: 1-385 <pea> A; Residues: 1-385 <pea> A; Cross-references: BMBL: 267961; PIDN: CAA91887.1; GSPDB: GN00066; SPDB: SPAC30D11.01c A; Experimental source: strain 972h-; cosmid c30D11 R; Pearson, D.; Churcher, C.M. R; Reference number: 86259 A; Accession: 86259 A; Accession: 86259 A; Accession: 86259 A; Residues: 1-384 <pe2> A; Residues: 1-384 <pe2> A; Residues: 1-384 <pe2> A; Coss-references: EMBL: 267961 A; Residues: DNA A; Residues: C.M.; Barrell, B.G.; Rajandream, M.A.; Walsh, S.V. Submitted to the EMBL Data Library, February 1996 A; Reference number: 221817 A; Reference number: 221817 A; Molecule type: DNA</pe2></pe2></pe2></pea></pea></pea></pea>	A; Residues: 352-993 < PED> A; Residues: 352-993 < PED> A; Cross-references: EMBL: 269728; PIDN: CAA93572.1; GSPDB:GN00066; SPDB:SPACS6F8.0. A; Experimental source: strain 972h-; cosmid c56F8 C; Genetics: As Pabe. SPAC30D11.01c; SPDB: SPAC56F8.01 A; Map position: 1L C; Superfamily: Schwanniomyces glucan 1,4-alpha-glucosidase GAM1; sucrase/isomaltase homof F; 165-384/Domain: sucrase/isomaltase homology (fragment) < SIM> Query Match Best Local Similarity 32.9%; Pred. No. 3.70-89; Marches 286: Conservative 156: Mismarches 287: Indels 141: Gans 20:	SLETOSRILRVRITDADHPRWEVPQDIIPRPAPGDVLHDAPPASSAPLQGRV 11 : : : : : : : : : : : : :	228 GVLLLSSNGMDVLYGGSYVTYKVIGGVLDFYFFAGPNPLAVVDQYTQLIARPAPMPYW	

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405 YPPDFMHPAAAEFWAREISLFRRTIPVDGLWIDMNEISNF-------YNPE 448
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                                                     SLYGLGEHTKSSFRLRHNDSFTLW---NADIGASYVDVNLYGSHPFYMDV-RAPGTAHGV
                                                                                   247 YIYGFGGHIHK--RFRHDLYWKTWPIFTRDBIPGDNNHNLYGHQTPFMGIGDTSGKSYGV
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C; Superfamily: sucrase/isomaltase; sucrase/isomaltase homology; trefoil homology
C; Keywords: carbohydrate digestion; glycosidase; hydrolase
F;199-846/Domain: sucrase/isomaltase homology <SIM>
F;937-983/Domain: trefoil homology <TRP>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Chandrasena, G.; Osterholm, D.E.; Sunitha, I.; Henning, S.J.

Gene 150, 155-360, 1994

A;Title: Cloning and sequencing of a full-length rat sucrase-isomaltase-encoding cDNA.

A;Reference number: Z17155; MUID:95121929; PMID:7821806

A;Accession: T10799

A;Residues: preliminary; translated from GB/EMBL/DDBJ

A;Residues: 1-1841 cCHA>

A;Residues: 1-1841 cCHA>

A;Cessereferences: EMBL:L25926; NID:9414818; PIDN:AAA65097.1; PID:9773669

A;Genetimental source: strain Sprague-Dawley, intestine

C;Genetics:
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C;Species: Rattus norvegicus (Norway rat)
C;Species: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 21-Jul-2000
C;Accession: T10799
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Sequence 120, Appl
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1393.955 Million cell updates/sec
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                                                                                             ; Search time 105.357 Seconds
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Sequence 3
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(cgn2 6/ptodata1/pubpaa/USO6 PUBCMB.pep:*
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GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
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4 US-10-043-418-3

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US-10-032-189-44

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Maximum Match 1008
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    protein search, using sw model

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Perfect score:
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Sequence 1, Appli
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Sequence 1315, A
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Sequence 9, Appli
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APPLICANT: Haslin, Elizabeth H.
APPLICANT: Maslin, Elizabeth H.
APPLICANT: Clark, Suzame E.
TITLE OF INVENTION: Modified barley alpha-glucosidase
FILE REPRENCE: 960296.97486
CURRENT APPLICATION NUMBER: US/10/043,418
CURRENT FILING DATE: 2002-06-25
PRIOR APPLICATION NUMBER: 60/260,787
NUMBER OF SEQ ID NOS: 7
SOFTWARE: Patentin Ver. 2.1
5 US-10-102-806-557

2 US-10-228-063-5

2 US-10-228-063-26

2 US-10-228-063-36

2 US-10-228-063-36

5 US-10-126-761-14497

US-09-734-569-135

US-09-734-569-135

US-09-734-569-135

US-09-734-569-136

US-09-423-126-3

US-09-423-126-4

US-09-423-126-5

US-09-423-126-5

US-09-423-126-5

US-09-423-126-5

US-09-423-126-5

US-09-280-197-2

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US-09-423-126-5

US-09-423-126-1
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5.05-10-156-761-11179

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2.05-09-940-3168-72

5.05-10-120-145-5

5.05-10-136-841-6

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US-09-971-536-69
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100.0%; Score 4630;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 877; Conservative 0; Mismatches
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; Publication No. US20020184662A1
; GENERAL INFORMATION:
   LENGTH: 877
TYPE: PRT
ORGANISM: Barley
  818
679.5
679.5
679.5
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PAPMDYWSFGFHOCRYGYLNVSDLERVVARYAKARIPLEVMWTDIDYMDGFKDFTLDRVN 338
                              59 DVQRLAVYASLETDSRLRVRITDADHPRWEVPQDIIPRPAPGDVLHDAPPASSAPLQG-- 116
                                                    FTAAELRPFVDRIHRNAQKYVI.ILDPGIRVDPIDATYGTFVRGMQQDIFLKRNGTNFVGN 398
                                                                                                                                                                                                                                                                                                                                                                        364 FPEDKMQSFVDTLHKNGQKYVLILDPGIGV---DSSYGTYNRGMEADVFIKRNGEPYLGE 420
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                                                                                                                                                       TSALPAGRASLYGLGEHTKSSFRLRHNDSFTLWNADIGASYVDVNLYGSHPFYMDVRA-- 222
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SGELFLDDGENLRMGAGGGNRDWTLVKPRCYVTGK--SVVLRSEVVNPEYASKMKWSIGK 837
                                                                                           ----RVLSPAGSDLVLTVH-ASPFRFTVSRRSTGDTLFDTAPG-----LVFRDKYLEV
                                                                                                                                                                           SSALPENRSNLYGIGEHTKRSFRLIPGETMTLWNADIGSENPDVNLYGSHPFYMDVRGSK
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   Gaps
   26;
 191; Indels
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Publication No. US20020184662A1
GENERAL INFORMATION.
APPLICANT: Henson, Cynthia A.
APPLICANT: Muslin, Elizabeth H.
APPLICANT: Clark, Suzanne B.
TILLE OF INFENTION: Modified barley alpha-glucosidase
FILE REFERENCE: 960296.97486
   136; Mismatches
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LLVGKKFEMRLRLT 902
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HTKSSFRLRHNDSFTLWNADIGASYVDVNLYGSHPFYMDVRAPGTAHGVLLLSSNGMDVL
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                HTKSSFRLRHNDSFTLWNADIGASYVDVNLYGSHPFYMDVRAPGTAHGVLLLSSNGMDVL
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                                                                                                                          DLERVVARYAKARIPLEVMMTDIDYMDGFKDFTLDRVNFTAAELRPFVDRLHRNAQKYVL
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Pred. No. 2.5e-226;
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GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Henson, Cynthia A.; APPLICANT: Usasin, Elizabeth H.
APPLICANT: Clark, Suzanne E.; TITLE OF INVENTION: Modified barley alpha-glucosidase; FILE REFERENCE: 960296.97486; CURRENT APPLICATION NUMBER: US/10/043,418; FILE REFERENCE: 960296.97486; CURRENT APPLICATION NUMBER: 60/260,787; PRIOR FILING DATE: 2001-01-10; NUMBER OF SEQ ID NOS: 7; SOFTWARE: PATENTIN Ver. 2.1; SEQ ID NO 4
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ORGANISM: Arabidopsis
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Best Local Similarity
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                                                                                                                                                                                                            APPLICANT: Henson, Cynthia A.
APPLICANT: Muslin, Elizabeth H.
APPLICANT: Clark, Suzanne B.
TITLE OF INTENTION: Modified barley alpha-glucosidase
FILE REFERENCE: 960296.97486
CURRENT APPLICATION NUMBER: US/10/043,418
CURRENT FILING DATE: 2002-06-25
PRIOR APPLICATION NUMBER: 60/260,787
PRIOR APPLICATION NUMBER: 60/260,787
NUMBER OF SEG ID NOS: 7
SOFTWARE: Patentin Ver: 2.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Conservative 147; Mismatches 235;
                                                                                                                                                                ; Sequence 2, Application US/10043418; Publication No. US20020184662A1; GENERAL INFORMATION:
                                                    VGEEFEL 871
                                                                                  894 LGREFKL 900
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity
Matches 466; Conserv
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                                                                                                                                                                                                                               55; Gaps
                                                                                                                                                                                             Query Match 52.3%; Score 2422.5; DB 14; Length 903; Best Local Similarity 53.6%; Pred. No. 1.4e-223; Matches 486; Conservative 132; Mismatches 234; Indels 55;
CURRENT APPLICATION NUMBER: US/10/043,418
             CURRENT FILING DATE: 2002-06-25
PRIOR APPLICATION NUMBER: 60/260,787
PRIOR FILING DATE: 2001-01-10
NUMBER OF SEQ ID NOS: 7
SOFTWARE: PATCHIIN Ver. 2.1
SEQ ID NO 3
LENGTH: 903
                                                                                                                                              ; ORGANISM: Spinach US-10-043-418-3
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FILING DATE: 2001-03-29
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                                                                           FYTLMYEAHMTGAPIARPLFFSYPHDVATYGVDRQFLLGRGVLVSPVLEPGPTTVDAYFP
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APPLICANT: Smithson, Glennda
TITLE OF INVENTION: Proteins and Nucleic Acids Encoding Same
FILE REFERENCE: 21402-228
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PRIOR APPLICATION NUMBER: 05/10/032,189
CURRENT FILING DATE: 2001-12-21
PRIOR FILING DATE: 2000-12-21
PRIOR FILING DATE: 2000-12-21
PRIOR APPLICATION NUMBER: 60/258,171
PRIOR FILING DATE: 2000-12-20
PRIOR FILING DATE: 2001-02-20
PRIOR FILING DATE: 2001-02-20
PRIOR FILING DATE: 2001-03-08
PRIOR FILING DATE: 2001-03-08
PRIOR APPLICATION NUMBER: 60/274,192
PRIOR APPLICATION NUMBER: 60/277,826
PRIOR PRILING DATE: 2001-03-08
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R FILING DATE: 2000-12-20
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R APPLICATION NUMBER: 60/274,192
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R PELLING DATE: 2001-03-08
R FILING DATE: 2001-03-08
R FILING DATE: 2001-03-22
R FILING DATE: 2001-03-22
R APPLICATION NUMBER: 60/277,826
R FILING DATE: 2001-03-22
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US-10-032-189-125
Sequence 125, Application US/10032189
Publication No. US20030170630A1
GENERAL INFORMATION:
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Grosse, William M
Lepley, Denlise M
Burgess, Catherine E
Shimkets, Richard A
Grosse, William M
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Gangolli, Esha A
Fernandes, Elma R
Rieger, Daniel K
Edinger, Shlomit R
Gunther, Erik
Millet, Isabelle
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APPLICANT: Tchernev, Velizar I
APPLICANT: Liu, Xisohong
APPLICANT: Spytek, Kinherly A
APPLICANT: Zerhusen, Bryan D
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Vernet, Corine A.M
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Casman, Stacie J
Boldog, Ferenc L
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897 LVGQAFKLEL 906
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404 VYFPDFMHPAAAEFWAREISLFRRTIPVDGLWIDMNEISNFYNPEPWNA-LDDPPYRINN 462
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647 LDDGESID-TQRGDYLLVQFS---ANNN--TLTGTEVVTGYYKNSTNLTLEXITILGYGN 700
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            175 WSLGFHLCRWGYTNVSEVKTVVDGMRKANIPLDVQWLDIDYMDGYKDFTWDPVRFPGPE- 233
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RPFVDRLHRNAQKYVLILDPGIRVDPIDATYGTFVRGMQQDIFLKR-NGTNFVGNVWPGD 403
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PRIOR APPLICATION NUMBER: 60/282,981
PRIOR FILING DATE: 2001-04-11
PRIOR PILING DATE: 2001-04-13
PRIOR PILING DATE: 2001-04-13
PRIOR PILING DATE: 2001-04-13
PRIOR FILING DATE: 2001-04-13
PRIOR FILING DATE: 2001-08-17
PRIOR FILING DATE: 2001-08-17
PRIOR PILING DATE: 2001-08-17
PRIOR PILING DATE: 2001-08-17
PRIOR PILING DATE: 2001-08-17
PRIOR APPLICATION NUMBER: 60/313,331
PRIOR PILING DATE: 2001-08-17
NUMBER OF SEQ ID NOS: 260
SOFTWARE: PATENTIN Ver: 2.1
SEQ ID NO 125
LENGTH: 707
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633 AHMTGAPIARPLFFSYPHDVATYGVDRQFLLGRGVLVSPVLEPGPTTVDAYFPAGRWYRL 692
                                                                                  YDY-SLAVATRIGKHVRLPAPADTVNVHLTGGTILPLQQSALTTSRARRTAFHLLVALAE 751
                                                                                                                                                                                                 DGTASGYLFLDDGDSPEYGRRSDWSMVRFNYKIPNNKGAIKVKSEVVHNSYAQSRTLVIS
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APPLICANT: Blarman, Karen
APPLICANT: MacDougall, John R
APPLICANT: Matchoon, Glennda
TITLE OF INVENTION: Proteins and Nucleic Acids Encoding Same
FILE REFERENCE: 21402-228
CURRENT APPLICATION NUMBER: US/10/032,189
CURRENT PILING DATE: 2001-12-21
PRIOR APPLICATION NUMBER: 60/257,495
PRIOR APPLICATION NUMBER: 60/259,171
PRIOR APPLICATION NUMBER: 60/259,171
PRIOR PILING DATE: 2000-12-20
PRIOR PILING DATE: 2000-12-20
PRIOR PLING DATE: 2000-03-08
PRIOR PLING DATE: 2001-03-08
PRIOR APPLICATION NUMBER: 60/277,826
PRIOR APPLICATION NUMBER: 60/277,826
PRIOR APPLICATION NUMBER: 60/277,826
PRIOR PLING DATE: 2001-03-22
PRIOR APPLICATION NUMBER: 60/277,826
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APPLICATION UNMBR: 60/282,981
ELING DATE: 2001-04-11
APPLICATION NUMBER: 60/283,656
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 44, Application US/10032189
Publication No. US20030170630A1
GENERAL INFORMATION:
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APPLICANT: Tchernev, Velizar T
APPLICANT: Liu, Xiaohong
APPLICANT: Spytek, Kimberly A
APPLICANT: Zerhusen, Bryan D
APPLICANT: Patturajan, Meera
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Shimkets, Richard A
Grosse, William M
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Boldog, Ferenc L
Gorman, Linda
Gangolli, Esha A
Fernandes, Blma R
Rieger, Daniel K
Edinger, Shlomit R
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Patturajan, Meera
Grosse, William M
Lepley, Denise M
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Millet, Isabelle
Sciore, Paul
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APPLICANT: Park, Jason
APPLICANT: Schulz, Stephanie
TITLE OF INVENTION: Compositions And Methods For Identifying And Targeting Cancer Cel
TITLE OF INVENTION: Alimentary Canal Origin
FILE REFERENCE: TJU2413
CURRENT PILLOCATION NUMBER: uS/09/819,247
PRIOR PILLOCATION NUMBER: 60/192,229
PRIOR FILLNG DATE: 2000-03-27
PRIOR FILLNG DATE: 2000-03-27
SOUFFWARE: Patentin version 3.0
SEQ ID NO 2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LLSSNGMDV-LYGGSYVTYKVIGGVLDFYFFAGPNPLAVVDQYTQLIARPAPMPYWSFGF
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                                                                                                                                                               Sequence 2, Application US/09819247
Patent No. US20010013633A1
GENERAL INFORMATION:
APPLICANT: Waldman, Scott A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                : ORGANISM: Homo sapiens
US-09-819-247-2
                                                         701 EPAA 704
                 SPAA 823
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; Sequence 40, Application US/10032189; Publication No. US20030170630A1; GENERAL INFORMATION:
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Patturajan, Meera
Grosse, William M
Lepley, Denise M
Burgess, Catherine E
Shimkets, Richard A
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APPLICANT: Tchernev, Velizar T
APPLICANT: Liu, Xiaohong
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Grosse, William M
Szekeres, Edward S
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Li, Li
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Boldog, Perenc L
Gorman, Linda
Gangolli, Esha A
Ferrandes, Elma R
Rieger, Daniel K
Edinger, Shlomit R
Gunther, Erik
Millet, Isabelle
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NUMBER OF SEQ ID NOS: 260
SOFTWARE: PatentIn Ver. 2.1
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Casman,
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LENGTH: 914
TYPE: PRT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        334 LTGPTESDVFKQYSHLTGTQAMPPLFSLGYHQCRWNYEDEQDVKAVDAGFDEHDIPYDAM 393
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             492 LFGLLEARATGRGVL-RDTGR-RPFVLSRSTFVGSGRYTAYWTGDNAATWGDLRYSINTM 549
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                                                                                                                                                                                                                                                                                                                                                                                                                     100 DVLTSKPSTVRLI----SCSGDTGSLILADGKGDLKCHITANPFKVDLVSEEEVVISIN 154
                                                                                                                                                                                                                                                                                                                                                                                                                                                        STG-----DILFDIAP----GLVFR--DKYLEVISALPA--- 170
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          155 SLGQLYFEHLQILHKQRAAKENEEETSVDTSQENQEDLGLWEEKFGKFVDIKANGPSSIG 214
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ----GRASLYGLGEHTKSSFRLRHNDSFTLWNADIGA--SYVDVNLYGSHPFYMDVRA 222
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             215 LDFSLHGFEHLYGIPQHAESHQLKNTGDAYRLYNLDVYGYQIYDKMGIYGSVP-YLLAHK 273
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                                                                                                                                                                                                                                                                                                                                                    44 RALLDSVTTDEDSTRPQII----NEASKVPLLAEIYGIEGNIFRLKINEETPLKPRFEVP 99
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match.
20.6%; Score 956; DB 12; Length 912;
Best Local Similarity 28.3%; Pred. No. 2.1e-82;
Matches 267; Conservative 165; Mismatches 336; Indels 174; Gaps
PRIOR APPLICATION NUMBER: 60/309,24,
PRIOR FILING DATE: 2001-07-31
PRIOR APPLICATION NUMBER: 60/311,754
PRIOR APPLICATION NUMBER: 60/313,331
PRIOR APPLICATION NUMBER: 60/313,331
PRIOR APPLICATION NUMBER: 60/313,331
PRIOR FILING DATE: 2001-08-17
NUMBER OF SEQ ID NOS: 260
SOFTWARE: PATCHIIN Ver. 2.1
SEQ ID NO 44
                                                                                                                                                                             ; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-032-189-44
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780 FNYKIPNNKGAIKVKSEVVHNSYAQSR-----TLVISKVVLMGHRSPAAPKKLTVHVNSA 834
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APPLICANT: Blarman, Karen
APPLICANT: MacDougall, John R
APPLICANT: Smithson, Glenda
TITLE OF INVENTION: Proteins and Nucleic Acids Encoding Same
FILE REFERENCE: 21402-28
CURRENT APPLICATION NUMBER: US/10/032,189
CURRENT FILING DATE: 2001-12-21
PRIOR APPLICATION NUMBER: 60/257,495
PRIOR APPLICATION NUMBER: 60/259,71
PRIOR PILING DATE: 2000-12-20
PRIOR PILING DATE: 2000-12-20
PRIOR PILING DATE: 2000-12-20
PRIOR PILING DATE: 2000-13-20
PRIOR PILING DATE: 2001-03-20
PRIOR PILING DATE: 2001-03-29
PRIOR PILING DATE: 2001-04-11
PRIOR PILING DATE: 2001-04-13
PRIOR PILING DATE: 2001-03-34
PRIOR PILING DATE: 2001-04-13
PRIOR PILING DATE: 2001-08-17
PRIOR PILING DATE: 2001-08-17
PRIOR PILING DATE: 2001-08-17
PRIOR PILING DATE: 2001-08-17
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SEQ ID NO 42
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                                                                                                                                                                                                                                                                                                                                                                                                                                                            418
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                                                                                                       74 RLRVRITDADHPRWEVPQDIIPRPAPGBVLHDAPPASSAPLQGRVLSPAGSDLVLTVHAS 133
                                                                                                                                                                -----DTLFDTAP-----GLVFR 158
                                                                                                                                                                                                                         --DKYLEVTSALPA-----GRASLYGLGEHTKSSFRLRH---NDSFTLWNADIGA- 203
                                                                                                                                                                                            138 PFKVDLVSEEEVVISINSLGQLYFEHLQILHKQRAAKENEEETSVDTSQENQEDLGLWEE 197
                                                                                                                                                                                                                                                                                                                                                           LILDPGIRVDPIDATYGTFVRGMQQDIFLK-RNGTNFVGNVWPGDVYFPDFMHPAAAEFW
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                                                                             Gaps
                                                            Best Local Similarity 28.8%; Pred. No. 3.7e-82;
Matches 260; Conservative 161; Mismatches 308; Indels 173;
                                               DB 12; Length 914;
                                                                                                                                                                                                                                                                                 204 -SYVDVNLYGSHPFYMDVRAPGTAHGVLLLSSN-----
                                            20.6%; Score 953.5; DB 1 28.8%; Pred. No. 3.7e-82;
                                                                                                                                                                134 PFR-----FTVSRRSTG-----
ORGANISM: Homo sapiens
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    ; ORGANISM: Hon
US-10-032-189-40
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RESULT 9

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Blerman, Karen
APPLICANT: Balerman, Karen
APPLICANT: Balerman, Glennda
TITLE OF INVENTION: Preceins and Nucleic Acids Encoding Same
FILE REFERENCE: 21402-228
FILE REFERENCE: 21402-228
CURRENT FILING DATE: 2001-12-21
PRIOR APPLICATION NUMBER: 60/259,495
PRIOR APPLICATION NUMBER: 60/259,171
PRIOR APPLICATION NUMBER: 60/259,171
PRIOR APPLICATION NUMBER: 60/259,171
PRIOR PILING DATE: 2001-02-20
PRIOR FILING DATE: 2001-03-20
PRIOR FILING DATE: 2001-03-20
PRIOR PELING DATE: 2001-03-20
PRIOR PELING DATE: 2001-03-20
PRIOR PELING DATE: 2001-03-29
PRIOR PELING DATE: 2001-03-29
PRIOR PELING DATE: 2001-03-29
PRIOR PELING DATE: 2001-03-29
PRIOR PELING DATE: 2001-04-11
PRIOR PELING DATE: 2001-04-13
PRIOR PELING DATE: 2001-08-17
Sequence 42, Application US/10032189
Publication No. US20030170630A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                         Spytek, Kimberly A Zerhusen, Bryan D Parturajan, Meera Grosse, William M Lepley, Denise M Burgess, Catherine E Shimkets, Richard A Grosse, William M
                                                                                                                                                                          APPLICANT: Alsobrook II, John P
APPLICANT: Tchernev, Velizar T
APPLICANT: Liu, Xiaohong
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Vernet, Corine A.M.
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Boldog, Ferenc L
Gorman, Linda
Gangolli, Esha A
Fernandes, Elma R
Reger, Daniel K
Edinger, Shlomit R
Gunther, Erik
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Sciore, Paul
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Best Local Similarity
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Denise

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Burgees, Catherine E
Shimkers, Richard A
Grosse, William M
Szekeres, Edward S
Vernet, Corine A.M.
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Gorman, Linda
Gangolli, Esha A
Fernandes, Elma R
Rieger, Daniel K
Edinger, Shlomit R
Gunther, Erik
Miller
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ORGANISM:
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                                                                 --DKYLEVTSALPA-----GRASLYGLGEHTKSSFRLRH---NDSFTLWNADIGA- 203
                                                                                                                                  204 -SYVDVNLYGSHPFYMDVRAPGTAHGVLLLSSN---------GMDV 239
                                                                                                                                                          QIYDKMGIYGSV?-YLLAHKLGRTIGIFWLNASETLVEINTEPAVEYTLTQMGPVAAKQK 315
                                                                                                                                                                                               LYGGSYVTYKVIGGVLDFYFFAGPNPLAVVDQYTGLIARPAPMPYWSFGFHQCRYGYLNV 299
                                                                                                                                                                                                                            316 VGSRTHVHWMSESGIIDVFLLTGPTPSDVFKQYSHLTGTQAMPPLFSLGYHQCRWNYEDE 375
                                                                                                                                                                                                                                                                  SDLERVVARYAKARIPLEVMWTDIDYMDGFKDFTLDRVNFTAAELRPFVDRLHRNAQKYV 359
                                                                                                                                                                                                                                                                                       376 QDVKAVDAGFDEHDIPYDAMMLDIEHTEGKRYFTWDKNRF--PNPKRMOELLRSKKRRLV 433
                                                                                                                                                                                                                                                                                                                                  360 LILDPGIRVDPIDATYGTFVRGMQQDIFLK-RNGTNFVGNVWPGDVYFPDFMHPAAAEFW 418
                                                                                                                                                                                                                                                                                                                                                   119 AREISLFRRTIPV-DG-----LWIDMNEISNFYNPEPMNALDDPPYRINNDGTGRPINN 471
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523 QTMQKNAIHHGNWEHRELHNIYGFYHQMATAEGLIKRSKGKERPFULTKSFFAGSQKYGA 582
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                                                                                               198 KFGKFVDIKANGPSSIGLDFSLHGFEHLYGIPQHAE-SHQLKNTGDGDAYRLYNLDVYGY
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209 RQGSKDPAEGDGAQPEETPRDGDKPEETQGKAEKDEPGAWBETFKTHSDSKPYGPMSVGL 268
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APPLICANT: Sllerman, Karen
APPLICANT: Blerman, Gennda
APPLICANT: MacDougall John R
APPLICANT: MacDougall John R
APPLICANT: Sinthson, Glennda
TITLE OF INVENTION: Proteins and Nucleic Acids Encoding Same
FILE REPERENCE: 21402-228
FILE REPERENCE: 21402-228
CURRENT PILLION DATE: 2001-12-21
PRIOR APPLICATION NUMBER: 60/257,495
PRIOR APPLICATION NUMBER: 60/259,940
PRIOR APPLICATION NUMBER: 60/259,940
PRIOR FILING DATE: 2001-02-20
PRIOR FILING DATE: 2001-03-08
PRIOR FILING DATE: 2001-03-08
PRIOR FILING DATE: 2001-03-08
PRIOR FILING DATE: 2001-03-09
PRIOR FILING DATE: 2001-03-19
PRIOR PELING DATE: 2001-04-11
PRIOR APPLICATION NUMBER: 60/283,656
PRIOR PELING DATE: 2001-04-11
PRIOR PELING DATE: 2001-04-11
PRIOR PELING DATE: 2001-04-11
PRIOR PELING DATE: 2001-04-11
PRIOR FILING DATE: 2001-04-11
PRIOR FILING DATE: 2001-03-19
PRIOR FILING DATE: 2001-03-19
PRIOR FILING DATE: 2001-04-11
PRIOR FILING DATE: 2001-04-11
PRIOR FILING DATE: 2001-04-11
PRIOR FILING DATE: 2001-03-17
PRIOR FILING DATE: 2001-08-17
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Sequence 120, Application US/10032189
Publication No. US20030170630A1
GENERAL INFORMATION:
APPLICANT: Alsobrook II, John P
APPLICANT: Liu, Xiaohong
APPLICANT: Edylek, Kimberly A
APPLICANT: Seytek, Kimberly A
APPLICANT: Patturen, Bryan D
APPLICANT: General
APPLICANT: Grosse, William M

US-10-032-189-120

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APPLICANT: Sciore, teacelle
APPLICANT: Sciore, paul
APPLICANT: Ellerman, Karen
APPLICANT: Bachean, Karen
APPLICANT: Bachean, Karen
APPLICANT: Bachean, Glennda
TITLE OF INVENTION: Deceins and Nucleic Acids Encoding Same
FIGE REFERENCE: 21402-228
CURRENT FILING DATE: 2001-12-21
FRIOR PAPLICATION NUMBER: 60/257,495
FRIOR APPLICATION NUMBER: 60/258,171
FRIOR APPLICATION NUMBER: 60/258,171
FRIOR APPLICATION NUMBER: 60/259,940
FRIOR APPLICATION NUMBER: 60/279,806
FRIOR APPLICATION NUMBER: 60/277,826
FRIOR APPLICATION NUMBER: 60/277,826
FRIOR APPLICATION NUMBER: 60/282,981
FRIOR APPLICATION NUMBER: 60/282,981
FRIOR APPLICATION NUMBER: 60/282,981
FRIOR APPLICATION NUMBER: 60/282,981
FRIOR APPLICATION NUMBER: 60/283,656
FRIOR FILING DATE: 2001-04-11
FRIOR APPLICATION NUMBER: 60/283,656
FRIOR FILING DATE: 2001-04-13
FRIOR APPLICATION NUMBER: 60/311,754
FRIOR APPLICATION NUMBER: 60/311,754
FRIOR APPLICATION NUMBER: 60/311,754
FRIOR APPLICATION NUMBER: 60/313,331
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                                                                                                                                                                                                                                                                                                                        378 FVRGMOODIFLK-RNGTNFVGNVWPGDVYFPDFMHPAAAEFWAREISL--FRRTIPVDGL 434
                                                                                                                                                                                                                                                                                                                                                                                                                                WIDMNEISNFYNPEPMNALDDPPYRINNDGTGRPINNKTVRPLAVHYGGVTEYEEHNLFG 494
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LLEARATGRGVLRDTG--RRPFVLSRSTFVGSGRYTAYWTGDNAATWGDLRYSINTMLSF 552
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GLFGMPMIGADICGFNGNTTEELCGRWIQLGAFYPFSRDHSAIFTVRRELYLWPSVAAS- 611
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          RAPGTAHGVLLL-----SSNG-----MDVLYGG----SYVTYKVIGGVLDF
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Publication No. US20030170630A1
GENERAL INFORMATION:
APPLICANT: Alsobrook II, John P
APPLICANT: Tchernev, Velizar T
APPLICANT: Liu, Xiachong
APPLICANT: Spytek, Kimberly A
APPLICANT: Spytek, Kimberly A
APPLICANT: Spytek, Kimberly A
APPLICANT: Gerbusen, Bryan D
APPLICANT: Gerbusen, Bryan D
APPLICANT: Gerbusen, Richard A
APPLICANT: Lepley, Denise M
APPLICANT: Burgess, Catherine E
APPLICANT: Szekeres, William M
APPLICANT: Szekeres, William M
APPLICANT: Vernet, Corine A.M.
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390 -RNGTNFVGNVWPGDVYFPDFMHPAAAEFWARBISL--FRRTIPVDGLWIDMNBISNFYN 446
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                                                                                                                                    73 SRLRVRITDADHPRWEVPQDIIPRPAPGDVLHDAPPASSAPLQGR-----VLSPAGSDLV
                                                                                                                                                                                                                                                                                                                                                                                                    270 DQYTQLIARPAPMPYWSPGFHQCRYGYLNVSDLERVVARYAKARIPLEVMMTDIDYMDGF
                                                     tch 19.7%; Score 911.5; DB 12; Length 943; al Similarity 31.0%; Pred. No. 4.3e-78; 271; Conservative 114; Mismatches 296; Indels 193;
                                                                                                                                                                                                                                                                                                                                  208 DKPERTQGKAEKDEPGAWEETFKTHSDSKPYGPMSVGLDF
                                                                                                                                                                                                                  128 LTVHASPFR------FTVSRR-----
ORGANISM: Homo sapiens
                                                     Query Match
Best Local Similarity
Matches 271; Conservat
                                                                                                                                                                                                                                                                                               147 -----
                  US-10-032-189-123
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Casman, Stacie J Boldog, Ferenc L Gorman, Linda Gangolli, Esha A Fernandes, Elma R Rieger, Daniel K Edinger, Shlomit R Gunther, Erik

APPLICANT: APPLICANT: APPLICANT:

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99 TRFRIDELEPRRPRYRVP------DVLVADPPIARLSVSGRDENSVELTMAEGPYK 148
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DB 12; Length 944;
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PRIOR APPLICATION NUMBER: 60/274,192
PRIOR FILING DATE: 2001-03-08
PRIOR FILING DATE: 2001-03-08
PRIOR FILING DATE: 2001-03-22
PRIOR APPLICATION NUMBER: 60/279,840
PRIOR APPLICATION NUMBER: 60/29,91
PRIOR APPLICATION NUMBER: 60/282,981
PRIOR FILING DATE: 2001-04-11
PRIOR FILING DATE: 2001-04-11
PRIOR FILING DATE: 2001-04-11
PRIOR PRILING DATE: 2001-04-11
PRIOR PRILING DATE: 2001-07-31
PRIOR PRILING DATE: 2001-07-31
PRIOR PRILING DATE: 2001-08-17
PRIOR PILING DATE: 2001-08-17
PRIOR FILING DATE: 2001-08-17
PRIOR PRILING DATE: 2001-08-17
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ORGANISM: Homo sapiens
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US-10-032-189-122
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       491 TRDGSDYEGWCWPGSAGYPDFTNPTMRAWWANMFSYDNYEGSAPNLFVWNDMNEPSVFNG 550
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                                                                                                                                                                                                                                                                                                                                                                                      167
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814 RVRRSSECMKDDPITLFVALSPQGTAQGELFLDDGYTFNYQTRQFFLLRRFSF-----SG 868
                                                     PEPMNALDDPPYRINNDGTGRPINNKTVRPLAVHYGGVTEYEEHNLFGLLEARATGRGVL
                                                                                                    PE-VIMLKD------AQHYGGWEHRDVHNIYGLYVHMATADGLR
                                                                                                                                                507 RDTG--RRPFVLSRSTFVGSGRYTAYWTGDNAATWGDLRYSINTMLSFGLFGMPMIGADI
                                                                                                                                                                                            QRSGGMERPFVLARAFFAGSQRFGAVWTGDNTAEWDHLKISIPMCLSLGLVGLSFCGADV
                                                                                                                                                                                                                                           565 CGFNGNTTEELCGRWIOLGAFYPFSRDHSAIFTVRRELYLWPSVAAS-GRKALGLRYQLL
                                                                                                                                                                                                                                                                                                                                                                   RARRIA-----FHLLVALAEDGTASGYLFLDDGDSPEYGRRSDWSMVRFNYKIPNNKG
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APPLICANT: Smithson Glennda
TITLE OF INVENTION: Proteins and Nucleic Acids Encoding Same
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     790 AIKVKSEVVHNSYAQSRTLVISKVVLMGHRSPAA 823
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CURRENT APPLICATION NUMBER: US/10/032,189
CURRENT FILING DATE: 2001-12-21
PRIOR APPLICATION NUMBER: 60/257,495
PRIOR FILING DATE: 2000-12-21
PRIOR APPLICATION NUMBER: 60/258,171
PRIOR APPLICATION NUMBER: 60/258,171
PRIOR PILING DATE: 2000-12-20
PRIOR PILING DATE: 2000-12-20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 122, Application US/10032189
Publication No. US20030170630A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Burgess, Catherine E
Shimkets, Richard A
Grosse, William M
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Boldog, Ferenc L
Gorman, Linda
Gangolli, Esha A
Fernandes, Elma R
Rieger, Daniel K
Edinger, Shlomit R
Gunther, Erik
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APPLICANT: Thernew, Velizar T
APPLICANT: Liu, Xiachong
APPLICANT: Spytek, Kimberly A
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Patturajan, Meera
Grosse, William M
Lepley, Denise M
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Vernet, Corine A.M
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Sciore, Paul
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206 LFSRQESKDPABGNGAQPEATPGDGDKPEETQEKAEKDEPGAWEETFKTHSDSKPYGPTS 265
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FDDHNMPCDVIWLDIEHADGKRYFTWDPTRFP----QPLNMLEHLASKRRKLVAIVDPH1 493
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                                                                                                                                                                                                                                         Gaps
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                                                                                                                                                                                             19.5%; Score 903.5; DB 12; Length 966; 29.5%; Pred. No. 2.7e-77;
                                                                                                                                                                                                                                                                                                                                                                 LTVHASPFR-----FTVSRRSTGDTLFD--TAPGLVFRDKYLEVTSAL-
                                                                                                                                                                                                                 Best Local Similarity 29.5%; Pred. No. 2.7e-77; Matches 265; Conservative 123; Mismatches 292;
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NUMBER OF SEQ ID NOS: 260
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 121
                                                                                   LENGTH: 966
TYPE: PRT
ORGANISM: Mus musculus
                                                                                                                                                   US-10-032-189-12
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                                                                                                                                                      RARRIA------FHILVALAEDGIASGYLFLDDGDSPEYGRRSDWSMVRFNYKIPNNKG
                                                                                          769 LPGQGEVWYDIQSYQ------KHGPQTLYLPVTLSSIPVFQRGGTIVP-----RWM
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APPLICANT: Sclore, Fall
APPLICANT: Sclore, Fall
APPLICANT: MacDougall, John R
APPLICANT: MacDougall, John R
APPLICANT: MacDougall, John R
TITLE OF INVENTION: Proteins and Nucleic Acids Encoding Same
FILE REFERENCE: 21402-228
CURRENT FILING DATE: 2001-22-21
PRIOR APPLICATION NUMBER: 60/257,495
PRIOR APPLICATION NUMBER: 60/259,171
PRIOR APPLICATION NUMBER: 60/259,171
PRIOR PILING DATE: 2000-12-21
PRIOR PILING DATE: 2001-02-02
PRIOR PILING DATE: 2001-02-02
PRIOR PILING DATE: 2001-03-08
PRIOR PLING DATE: 2001-03-08
PRIOR PLING DATE: 2001-03-29
PRIOR PLING DATE: 2001-03-29
PRIOR PLING DATE: 2001-03-29
PRIOR PLING DATE: 2001-04-11
PRIOR APPLICATION NUMBER: 60/282,981
PRIOR PAPLICATION NUMBER: 60/282,981
PRIOR PLING DATE: 2001-04-13
PRIOR PLING DATE: 2001-04-13
PRIOR PLING DATE: 2001-04-13
PRIOR PLING DATE: 2001-07-31
PRIOR PLING DATE: 2001-07-31
PRIOR PLING DATE: 2001-07-31
PRIOR PLING DATE: 2001-08-17
                                                                                                                                                                                                                                       790 AIKVKSEVVHNSYAQSRTLVISKVVLMGHRSPAA 823
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Publication No. US20030170630A1
GENERAL INFORMATION:
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Grosse, William M
Szekeres, Edward S
Vernet, Corine A.M.
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Shimkets, Richard A
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Gangolli, Esha A
Fernandes, Elma R
Rieger, Daniel K
Edinger, Shlomit R
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APPLICANT: Tchernev, Velizar T
APPLICANT: Liu, Xiaohong
APPLICANT: Spyrek, Kimbelly A
APPLICANT: Zerhusen, Bryan D
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Grosse, William M
Lepley, Denise M
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Boldog, Ferenc L
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Sciore, Paul
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103 RLKINEETPLKPRFEVPDVLTSKPSTVR1----SCSGDTGSL1LADGKGDLKCH1TAN 156
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                                                                                                                                                                                                                                                                                                                                                                                                                             GPNPLAVVDOYTQLIARPAPMPYWSFGFHQCRYGYLNVSDLERVVARYAKARIPLEVMWT 321
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                                                                                                                                         382 MQQDIFLK-RNGTNFVGNVWPGDVYFPDFMHPAAAEFWAREISLFRRTIPVDG-----L
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                                               PPR-----PTVSRRSTGDTLFD--TAPGLVFRDK-
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Alsobrook II, John P
APPLICANT: Tchernev, Velizar T
APPLICANT: Liu, Xiaohong
APPLICANT: Spytek, Kimberly A
APPLICANT: Zerhusen, Bryan D
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19.4%; Score 900; DB 12; Length 967;
Best Local Similarity 27.6%; Pred. No. 5.8e-77;
Matches 256; Conservative 158; Mismatches 321; Indels 194;
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APPLICANT: MacDougall, John R
APPLICANT: MacDougall, John R
APPLICANT: Smithson, Glennda
TITLE OF INVENTION: Proteins and Nucleic Acids Encoding Same
FILE REFERENCE: 21402-228
CURRENT FILING DATE: 2001-12-21
PRIOR APPLICATION NUMBER: 60/257,495
PRIOR APPLICATION NUMBER: 60/259,71
PRIOR APPLICATION NUMBER: 60/259,71
PRIOR APPLICATION NUMBER: 60/269,940
PRIOR FILING DATE: 2000-12-20
PRIOR FILING DATE: 2001-03-20
PRIOR APPLICATION NUMBER: 60/279,840
PRIOR FILING DATE: 2001-03-20
PRIOR PELING DATE: 2001-03-22
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PRIOR PELING DATE: 2001-03-22
PRIOR PELING DATE: 2001-03-29
PRIOR PELING DATE: 2001-03-29
PRIOR PELING DATE: 2001-03-29
PRIOR PELING DATE: 2001-03-19
PRIOR PELING DATE: 2001-04-11
PRIOR APPLICATION NUMBER: 60/283,656
PRIOR PELING DATE: 2001-04-13
PRIOR APPLICATION NUMBER: 60/309,247
PRIOR PELING DATE: 2001-08-17
                                                           Sequence 38, Application US/10032189
Publication No. US20030170630A1
GENERAL INFORMATION:
APPLICANT: Alsobrook II, John P
APPLICANT: Tchernev, Velizar T
APPLICANT: Tchernev, Velizar T
APPLICANT: Spytek, Kimberly A
APPLICANT: Serlusen, Bryan D
APPLICANT: Gerlusen, Bryan D
APPLICANT: Grosse, Milliam M
APPLICANT: Grosse, Milliam M
APPLICANT: Lepley, Denise M
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Shimkets, Richard A
Grosse, William M
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Casman, Stacie J
Boldos, Ferenc L
Gorman, Linda
Gangolli, Esha A
Fernandes, Elma R
Rieger, Daniel K
Edinger, Shlomit R
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Vernet, Corine A.M.
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Millet, Isabelle
Sciore, Paul
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US-10-032-189-38
                                            US-10-032-189-38
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LENGTH: 967
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201 PEEAPGD - GDKP --- EEIQGK --- ARKD --- EPGAWEETFKTHSDSKPYGPTSVG 245
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19.0%; Score 878.5; DB 12; Length 944;
Best Local Similarity 33.0%; Pred. No. 6.5e-75;
Matches 256; Conservative 104; Mismatches 294; Indels 121; Gaps
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APPLICANT: MacDougall, John R
APPLICANT: Smithson, Glennda
TITLE OF INVENTION: Proteins and Nucleic Acids Encoding Same
FILE REFERENCE: 21402-228
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PRIOR PLING DATE: 2000-12-21
PRIOR PELLING DATE: 2000-12-21
PRIOR FILING DATE: 2000-12-20
PRIOR FLING DATE: 2001-02-20
PRIOR PELLING DATE: 2001-02-20
PRIOR APPLICATION NUMBER: 60/274, 192
PRIOR APPLICATION NUMBER: 60/277, 826
PRIOR PELLING DATE: 2001-03-20
PRIOR APPLICATION NUMBER: 60/277, 826
PRIOR APPLICATION NUMBER: 60/279, 840
PRIOR PILING DATE: 2001-03-22
PRIOR APPLICATION NUMBER: 60/289, 981
PRIOR PELLING DATE: 2001-04-11
PRIOR PELLING DATE: 2001-04-11
PRIOR PELLING DATE: 2001-04-13
PRIOR PELLING DATE: 2001-04-13
PRIOR PELLING DATE: 2001-04-13
PRIOR PELLING DATE: 2001-07-13
PRIOR PELLING DATE: 2001-07-17
PRIOR PELLING DATE: 2001-08-17
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                                                                           Burgess, Catherine E
Shimkets, Richard A
Grosse, William M
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Boldog, Ferenc L
Gorman, Linda
Gangolli, Baha A
Fernandes, Blma R
Rieger, Daniel K
Edinger, Shlomit R
Gunther, Erik
Millet, Isabelle
Sciore, Paul
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Vernet, Corine A.M.
Patturajan, Meera
Grosse, William M
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US-10-032-189-124
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LENGTH: 944
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                                               307 ARYAKARIPLEVMWTDIDYMDGFKDFTLDRVNFTAAELRPFVDRLHRNAQKYVLILDPGI 366
                                                                 367 RVDPIDATYGTFVRGMQQDIFLK-RNGTNFVGNVWPGDVYFPDFMHPAAAEFWAREISLF 425
                                                                                                                               622 EWDHLKISIPMCLSLGLVGVSFCGADVGGFFKNPEPELLVRWYQMGAYQPFFRAHAHLDT 681
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                                                                                                                                                                                           HYGGVTEYEEHNLFGLLEARATGRG-VLRDTG-RRPFVLSRSTFVGSGRYTAYWTGDNAA 537
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Sequence

Sequence 2, M. Sequence 4, M. Sequence 4, M. Sequence 1692, Sequence 1692, Sequence 14, M. Sequence 6, M. Sequence 2231(Sequence 2231(Sequence 26, Sequence 26, S

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Fatent No. 5763252
GENERAL INFORMATION:
APPLICANT: Skadsen, Ronald W
APPLICANT: Tibbot, Brian K
ITLE OF INVENTION: Cloned Alpha-Glucosidase from Barley
NUMBER OF SEQUENCES: 7
CORRESPONDENCE ADDRESS:
ADDRESSEE: Quartles & Brady
STREET: 1 South Pinckney Street
CUTTY: Madison
STATE: Will
COUNTRY: US
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US-09-417-822-2

US-09-104-623A-4

US-09-019-532-4

US-09-019-532-4

US-09-252-911A-16929

US-09-679-279-14

US-08-679-279-14

US-08-679-279-14

US-08-679-279-14

US-08-296-10661A-6

PCT-US95-10661A-6

US-09-252-991A-21126

US-09-252-991A-21126

US-09-252-991A-21126

US-09-252-991A-21126

US-09-164-222B-26

US-08-164-222B-26

US-09-103-310-26
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/430,925A
FILING DATE:
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Best Local Similarity 100.0%; Pred. No. 0;
Matches 877; Conservative 0; Mismatches
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Patent No. 5183745
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Sequence 8, Appli
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                                                                                                                                                                                                                                        October 27, 2003, 10:19:13; Search time 15.8523 Seconds (without alignments) 2340.767 Million cell updates/sec
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                                                                                                                                                                                                                                                                                                                                                                                                                                             .....IGGLSLVVGEEFELKVAMSY 877
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5: /cgn2_6/ptodata/2/iaa/PCTUS_COMB.pep:*
6: /cgn2_6/ptodata/2/iaa/PCTUS_COMB.pep:*
                                    GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
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US-08-633-770A-2
US-08-633-770A-2
US-08-633-768A-1
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US-09-437-054A-10
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US-09-410-551B-31
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Gaps

50 ATGGRSSTGDVORLAVYASLETDSRLRVRITDAD-----HPRWEVPODIIPRPAPGDVL 103

7 LLLCLCLCLFAPRLCSSKBE-----GPLAAR----

--TVLAVAVTM-EGALRAEA

Length 914;

19.1%; Score 883; DB 4; 29.4%; Pred. No. 6.8e-78;

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Best Local Similarity 29.4%; Pred. No. 6.8e-78;
Matches 278; Conservative 123; Mismatches 338; Indels
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                                     HTKSSFRLRHNDSFTLWNAD1GASYVDVNLYGSHPFYMDVRAPGTAHGVLLLSSNGMDVL
                                                                            HTKSSFRLRHNDSFTLMNADIGASYVDVNLYGSHPFYMDVRAPGTAHGVLLLSSNGMDVL
                                                                                                           YGGSYVTYKVIGGVLDFYFFAGPNPLAVVDQYTQLIARPAPMPYWSFGFHQCRYGYLNVS
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                                                                                                                                                                                                                                                                                                                                                                                                                                               B--EMORKILASKGRHMVIIVDPHIK---RDENFHLHKEASQKGYYVKDASGNDFDGMCWP 467
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                                                HDAPPASSAP--LOGRVLSPAGSDLVLTVHASPFRFTVSRRSTGD----TLFD--- 150
                                                                                         125 W-LPKIŚSVENGĽSSSVYLSDGHSAVĽ--RHDPFELFIRDDSSGDRVISLNSHDĽFDFEQ 181
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67 LIPKHDSQSETKPLLLILSVYQRGILRLKI-DEDPSLSPPKKRFEVP-DVIVSEFPSTKL 124
                                                                                                                                                                                   LKHKSEDDNWEBOFRSHTDRRPYGPOSISFOVSFYGADFVYGIPERA-ASLALKPTRGPN
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Homologs

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Sequence 8, Application US/09437054A
Patent No. 6316698
GENERAL INFORMATION:
APPLICANT: Rinney, Anthony J.
TITLE OF INVENTION: Plant Alpha-Glucosidase II
TITLE OF INVENTION: Plant Alpha-Glucosidase II
FILE REFERENCE: BB1273 US NA
CURRENT APPLICATION NUMBER: US/09/437,054A
CURRENT FILING DATE: 2001-05-14
PRIOR APPLICATION NUMBER: 60/107,909
PRIOR FILING DATE: 1999-No. 6316698ember-10
NUMBER OF SEQ ID NOS: 19
SOFTWARE: Microsoft Office 97
SEQ ID NO 8
LENGTH: 914

US-09-437-054A-8

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146 LTAQPPRLDLLEDRSLLLSVNARGLMAPEHQRAPRVPQESKDPAEGNGAQPEATPGDGDK 205
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                                                                                                                                                               829 QGAFILKWEAXIPQMQPRLQLAVTHFPSE------CTVERIILIG-LSPGA-KTA 875
                                                                                                                                                                                                                                                                                                                                                  Sequence 1, Application US/08897843A

Patent No. 6514493

GENERAL INFORMATION:
TITLE OF INVENTION: CDNA CLONE FOR MURINE TUMOR
TITLE OF INVENTION: REJECTION ANTIGEN GP110 AND TUMOR PEPTIDE VACCINE
NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:
ADDRESSEE: Diane R. Meyere
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    148 LFDT-----APGLVFRDKYLEVTSALPAGRAS------LYGLGEHTKSSFRL
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                                                                                                                                        771 RRS---DWSMVRPNYKIPNNKGAIKVKSEVVHNSYAQSRTLVISKVVLMGHRSPAAPKKL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/897,843A
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STREET: 600 Grant Street, 42nd Floor
CITY: Pittsburgh
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DEVELOPMENTAL STAGE: Embryo
TISSUE TYPE: Embryo
CELL LINE: NIH 3T3
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INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
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amino acid
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876 LIEPGNKKVE 885
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                                                                                                                                                                                                                      828 TVHVNSAEVE 837
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                                                      GENERAL INFORMATION:
APPLICANT: Allen, Stephen M.
APPLICANT: Allen, Stephen M.
APPLICANT: Kinney, Anthony J.
ATTILE OF INVENTION: Plant Alpha-Glucosidase II Homologs
FILE REFERENCE: BB1273 US NA
CURRENT APPLICATION NUMBER: US/09/437,054A
CURRENT FILING DATE: 2001-05-14
PRIOR FILING DATE: 1998-No. 6316698ember-10
NUMBER OF SEQ ID NOS: 19
SOFTWARE: Microsoft Office 97
LENGTH: 919
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                Sequence 17, Application US/09437054A
Patent No. 6316698
                                                                                                                                                                                                                                                                                                                                          ORGANISM: Solanum tuberosum
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US-09-437-054A-17
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QY 134 PFRFTVSRR-STGDTLFDTAPGLVFRDKYLEVTSALPAGRASLYGLGEHTKSSFRL-RHN 191 Db 23 PIEFPLEQKISSNKSLSELGLTIVQQGNKVIVBKSLDL-KEHIIGLGEKAFELDRKR 78	Qy 192 DSFTLMNADIGASYVDVNLYGSHPYMDVRAPGTAHGVLLLSSNGMDVLYGGSYVTY- 248 : ::	OY 249 KVIGGVLDFYFFAGENPLAVVDQYTQLIARPAPMPYWSFGFHQCRYGYLNVSDLER 304	OY 305 UVARYAKARIPLEUMWTDIDYMDGFKDFTLDRYNFTAAELRPFUDRLHRNAQKYULILDP 364 :	Qy 365 GIRVDPIDATYGTFVRGMQQDIFLKRNGTNFVGNVWPGDVYFPDFMJPAAEFWAREISL 424	Qy 425 FRRTIPUDGLWIDKNEISNFYNP-EPWNALDDPPYRINNDGTGRPINNKTVRPLAVHY 481 :	Qy 482GGVTEYEE-HNLFGLLEARAIGRGVLRDIGRRPFVLSRSTFVGSGRYTAYWIGDNAAI 538 Qy 482GGVTEYEE-HNLFGLLEARAIGRGVLRDIGRRPFVLSRSGRYTAYWIGDNAAI 538 DD 361 LRGKRVKHEKVRNAYPLYEAMAIFKGFRISHRNEIFILSRAGYAGIQRYAFIWIGDNIFS 420	OY 539 WGDLRYSINIMLSFGLFGMPMIGADICGFNGNTTEELCGRWIQLGAFYPFSRDH 592	Qy 593 SAIFTVRRE-LYLWPSVAASGRKALGLRYQLLPYFYTLMYEAHMTGAPIARPLFFSYPHD 651	Qy 652 VATYGVDRQFLLGRGVLVSPVLEPGPTTVDAYFPAGRWYRLXDYSLAVATRTGRHV 707 1	Qy 708 -RLPAPADTVNVHLTGGTILPLQQSALTTSRARRTAFHLLVALAEDGTASGYLFLDDGDS 766	Qy 767 PEYGRRSDWSMVRF-NYKIPNNKGAIKVKSEVVHNSYAQSRTLVISKVVLMGHRSPAAPK 825 : : : :	Qy 826 KLTVHVNSAEVEASSAGTRY 846	APPLICANT: Yu, Shukun APPLICANT: Kragh, Kareten APPLICANT: Christensen, Tove APPLICANT: Marcussen, Jan	NVENTION: ALPHA-1,4-GLUCAN LYAS NVENTION: PURIFICATION GENE CLC SEQUENCES: 12 ENCE ADDRESS: E: Knobbe, Martens, Olson & Bea	STREET: 620 Newport Center Drive 16th Floor CITY: Newport Beach STATE: CA COUNTRY: U.S.A. ZIP: 92660
QY 189 RHNDSFILWNADIGASYVDVNLYGSHPFYMDVRAPGTAHGVLLL 232 :	Qy 233SNGMDVLYGGSYVTYKVIGGVLDFYFFAGENPLAVVDQYTQ 274	QY 275 LIARBAPMYWSFGFHQCRYGYLNVSDLERVVARYAKARIPLEVMWTDIDYMDGFKDFTL 334 1 1 1 1 1 1 1 1 1	QY 335 DRVNFTAAELRPFUDRLHRNAQKYVLILDPGIRVDPIDATYGTFVRGMQQDIFLK-RN 391	OY 392 GTNFVGNVWPGDVYFPDFXHPAAAEFWAREISLFRRTIPVDGLWIDMKEISNFYNPEP 449	QY 450 MMALDDPPYRINNDGTGRPINNKTVRPLAVHYGGVTEYEEHNLFGLLEARATGRGVLRDT 509 :	QY 510 GRRPEVLSRSTFVGSGRYTAYWTGDNAATWGDLRYSINTMLSFGLFGMPMIGADICGF 567	QY 568 NGNTTEELGGRWIQLGAFYPESRDHSAIFTVRRELYLWPSVAASGRKALGLRYQLLPY 625	Qy 626 FYTLMYEAHMTGAPIARPLFFSYPHDVATYGVDRQFLLGRGVLVSPVLEPG 676	Qy 677 PTTVDAYFPAGRWYRLYDYSLAVATRTGKHVRLFAPADTVNVHLTGGTILPLQQ 730 Db 756 AHGGRSICLAKKRCGMTFRAIRSIMGFRPCICPVTLSSIPVFQGGGTIVP 805	CY 731 SALITSRARRIAFHLLVALABDGTASGYLFLDDGDSPEYGRRSDWSWVRFNYK 783	Qy 784 IPNNKGAIKVKSEVVHNSYAQSRTLVISKVVLMGHRSPAA 823 : : :	RESULT 5 10S-09-376-343-2 1Sequence 2, Application US/09376343 1Sequence 2, Application US/09376343 1Sequence 2, Application US/09376343 1Sequence 2, Application US/09376343 1Sequence 2, Application Sequence 2, CURRENT APPLICATION Hyperthermophilic Alpha-Glucosidase Gene and Its Use 11LE REFERENCE: N1231-200 1SEQUENCE APPLICATION NUMBER: US/09/376,343 1CHRAENT FILING DATE: 1949-08-18		SEQ ID NO 2 LENGTH: 6 TYPE: PRT ORGANISM: S-09-376-343	<pre>Cuery Match Best Local Similarity 27.8%; Pred. No. 5.8e-58; Matches 206; Conservative 130; Mismatches 292; Indels 113; Gaps 30;</pre>

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619 RYQLLPYFYTLMYEAHMTGAPIARPLFFSYPHDVATYG-----VDRQFLLGRGVLVSPVL 673
                                                                                                                                                              674 E-----PGPTTVDAYFPA-GRWY----RLYD---YSLAVATRTGKHV----RLPAPAD-- 714
                                                                                                                                                                                               809 HSRKEIPGENR-DVYLPLYHTWYPSNIRPWDDQGVALGNPVEGGSVINYTARIVAPEDYN 867
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APPLICATION NUMBER: US/08/633,770A
FILING DATE: Usly 8, 1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ADDRESSEE: Knobbe, Martens, Olson & Bear
STREET: 620 Newport Center Drive 16th Floor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME: Altman, Daniel E
REGISTRATION NUMBER: 34,115
REFERENCE/DOCKET NUMBER: DYOUG.001APC
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/EP94/03398
FILING DATE: OCT-15-1994
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 2, Application US/08633770A
Patent No. 5908760
GENERAL INFORMATION:
APPLICANT: Bojsen, Kirsten
APPLICANT: Yu, Shukun
APPLICANT: Kragh, Karsten
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1070 amino acids
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELEFAX: 714-760-9502
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MOLECULE TYPE: protein
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COMPUTER READABLE FORM:
MEDIUM TYPE: Diskett
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CITY: Newport Beach
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          amino acid
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982 TRTVTI 987
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         235 PTFMNYFNFD-NMQYQQVYAQGALDSREPLYHSDPFYLDVNSNPEHKNITATFIDNYSQI 293
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            236 GMDVLYGGSYVTYKVIG---GVLDFYFFAGPNPLAVVDQYTQLIARPAPMPYWSFGFHQC 292
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        293 RYGYLNVSDLERVVARYAKARIPLEVMWTDIDYMDGFKDFTLDRVNFTAAELRPFVDRLH 352
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             409
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ---YFPDFMHPAAA 415
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TGDNAATWGDLRYSINTMLSFGLFGMPMIGADICGF----NGNTTE-----ELCGRWIQ 581
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TGDNASNWEFWKISVSQVLSLGLMGVCIAGSDTGGFEPYRDANGVEEKYCSPELLIRWYT 692
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            353 RNAQKYVLILDPGIRVDPIDATYGTFVRGMQQDIFLK----RNGINFVGN-----
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10.1%; Score 466; DB 2; Length 1066;
Best Local Similarity 23.4%; Pred. No. 1.7e-36;
Matches 212; Conservative 119; Mismatches 343; Indels 232;
                MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: Patentin Release #1.0, Version #1.25 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/633,770A
FILING DATE: July 8, 1996
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/EP94/03398
FILING DATE: OCT-15-1994
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             100 GDVLHDAPPASSAPLOGRVLSPAGSDLVLTVHASPFRFTVSR----
                                                                                                                                                                                                                                                                                            NAME: Altman, Daniel E
REGISTRATION NUMBER: 34,115
REGISTRATION NUMBER: DYOUG.001APC
TELECOMUNICATION INFORMATION:
TELEPHONE: 714-760-0404
                                                                                                                                                                                                                                                                                                                                                                                                                                                        INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 1066 amino acids
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COMPUTER READABLE FORM
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APPLICANT: Bojsen, Kirsten
APPLICANT: Yu, Shukun
APPLICANT: Kragh, Karsten
APPLICANT: Kragh, Karsten
APPLICANT: Marcussen, Jan
APPLICANT: Marcussen, Jan
TITLE OF INVENTION: ALPHA-1,4-GLUCAN LYASE FROM A FUNGUS, ITS
TITLE OF INVENTION: PURIFICATION GENE CLONING AND EXPRESSION IN MICROORGANISMS NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:
ADDRESSEE: Knobbe, Marren C. STREES 715 ----TVNVHLTGGTILPLQQSALTISR--ARRTAFHLLVALABDGTASGY-LFLDDG--- 764 868 LFHSVVPVYVREGAIIPQIEVROWIGOGGANRIKFNIY-----PGKDKEYCTYLDDGVSR 922 ----DSPEYGRRSDWSMV-----RFNYKI----PNNKGAIKVKSEVVHNSYAQ 804 923 DSAPEDLPQYKETHEGSKVEGAEIAKQIGKKTGYNISGTDPEAKGYHR-KVAVTQTSKDK 981

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161 YLEVTSALP-----AGRASLYGLGEHTKSSFRLRHNDSFTLWN-----ADIGASYVD 207
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                315 PLEVMWTDIDYMDGFKDFTLDRVNFTAAELRPFVDRLHRNAQKYV•---LILDPGI---- 366
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    | | : | : | : | : | : | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | 
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          314 YIPMYYAAPWLVVQGCAGTSKQYSYGWFMDNVSQSYMNTGDTAWNCGQENLAYMGAQY--
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8.3%; Score 385.5; DB 4; Length 1092;
Best Local Similarity 21.7%; Pred. No. 1.6e-28;
Matches 175; Conservative 136; Mismatches 298; Indels 199; Gaps
                                     APPLICANT: JSEN, Kirsten
APPLICANT: MARCUSSEN, Jan
TITLE OF INVENTION: ALPHA-1, 4-GLUCAN LYASE AND
TITLE OF INVENTION: ITS USE IN THE PRODUCTION OF 1, 5-ANHYDROFRUC
TITLE OF INVENTION: TOSE
NUMBER OF SEQUENCES: 21
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                ADDRESSEE: Knobbe, Martens, Olson & Bear
STREET: 620 Newport Center Drive 16th Floor
CITY: Newport Beach
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: Windows
SOFTWARE: FastSEQ for Windows Version 2.0b
CURENT APPLICATION DATA:
APPLICATION NUMBER: US/09/275,608
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/EP95/02172
APPLICATION NUMBER: 08/836,156
PILING DATE: 15-APR-1997
APPLICATION NUMBER: PCT/EP94/03397
PILING DATE: 15-CCT-1994
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              REGISTRATION NUMBER: 34,115
REFERENCE/DOCKET NUMBER: DYOU9.001C1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELECOMMUNICATION INFORMATION:
TELEPHONE: 714-760-0404
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 1092 amino acids
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REGISTRATION NUMBER: 34
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TELEFAX: 714-760-9502
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                                                                                                                                                                                                                                                                                                                                                                                                                        ZIP: 92660
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskett
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: amino acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FILING DATE
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                                                                                                                                                                                                                                                                                                                                CITY: Nev
STATE: CA
COUNTRY:
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                                                                                                                                                                                                                              60 VORLAVYASLETDS----RLRVRITDADHPRWEVPQDIIPRPAPGDVLHDAPPASSAPLQ 115
                                                                                                                                                                                                                                                                                                                                                               -----RSTGDTLFDTAPGL- 155
                                                                                                                                                                                                                                                                                                                                                                                                 -----VFRDKYLEVTSALPAGRASLYGLGEHTKSSFRLRHNDSFTLWNADIGASYV 206
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 G---GVLDFYFFAGPNPLAVVDQYTQLIARPAPMPYWSFGFHQCRYGYLNVSDLERVVAR 308
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GTRYGGIDCYGISADTVPEIVRLYTGLVGRSKLKPRYILGAHQACYGYQQESDLHAVVQQ 367
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            309 YAKARIPLEVMWIDIDYMDGFKDFILDRVNF-------TAAELRPFV---D 349
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 R-----LHRNAQKYVLILD----PGIRVDPIDATY-----GTFVRGMQQDIFLKRN--- 391
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         428 RPNGYSTLNEGYDKKYFIMDDRYTEGTSGDPQNVRYSFYGGGNPVEVNPNDVWARPDFGD 487
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ----GINF------VGNVWPGDVYFPDFMHPAAAEFWAREIS-LFRRTIPVD 432
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                                                                                                 1 MATVGVLLLCLCLCLFAPRLCSSKEBGPLAARTVLA-VAVTMEGALRAEAATGGRSSTGD
                                        Gabs
Best Local Similarity 22.7%; Pred. No. 2.4e-36;
Matches 216; Conservative 122; Mismatches 355; Indels 257;
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                                                                                                                                                              58 MCVVQFVRPCVWRVRYDPSVKTSDEYGDENTRTIVQDYMTTLVGNL
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Sequence 3, Application US/09275608 Patent No. 6541237 GENERAL INFORMATION:

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      368 LAYMGAQCGPFDQHFVYGDGDGLEDVVQAFSLLQGKEFENQVLNKRAVMPPKYVFGYFQG 427
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      293 RYGYL------NVSDLERVVARYAKARIPLEVMWTDIDYMDGPKDFTLDRVNFT 340
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          VDGLWIDMNEISNFYNPEPM----NALDD-PPY---RINNDGTGRPINNKTVRPLAVHY 481
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                                                                                                                                                                                                                                                                                                                                                             Query Match 7.7%; Score 356; DB 3; Length 1091; Best Local Similarity 23.8%; Pred. No. 1.4e-25; Matches 197; Conservative 117; Mismatches 308; Indels 204; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          212 GSHP-FY--MDVRAPGTAHGVLLLSSNGMDVLYGGSYV-----TYKVIGGV---
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                                                                                          7;
                                                                                                                                                    1091 amino acids
714-760-0404
                                                                                       INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                             TELEFAX: 714-760-9502
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MOLECULE TYPE: protein
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                                                             INNDGTGRPINNKTVRP-----LAVHYGGVTEYEEHNLFGLLEARATGR-GVLRDTG 510
                                                                                                                                                                                 -----RRPFVLSRSTFVGSGRYTAYWTGDNAATWGDLRYSINTMLSFGLFGWPMIGADIC 565
                                                                                                                                                                                                                     GF-----NGNTTEELCGRWIQLGAFYPFSRDHSAIFTVRR-----ELYLWPSVAASG 612
                                                                                                                                                                                                                                                                                                                                                                                                                                 RKALGLRYQLLPYFYTLMYEAHMTGAPI--ARPLFFSYPHDVATY-GVDRQFLL----GR 665
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ------LYDYSLAVATRIGK 705
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             706 HVRLPAPADIVNVHLIGGIILPLQQSALITSRARRI------AFHLLVALAEDGTASGY 758
577 DWGRPDVAQWWGENYKKLF--SIGLDFVWQDMTVPAMMPHRLGDAVNKN--SGSSAPGWP 632
                                                                                                                    633 NENDPSNGRYNWKSYHPQVLVTDMRYGAEYGREPMVSQRNIHAYTLCESTRREGIVGNAD 692
                                                                                                                                                                                                                                                                                                                                                813 KKFVEFRYRWQEVLYTAMYQNATTGEPIIKAAPM---YNNDVNVYKSQNDHFLLGGHDGY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         : | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | : | | : | | : | : | | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GENERAL INFORMATION:
APPLICANT: YU, SHUKUN
APPLICANT: KRAGH, KARSTEN
APPLICANT: BOJSKO, MAJA
APPLICANT: BOJSKO, MAJA
APPLICANT: NIELSEN, JOHN
APPLICANT: MARCUSSEN, JAN
APPLICANT: MARCUSSEN, JAN
APPLICANT: MARCUSSEN, JAN
APPLICANT: ALBHA-1,4-GLUCAN LYASE FROM
ITILE OF INVENTION: A FUNGUS INFECTED ALGAE, ITS PURIFICATION
NUMBER OF SEQUENCES: 25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            3: Knobbe, Martens, Olson & Bear
620 Newport Center Drive 16th Floor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        666 GVLVSPVLEPGPTTVDAYFPA-GRWYR------
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NAME: Altman, Daniel E
REGISTRATION NUMBER: 34,115
REFERENCE/DOCKET NUMBER: DYOU7.001APC
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SOFTWARE: FaetSEQ Version 1.5
SOFTWARE: FaetSEQ Version 1.5
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/633,768A
FILING DATE: 02-UUL-1996
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 2, Application US/08633768A Patent No. 6013504
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRIOR APPLICATION DATA:
APPLICATION NUMBER: 9321301.5
PILING DATE: 15-0CT-1993
ATYORNEY/AGENT INPORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ZIP: 92660
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskett
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CORRESPONDENCE ADDRESS:
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STREET: 62
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-----VTTNAEDNGKFSVVKVAAB----QDGGTETITFTNDCYBYVFGGPFYVRVRGA 1025
                              771 RRSDWSMVRFNYKIPNNKGAIKVKSEVVHNSYAQSRTLVISK-------VVLMGH 918
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               721 TGGTILPLQQSALTTSRART-----AFHLLVALAEDGTASGYLFLDDGDSPEYG 770
339 FTAAELRPFVDRLHRNAQKYV----LILDPGI----RVDPIDATYGTFVRGMQQDIFLKR 390
                                                                                                                             539 DSLTGTDFGMTDDGPSDAYIGHLDYGGGVECDALFPDWGRPDVAEWWGNNYKKLF--SIG 596
                                                                                                                                                                         431 VDGLWIDM-----NEISNFYNPEP----MNALDDPPYRINNDGTGRPINNKTVRPLAV 479
                                                                                                                                                                                                   480 HYGGUTE--YEEH-----NLFGLLEARATGR-GVLRDTG-----RRPFVLSRSTFV 522
                                                                                                                                                                                                                                                                                             GSGRYTAYWTGDNAATWGDLRYSINTMLSFGLFGMPMIGADICGF----NGN----TTEE 574
                                                                                                                                                                                                                                                                                                                                                                                 575 LCGRWIQLGAFYPF-----SRDHSAIFTVRRELYLWPSVAASGRKALGLRYQLLP 624
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 625 YFYILMYEAHMTGAPIARPLFFSYPHDVATYGVDRQFLL----GRGVLVSPVLEPGPTTV 680
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           821 VLYTAMYONAAFGKPIIKAASMYNNDSNVRRAQNDHFLLGGHDGYRILCAPVVWENSTER 880
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         927 REGAILPTRYTLNGENKSLNTYTDEDPLVFEVFPL-----GNNRADGMCYLDDGG----- 976
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: YU, Shukun
APPLICANT: JSEN, Kirsten
APPLICANT: JSEN, Kirsten
APPLICANT: JSEN, Kirsten
APPLICANT: MARCUSSEN, ALPA-1, 4-GLUCAN LYASE AND
TITLE OF INVENTION: ITS USE IN THE PRODUCTION OF 1,5-ANHYDROFRUC
TITLE OF INVENTION: TOSE
NUMBER OF SEQUENCES: 21
CORRESPONDENCES ADDRESS:
ADDRESSEE: Knobbe, Martens, Olson & Bear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  E: Knobbe, Martens, Olson & Bear
620 Newport Center Drive 16th Floor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                OPERATING SYSTEM: Windows SOFTWARE: FASTSO for Windows Version 2.0b CURRENT APPLICATION DATA:
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1026 QSPS-----NIHV-----SSGAGSQ 1040
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              819 RSPAAPKKLTVHVNSAEVEASSSAGTR 845
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DAYFPA-GRWY------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER: IBM Compatible
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COUNTRY: U.S.A.
ZIP: 92660
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  251 RNDAVKQEGFYGAGE-----VNCKYQDTYILERTGIAMTNYNYDNLNYNQWDLRPPHHDG 305
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GSYVTYKVIGGVLD--FYFFAGPNPLAVVDQYT-----QLIARPAPM-PYWSFGFH 290
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             291 QCRYGYL------NVSDLERVVARYAKARIPLEVMWTDIDYMDGFKDFTLDRVN 338
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      420 GGVFGTSSLLRAHMPAGENNIS-VEEIVEGYQNNNFPFEGLAVDVDMQDNLRVFTTKGEF 478
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            192 DLSVIIYGN-FKTRVTRKSDGKVIMENDEVGTASSGNKCRGLMFVDRLYGNAIASVNKNF
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      Sequence 1, Application US/08633768A

Patent No. 6013504

GENERAL INFORMATION

APPLICANT: BOJSEN, KIRSTEN

APPLICANT: BOJSEN, MAJA

APPLICANT: BOJSEN, JOHN

APPLICANT: MARCUSSEN, JAN

TITLE OF INVENTION: ALPHA-1, 4-GLUCAN LYASE FROM

TITLE OF INVENTION: A FUNGUS INFECTED ALGAE, ITS PURIFICATION

NUMBER OF SEQUENCES: 25

CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 7.5%; Score 349; DB 3; Length 1088; Best Local Similarity 21.1%; Pred. No. 6.7e-25; Matches 196; Conservative 139; Mismatches 308; Indels 284;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ---PAGRASLYGLGEHTKSSFRLRHNDSFTLWNADIGA---SYVDVN----
                                                                                                                                                                                                                                                                                                       E: Knobbe, Martens, Olson & Bear
620 Newport Center Drive 16th Floor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NAME: Aleman, Daniel E
REGISTRATION NUMBER: 34,115
REFERENCE/DOCKET NUMBER: DYOUT.001APC
TELECOMMUNICATION INFORMATION:
TELEPHONE: 714-760-0404
TELEPAK: 714-760-0404
                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDIUM TYPE: Diskette
COMPUTER: IBM Comparible
OPERATING SYSTEM: DOS
SOFTWARE: FastSEN Version 1.5
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/633,768A
FILING DATE: 0-JUL-1996
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 9321301.5
FILING DATE: 15-CT-1993
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LENGTH: 1088 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ; TOPOLOGY: linear;
; MOLECULE TYPE: protein
US-08-633-768A-1
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                                                                                                                                                                                                                                                                                                                                                                                                                  ZIP: 92660
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskett
                                                                                                                                                                                                                                                                                                                                            CITY: Newport Beach
STATE: CA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: amino acid
STRANDEDNESS: sin
                                                                                                                                                                                                                                                                                                                                                                                                 U.S.A.
                                                                                                                                                                                                                                                                                                         ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                 COUNTRY:
                                                                                                                                                                                                                                                                                                                                   STREET:
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TITLE OF INVENTION: Polynucleotides, materials incorporating
TITLE OF INVENTION: them and methods for using them.
FILE REFERENCE: 11000.1043U1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ch 4.3%; Score 197; DB 4; Length 390; 1 Similarity 24.6%; Pred. No. 1.2e-10; 95; Conservative 35; Mismatches 166; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CURRENT APPLICATION NUMBER: US/09/634,238
CURRENT FILING DATE: 2000-08-08
NUMBER OF SEO ID NOS: 422
SOFTWARE: FASCISEO for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        651 DVATYG--VDRQFLLGRGVLVSPVLE 674
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       332 IPEAYTDLVKYEYLWGDNPLVAPIYO 357
                                                                                                                                                               ; Sequence 331, Application US/09634238; Patent No. 6544772; GENERAL INFORMATION:
                                                                                                                                                                                                                                   Glenn, Matthew
Havukkala, Ilkka J.
Blokaberg, Leonard, N.
Lubbers, Mark W.
Dekker, James
Christensson, Anna C.
Holland, Ross
O'Toole, Paul W.
Reid, Julian R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; ORGANISM: Lactobacillus rhamnosus US-09-634-238-331
645 FFSYPHDV 652
                                | :|:
| SS4 SM-YNNDM 560
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US-09-437-054A-10
                                                                                                                                              US-09-634-238-331
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQ ID NO 331
LENGTH: 390
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     72 AGQKDLAYMGAQ-----CGPFDQHFVYEAGDGLEDVVTAFSYLQGK------ 112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     263 PNPLAVVDQYTQ--LIARPAPMPYWSFGFHQCRYGYL-------NVSDLERVVAR 308
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 113 -----EYENQGLNIRSAMPPKYVFGFFQGVFGATSLLRDNLPAGENNVS-LEETVEG 163
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    342 -----AELRPF-VORLHRNAQKYVLILDPGIRVDPID-ATYGTFVRGMQQDIFLKRNG 392
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            393 TNFVGNVWPG-----DVYFPDFMHPAAAEFWAREI-SLFRRTIPVDGLWIDMNEISNFYN 446
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ---INNKTVRPLAV-----HYG 482
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        320 PAMM-----PHRLGDPVGTNSGETAPGWPNDKDPSNGRYNWKSYHPQVLVTDMRYDDYG 373
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        483 GVTEYEEHNLFGLLEARATGR-GVLRDTG----RRPFVLSRSTFVGSGRYTAYWTGDNA 536
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   434 STEDYLAMMVINVINMNMSGVPLVGSDIGGFTEHDKRNPCTPDLMMRFVQAGCLLPWFRN 493
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      203 ASYVDVNLYGSHPFYMDVRAPGTAHGVLLSSNGMDVLYGGSYVTYKVIGGVLDFYFFAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            7 DNLNYNOP-DLIP---PG---HDSDPDYYIPM------YFAAPWVIAHGYR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 6.0%; Score 279; DB 4; Length 570; Best Local Similarity 21.4%; Pred. No. 1.8e-18; Matches 143; Conservative 87; Mismatches 226; Indels 212;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              224 NVTCFLKNEKAPYEVNQSLREKQLYT-----KSDSLDNIDFGTTPDGPSD--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 309 YAKARIPLEVMWIDIDYMDGFKDFTLDRVNFTA-----
              PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/EP95/02172
FILING DATE: 06-JUN-1995
APPLICATION NUMBER: 08/836,156
FILING DATE: 15-APR-1997
APPLICATION NUMBER: PCT/EP94/03397
FILING DATE: 15-07-1994
ATTORNEY/AGENT INFORMATION:
NAME: Altman, Daniel E
                                                                                                                                                                                                          NAME: Altman, Daniel E
REGISTRATION NUMBER: 34,115
REFERENCE/DOCKET NUMBER: DYOU9.001C1
TELECOMEUNICATION INFORMATION:
TELEPHONE: 714-760-0404
TELEFAX: 714-760-9502
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PEPMNALDDPPYRI ----NNDGTGRP
                                                                                                                                                                                                                                                                                                                                                                     INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 570 amino acids
TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TOPOLOGY: linear; MOLECULE TYPE: protein US-09-275-608-4
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130 NLSPVDPA-----VKALKTDVAWVGS 166
                                                          309 YAKARIPLEVMWTDIDYMDGFKDFTLDRVNFTAAELRPFVDRLHRNAQKYVLILDPGIRV 368
                                                                                                                                                                                        369 DPIDATYGTFVRGMQQDIFLKRNGTNFVGNVWPGDVYFPDF--MHPAAAEFWAREISLFR 426
                                                                                                                                                                                                                                                         88 -PNDG-YGA---GYGQIDTLAGNLQNLKS------FADYADQHGVATGLWTQQ---- 129
                                                                                                                                                                                                                                                                                                                           427 RTIPVDGLWIDMNEISNFYNPEPMNALDDPPYRINNDGTGRPINNKTVRPLAVHYGGVTE 486
                                                                                                                                                                                                                                                                                                                                                                                                                                                      487 YEEHNLFGLLEARATGRGYLRDTGRRPFVLSRSTFVGSGRYTAYWTGD-NAATWGDLRYS 545
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Gaps
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Patent No. 631669
GENERAL INPORMATION:
APPLICANT: Allen, Stephen M.
APPLICANT: Kinney, Anthony J.
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Gaps

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------GOVERLEGYLRGSVDVAAVAQGLVRE-- 3915
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                                                                                                                                                                                                                                                                                                                                                                                    3557 SDTGVFMGAFSHGYGAGVDL---GG----FGATATQNSVLSGRLS-YFFGMEGPAVTVDT 3608
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           3778 KSNIGHTQTTAGVAGVIKMYMAMRHG-----IAPKTLHVDEPSSHVDWTEGAVELLTEA 3831
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                                                                                                                                                         3336 FAORLAELPDADRGAALTTLVSDAT-----AAVLGHADASEIAPTTTFKDLGIDSLT 3387
                                                                                                                                                                                                                                                                                     3388 AIELRNKLAEÄTGLRLSATLVFÖHPTPRVLAAKLKTDLFGTAVPTPARTARTHHDEPLAI 3447
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                                                                                                                                                                                                                              74 -- RLRVRITDA------DHP-----RWEVPQDIIPRPA-PGDVLHDAPPA- 109
                                                                                                                                                                                                                                                                                                                                                   110 --SSAPLQGRVLSP-----AGSDLVLTVHASPFRFTVSRRSTGDTLFD---TAPGLV 156
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         157 F--RDKYLEVTSALPAG-RASLYGLGEHTKSSFRLRHNDSF-TLWNADIGASYVDVNLYG 212
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                                                                                                     16 FAPRLCSSKEEGPLAARTVLAVAVTMEGALRAEAATGGRSSTGDVQRLAVYASLETDS--
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   20.4%; Pred. No. 0.4;
tive 73; Mismatches 294; Indels 357;
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                                       Matches 186; Conservative
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      Best Local Similarity
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US-09-198-452A-966
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GENERAL INFORMATION:
APPLICANT: REEVES, CHRISTOPHER
APPLICANT: REEVES, CHRISTOPHER
APPLICANT: RHOSLA, CHRISTOPHER
APPLICANT: SANTI, DANIEL
APPLICANT: SANTI, DANIEL
APPLICANT: SANTI, DANIEL
APPLICANT: WU, KAI
ITILE OF INVENTION: CONSTRUCTS THEREFOR
ITILE OF INVENTION: CONSTRUCTS THEREFOR
FILE REFRENCE: 30662-20026.00
CURRENT APPLICATION NUMBER: US 60/139,650
PRIOR FILING DATE: 1999-06-11
PRIOR FILING DATE: 1999-06-11
PRIOR FILING DATE: 1999-06-11
PRIOR FILING DATE: 1999-03-11
PRIOR FILING DATE: 1999-03-11
PRIOR FILING DATE: 1998-10-02
NUMBER OF SEQ ID NOS: 72
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 72
LENGTH 6396
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TITLE OF INVENTION: Plant Alpha-Glucosidase II Homologs FILE REFERENCE: BB1273 US NA CURRENT APPLICATION NUMBER: US/09/437,054A CURRENT FILING DATE: 2001-05-14 PRIOR APPLICATION NUMBER: 60/107,909 PRIOR FILING DATE: 1998-No. 6316698ember-10 NUMBER OF SEQ ID NOS: 19 SOFTWARE: Microsoft Office 97 SEQ ID NOS: 19 SEQ ID NOS: 10 SEQ ID NOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DB 4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            4.2%; Score 195.5; DB 4 30.4%; Pred. No. 3.2e-11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           27; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               : Streptomyces hygroscopicue
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                                                                                                                                                                                                                                                                                                                      TYPE: PRT ORGANISM: Triticum aestivum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity 30.44
Matches 49; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                            (73)..(74)
UNSURE
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US-09-437-054A-10
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Sequence 966, Application US/09198452A Patent No. 6559294 GENERAL INFORMATION:

Score 122.5; DB 4; Length 6396;

2.6%;

Query Match

4047

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TITLE OF INVENTION: Chlamydia pneumoniae genomic sequence and polypeptides, fragments TITLE OF INVENTION: thereof and uses thereof, in particular for the diagnosis, preve TITLE OF INVENTION: and treatment of infection FILE REPERENCE: 9710-003-999 CURRENT APPLICATION NUMBER: US/09/198,452A CURRENT FILING DATE: 1998-11-24 NUMBER OF SEQ ID NOS: 6849
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 -----RAPGTAHGVLLLSSN---- 235
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       236 GMDVLYGGSY-----VTYKVIGGVLDFYFFAGP---NPLAVVDQYTQLIARPAP 281
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 166 GHEIFNGKIÝCLAGDGCFMEGVSHEVCS-----FAGSLNLNNLVVIYDYNNVVLD--- 215
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             282 MPYWSFGFHQCRYGYLNVSDLERVVARYAKARIPLEVMWTDIDYMDGFKDFTLDRVNFTA 341
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 342 AELRPFVDRLHRNAQKYVL----ILDPGIRVDPIDATYGTFVRGMQQDIFLKRNGTNFV 396
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                255 ------IKRGQERPVLVIAHIIGHGSPKEGTNKAHGSPL-GVE-----GTHET 296
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          448
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    297 KQFW----HLPEEKFFVPPAVKNFFAHKIQEDRK---AQEQWLDEVRVWSKQFPELHEBF 349
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 -----PMN-----ALDDPPYRINNDGTGRPINNKTVRPLAVH----YGGVTEYEEH 490
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             350 VALTSHKLPKNLESLVQSVEMP-----DSIAGRAASNKLIQVLVQHIPYLIGGSADLSS- 403
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       491 NLFGLLEARATGRGVLRDTGRRPFVLSRSTFVGSGR---YTAYWTGDNAATWGDLRYSINT 548
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     549 MLSFGLFGMPMIGADICGFNGNTTEELCGRWIQLGAFYPFSRDHSAIFTVRRELYLWPSV 608
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        723 GTILPLOOSALTTSRARRTAFHLLVALAEDGTASG-YLFL-DDGDSPEYGRRSDWSYVRF 780
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                                                                                                                                                                                                                                                                                                                                                                                                                                    106 DVSLEDLQEFRQLHSRTPGHPEYGETVGVEATTGPLGQGLGNAVGMALSMKMLESRFNRP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         216 ------GYLNEISVEDTKKRF------EAYGWEYYEIDGY-DFTHIHETFSS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          397 GNVWPGDVYFPD---FMHPAAAEFWAREISLFRKTIPVDGLWIDMNEISNFYNPE----
                                                                                                                                                                                                                                                                                                                                                                                                          168 LPAG----RASLYGLGEHTKSSFRLRHNDSFTLW-NAD---IGASYVDVNLYG----
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                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                               Query Match
2.6%; Score 121.5; DB 4; Length 692;
Best Local Similarity 18.9%; Pred. No. 0.0099;
Matches 140; Conservative 85; Mismatches 209; Indels 305;
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                                                                                                                                                                                                                           TYPE: PRT
ORGANISM: Chlamydia pneumoniae
APPLICANT: Griffais, R.
                                                                                                                                                                                                                                                         ; ORGANISM: CD1ar
US-09-198-452A-966
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Potato alpha-gluco
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An enzyme with sug
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Buckwheat alpha-gi
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2942.169 Million cell updates/sec
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GenCore version 5.1.6
(c) 1993 - 2003 Compugen Ltd.
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Gapop 10.0 , Gapext 0.5
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Match Length DB
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ABBS7174 AAW15191 AAW15191 AAAU9002 AAAU9002 AAAP81191 AAR07575 AAR7575 AAR69611 ABF52437 AAG69611 AAG69611 AAG69611 AAG69611 AAG69610 AAM19580 AAM18580 AAM18580 AAM18580 AAM18580 AAM18580 AAM18580 AAM18580 AAM18580	ABP96616 ABP96615 ABP96615 AAR04869 AAR04869 AAU23490 AAU19420 AAM00087 AAR72711
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ALIGNMENTS 1.1 1040 AAW59040 standard; Protein; 877 AA. AAW59040; 07-AUG-1998 (first entry) Barley alpha-glucosidase; barley; starch grain hydrolysis; alpha-amylase; glucoamylase; industry; germplasm; hydrolytic enzyme. Hordeum vulgare. USS763252-A.

DNA encoding barley alpha-glucosidase protein - useful for producing recombinant protein to increase rate of starch grain hydrolysis when

(WISC) WISCONSIN ALUMNI RES FOUND.

Skadsen RW, Tibbot BK; WPI; 1998-347329/30. N-PSDB; AAV11736.

95US-0430925.

28-APR-1995; 28-APR-1995; N

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                                  This sequence represents a novel barley alpha-glucosidase protein. Recombinant alpha-glucosidase can be used to increase the rate of starch grain hydrolysis when used together with alpha-amylase or can supplement glucoamylase in industrial starch hydrolysis systems. Useful DNA sequence characteristics from this enzyme can be identified which can be used as hybridisation probes for identifying germplasm with high levels of efficient hydrolytic enzymes.
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                                                                                                                                                                                                                                                                                                                    QRLAVYASLETDSRLRVRITDADHPRWEVPQDIIPRPAPGDVLHDAPPASSAPLQGRVLS
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                                                                                                                                                                                     DB 19; Length 877;
                                                                                                                                                                                                                0; Indels
                                                                                                                                                                                  100.0%; Score 4630;
100.0%; Pred. No. 0;
ive 0; Mismatches
         Claim 1; Col 21-26; 19pp; English.
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Best Local Similarity 100.
Matches 877; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A recombinant vector containing alpha-glucosidase gene, a transformant useful for preparation of alpha-glucosidase
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SAGTRYONAGGLGGVAHIGGLSLVVGEEFELKVAMSY
                                                                                                                                                                                                                                                                                                                                                                                                                    Common buckwheat alpha-glucosidase polypeptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Common buckwheat; alpha-glucosidase; enzyme;
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                                                                                                                                                                                                        standard; Protein;
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N-PSDB; ABK86269.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   819 RSPAAPKGLTVHVNSAEVBASSSAGTRYQNAG-GLGGVAHIGGLSLVVGEEFELKVAMS 876
                                                                                                                                                                                                                  7 LLLCLCLCLFAPRLCS---SKEEGPLAA---RTVLAVAVTMEGALRAEAATGGRSST--G
                                                                                                                                                                                                                                                                          DVQRLAVYASLETDSRLRVRITDADHPRWEVPQDIIPRPAPGDVLHDAPPASSAPL---Q
                                                                                                                                                                                                                                                                                           126 AAVLTHPNSDLIFRLHDTNPFGFSVTRRSTNDVLFDTRSADPBTDPVGLVFKDQYIQLSS
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                                                                                                                                                                                                                                             LILILAATILIF----CSLFVVSESGEVVGYGYRVVRAKVDSSSNTLTAFLKLINASSLYGQ
                                                                                                                                                                                                                                                                                                                                                                                        ALPAGRASLYGLGEHTKSSFRLRHNDSFTLWNADIGASYVDVNLYGSHPFYMDVRAP-GT
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                                                           The present sequence represents an alpha-glucosidase isolated from buckwheat (Fagopyrum esculentum Moeench). The alpha-glucosidase gene can be used for the preparation of alpha-glucosidase derived from
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 50.2%; Score 2324.5; DB 23; Length 901; Best Local Similarity 53.2%; Pred. No. 4.8e-192; Matches 478; Conservative 121; Mismatches 259; Indels 41;
       gene
    buckwheat-derived alpha-glucosidase
                                Claim 1; Page 7-9; 21pp; Japanese
                                                                                                                                  901 AA;
                                                                                                    buckwheat
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SFGFHQCRYGYRNVSVVENVVKAYATMRIPLEAIWTDIDYMEANKDFTVDPVNFPLDKMQ
                                                                                                      SGRYTAYWTGDNAATWGDLRYSINTMLSFGLFGMPMIGADICGFNGNTTEELCGRWIQLG
                                                                                                                                                                                                                  AFYPFSRDHSAIFTVRRELYLWPSVAASGRKALGLRYQLLPYFYTLMYEAHMTGAPIARP
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/label= signal
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                                                                                                                                                                                   AFYPFSRDHSAIPTVRRELYLWPSVAASGRKALGLRYQLLPYFYTLMYEAHMTGAPIARP 643
                                                                                                                                                                                                                AFYPFSRDHSDNLSEPQELTQMGSVTESARKVLGLRYRLLPYYYTLMYEAHKKGTPIARP 663
                                                                                                                                                                                                                                                   LFPSYPHDVATYGVDRQFLLGRGVLVSPVLEPGPTTVDAYFPAGRWYRLYDYSLAVAT-R 702
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SRGSQVKGYTM-LSIGRVVTTSAKGARKCSKGTGKFDVVEIPNLSLLVGRNFKLDIQIT 899
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PPDFLNPKTTIPWISEIQTFFNALPVDGLWIDMNEVSNFISSPPIPDSPLDNPPYVINNS
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                                                  GTGRPINNKTVRPLAVHYGGVTEYEEHNLPGLLEARATGRGVLRDTGRRPFVLSRSTFVG
                                                                     SGRYTAYWTGDNAATWGDLRYSINTMLSFGLFGMPMIGADICGFNGNTTEELCGRWIQLG
                                                                                                                                      The present sequence represents an alpha-glucosidase isolated from buckwheat (Fagopyrum esculentum Moeench). The alpha-glucosidase gene can be used for the preparation of alpha-glucosidase derived from
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Buckwheat; alpha-glucosidase; enzyme; Fagopyrum esculentum Moeench;
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/label= alpha_glucosidase
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The invention relates to a recombinant vector containing alpha-glucosidase gene derived from buckwheat. A transformant containing the recombinant vector can be used for preparing alpha-glucosidase by culturing the transformant and isolating alpha-glucosidase from the culture. This sequence represents a buckwheat alpha-glucosidase protein.
842 SRGSQVKGYTM-LSIGRVVTTSVKGARKCSRGTGKFDVVEIPNLSLLVGRNFKLDIQIT 899
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               126 AAVLTHPNSDLIFRLHDTNPFGFSVTRRSTNDVLFDTRSADPETDPVGLVFKDQYIQLSS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            346 PFVDRLHRNAQKYVLILDPGIRVDPIDATYGTFVRGMQQDIFLKRNGTNFVGNVWPGDVY
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        49.6%; Score 2297.5; DB 23; Length 901; 54.2%; Pred. No. 1.1e-189;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A recombinant vector containing alpha-glucosidase gene, a transformant useful for preparation of alpha-glucosidase
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                                                                                                                                                                                   Common buckwheat alpha-glucosidase polypeptide #2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          231;
                                                                                                                                                                                                                    buckwheat; alpha-glucosidase; enzyme;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Conservative 124; Mismatches
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                                                                                   AAU97732 standard; Protein; 901
                                                                                                                                                                                                                                                                                                                                                                                                                                     (NISO ) NIPPON SHOKUHIN KAKO
                                                                                                                                                                                                                                     Pagopyrum esculentum Moeench
                                                                                                                                                                                                                                                                                                                                                                      31-AUG-2000; 2000JP-0262104
                                                                                                                                                                                                                                                                                                                                                                                                     31-AUG-2000; 2000JP-0262104
                                                                                                                                                   (first entry
                                                                                                                                                                                                                                                                     Fagopyrum esculentum
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                                                                                                                                                   23-AUG-2002
                                                                                                                                                                                                                                                                                                                                     05-MAR-2002
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                                                                                                                    AAU97732;
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Matches
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Potato alpha-glucosidase protein fragment
                                                                                                                                                                                                (AGRE ) HOECHST-SCHERING AGREVO GMBH.
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                                                                                                                                                     98DE-1036097.
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Matches 376; Conservative
                                                                                                                                                                                                                                            WPI; 2000-225174/20.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       682 AA;
                                                                                Solanum tuberosum
                                                                                                                                                                                                                                                       N-PSDB; AAZ89108
                                                                                                       DE19836097-A1
                                                                                                                                                   31-JUL-1998;
                                                                                                                                                                         31-JUL-1998;
                                                                                                                                                                                                                       Frobberg C;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   663
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LFFSYPHDVATYGVDRQFLLGRGVLVSPVLEPGPTTVDAYFPAGRWYRLYDYSLAVAT-R 702
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SRGSQVKGYIM-LSIGRVVTTSAKGARKCSKGTGKFDVVEIPNLSLLVGRNFKLDIQIT 899
                                                                                                          167 ALPAGRASLYGLGEHTKSSFRLRHNDSFTLWNADIGASYVDVNLYGSHPFYMDVRAP-GT
                                                                                                                                                                                                  SLPADRSNLYGIGEHTKPTFRLARNOTLTLWNADIASYNVDLNLYGSHPFYLDVRAPLGT
                                                                                                                                                                                                                                 AHGVLLLSSNGMDVLYGGSYVTYKVIGGVLDFYFFAGPNPLAVVDQYTQLIARPAPMPYW
                                                                                                                                                                                                                                            SHGVLLLNSNGMDVBYTGDKITYKVIGGIVDLYVFEGPTPDEVVQQYTELIGRPAPMPYM
                                                                                                                                                                                                                                                                              SFGFHQCRYGYLNVSDLERVVARYAKARIPLEVMWTDIDYMDGFKDFTLDRVNFTAAELR
                                                                                                                                                                                                                                                                                                    306 SFGFHQCRYEYRNISVVENVVKAYSTWRIPLEAMWTDIDYMEANKDFTVDPVNFPLDKMQ
                                                                                                                                                                                                                                                                                                                                         366 RFVNKLHKNGQKYVAILDPGININ--TTTYGTFQRAMKADIPIKRQGEPYQGEVWFGFVY
                                                                                                                                                                                                                                                                                                                                                                       FPDFMHPAAAEFWAREISLFRRTIPVDGLWIDMNEISNFYN--PEPMNALDDPPYRINND
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                                                                                                                                                                                                                                                                                                                                                                                                                                GGRRPINEKTIPVSSVHYGNVSDYNVHNLYGYLEATATNVALKKVTKQRPFVLSRSTFIG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                             604 AFYPFSRDHSDNLSEPQELTQWGSVTESARKVLGLRYRLLPYYYTLMYEAHKKGTPIARP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TGKHVRLPAPADTVNVHLTGGTILPLQQSALTTSRARRTAFHLLVALAEDGTAS--GYLF
                                                                                           59 DVQRLAVYASLETDSRLRVRITDADHPRWEVPQDIIPRPAPGDVLHDAPPASSAPL---Q
                                                                                                                                        GRVLSPAGSDLVLTVH-ASPFRFTVSRRSTGDTLFDTAP-----GLVFRDKYLEVTS
                                                                                                                                                                                                                                                                                                                          PFVDRLHRNAQKYVLILDPGIRVDPIDATYGTFVRGMQQDIFLKRNGTNFVGNVWPGDVY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                819 RSPAAPKKLTVHVNSAEVEASSSAGTRYQNAG-GLGGVAHIGGLSLVVGEEFELKVAMS
                                                                     Gaps
                                                                     29;
                                              DB 23; Length 901;
                                                                    455; Conservative 124; Mismatches 231; Indels
                                              49.6%; Score 2297.5; DB 23 54.2%; Pred. No. 1.1e-189;
                                                          Similarity
                         901 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       544
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buckwheat
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This invention describes a novel potato alpha-glucosidase (I). (I) is used to produce transgenic plants (or plant to bacterial cells) that produce starch with modified degrees of branching, amylose/amylopectin ratio, phosphate content, starch granule size and/or sidechain structure, and thus altered physical and chemical properties. This starch is used for all usual applications, particularly in preparation of foods, packaging materials and disposable articles, but also for hydrolysis to glucose (for manufacture of other chemicals or for fermentation), in paper/pulp manufacture; in adhesives; for treating textiles; for soil stabilization, as wetting agent in plant protection and fertilizer compositions; as binding agent in plant protection and fertilizer compositions; as binding agent in plant protection and cosmetics; as additive for rubber, building materials, leather and in casting; as floculant for soil or coal slutries; and in polyment as simple filler or reactive component, e.g. in polywrethane foams. Modified starch produced using plants that contain (I) are easily hydrolyzed, reducing the requirement for expensive enzymes. This sequence represents the popure of the requirement for expensive enzymes. This sequence represents the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                284 YWSFGFHQCRYGYLNVSDLERVVARYAKARIPLEVMMTDIDYMDGFKDFTLDRVNFTAAE 343
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         94 YWSFGFHQCRWGYKNIDDVELVVDSYAKSRIPLEVMWTDIDYMDGFKDFTLDPVNFPLER 153
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     VYFPDFMHPAAAEFWAREISLFRRTIPVDGLWIDMNEISNFYN--PEPMNALDDPPYRIN 461
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             6
Alpha-glucosidase; potato; transgenic plant; starch; branching; amylose; amylogectin; granule size; sidechain; food; packaging; hydrolysis; paper; pulp; adhesive; soil stabilization; wetting agent; plant protection; fertilizer.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   New nucleic acid encoding potato alpha-glucosidase, used to produce transgenic plants that contain modified starch \, -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               682;
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57.2%; Pred. No. 1.5e-163;
Live 98; Mismatches 164; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             404
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AAY51670 standard; Protein;

RESULT 6

AAY51670;

01-JUN-2000 (first entry)

Aspergillus niger glucosylti GTase; glucoamylase; GAase; N-terminal deletion; C-termi Aspergillus niger #499.	X & X & X & X & X & X & X & X & X & X &	Zue 3e E
	XXXX	
RESULT 8 ARAR4214 ID AAR42214 standard: Protein:	RESI AAR4 ID	PT Prepn. of glucosyl:transferase - using glucosyl:transferase gene PT from recombinant DNA of Aspergillus niger XX Disclosure; Page 6-9: 10pp: Japanese.
: : : : : 855 LPMQBPALTTREARQTPWA	ag ag	R WPI; 1993-364282/46. R N-PSDB; AAG50468. x
796 VPVLBPLVNTVKGVFPGVC	A &	A (JOZU/) UOZUMI T. A (JOZU/) UOZUMI T.
670 SPVLEPGPTTVDAYPPA	ò	7 27-MAR-1992; 92JP-0101760. X
: : :	ପୁ	F 27-MAR-1992; 92JP-0101760.
610 ASGRKALGLRYQLLPYFY	ò	A 19-0CT-1993.
676 LSFSLFGIPMFGADTCGFN	4 0	X
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	ò	Glycosyltransferase.
SAFATTATISTICATION SEEDS AND SEEDS AND SEEDS ASSESSED SEEDS ASSESS	∂ 6	x 16-MAY-1994 (first entry) x
496 SFCVGSCGTGNLTLNPAHE	a :	X AAR42995;
	8	4299 AA
436 DDVFLKNPDGSLYIGAVWE	qu	C:1112
384 QDIFLKR-NGINFVGNVWE	ò	Db 629 VRGLKSYELVGSHQQGNTTMKESLKQSGQFVTMEISGMSILIGKEFKLEL 678
::: : : 376 HGYRNFDNDQHRFSYSEGE	qa	Oy 821 PAAPKKLTVHVNSAEVEASSSAGTRYQNAGGLGGVAHIGGLSLVVGEEFELKV 873
327 DGFKDFTLDRVNFTAAELE	8 8	OY (AZ DUGDEZELGKENEL MENNYEN KALENKASEN WANNEL VERNYEN SEU
268 VVDQY-TQLIARPAPMPYM	ò	511 NGGTYMTLDAPPDHINVHVREGNILVMQGEAMTTQAAQRTAFKLLVVLSSSKNSTGELFV
: 256 YIPVKSSEADASQDYISLS	q	Qy 702 RIGKHVRLPAPADTVNVHLTGGTILPLQQSALTTSRARRTAFHLLVALAEDGTASGYLF: 761
222 -APGTP	8	DD 451 RPLFFSFPQDAKTFDISTQFLLGKGVMISPILKQGATSVDAYFPAGNWFDLFNYSRSVSL 510
:	음	Qy 642 RPLFFSYPHDVATYGVDROFLIGRGYLVSPVLEPGPTTVDAYFPAGRWYRLYDYSLAVAT 701
142 LNASVSQSULFVSWSN 172 RASLYGLGEHTKSSFRLRE	8 8	OY DAG LOAR FESCHOLARIE I VEKEELINPE VALLE TO THE TENTE AND LOAR FESCHOLARIE A 641
114 LOGRVLSPAGSDLVLTVH	ò	Db 331 LGSGRYTSHWTGDNAATWNDLAYSIPTILSFGLFGIPMVGADICGFSSNTTEELCRRWIQ 390
: : : : 95 DVESLTLSVEYQDSDRINI	q a	Oy 522 VGSGRYTAYWTGDRATWGDLRYSINTMLSFGLFGMPMIGADICGFNGNTTEELCGRWIQ 501

59 DVQRLAVYASLETDSRLRVRI----TDADHPRWE-VPQDIIPRRAPGDVLHDAPPASSAP 113

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FNGNTTEELGGRWIQLGAFYPFSRDHSAIFTVRRELYLWPSVA 609
                                             MASP-PRFTVSRRSTGDTLPDT-APGLVFRDKYLEVTSALPAG 171
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              -----KAS 141
                                                                      HNDSFTLWNADIGASYVDVNLYGSHPFYMDVR----- 221
                                                                                                                                     WSFGFHQCRYGYLNVSDLERVVARYAKARIPLEVMWTDIDYM 326
                                                                                                                                                                                                                                                                     LRPFVDRLHRNAQKYVLILDPGIRV-DPIDAT--YGTFVRGMQ 383
                                                                                                                                                                                                                                                                                                                                        |: :|| : : || |: | : : :| :| | |: || 35
3DEFLSKLHESGRYYVPIVDAALYIPNPENASDAYATYDRGAA 435
                                                                                                                                                                                                                                                                                                                                                                                    PGDVYFPDFMHPAAAEFWAREISLFRRTIPVDGLWIDMNEIS 442
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TLMYEAHMIGAPIARPLFFSYPHDVATYGVDROFLLGRGVLV 669
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PAHGVLLLSSNGMDVLYGGSYVTYKVIGGVLDFYFFAGPNPLA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; recombinant production; truncated; minal deletion.
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:: | |: ::::| NIQILPTHVDSTNASWYFLSENLVPRP
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24;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The present sequence represents a sugar transferase protein of Acremonium sp. 84G13. The protein preferably catalyses the glucose transfer of an alpha-1 right arrow 3 bond or the glucose transfer of an alpha-1 right arrow 4 bond to a sugar receptor by reacting with a substrate selected from starch and its decomposition
                                                                                                                                                           796 VPVLEPLVNIVKGVFPGVGHGEVMYDMYIQA-AVDAKPGVNIIISAPLGHIPVYVRGGNI 854
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     59 DVQRLAVYASLETDSRLRVRITDADHPRWEVPQDIIPRPAPGDVLHDAPPASSAPLQGRV 118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DLKDLILEVIYETENRLHVKIODKGNOVYQIPESVFPRP.-------GGS 107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LSPAGSDLVLTVHASPFRFTVSRRSTGDTLFDT-APGLVFRDKYLEVTSALPAGRASLYG 177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  108 IDPESSSIRFAYAEEPFSFNITRADTDEVLFDTSAASIVFESQYLRLRTSIPTD-PYLYG 166
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LGEHTKSSFRLRHNDSF-----TLWNADIGASYVDVNLYGSHPFYMDVRAPGTAHG 228
ASGRKALGLRYQLLPYFYTLMYEAHMTGAPIARPLFFSYPHDVATYGVDRQFLLGRGVLV
                                                                                 SPVLEPGPTTVDAYFPA---GR-WYRLYDYSLAVATRIGKHVRLPAPADTVNVHLTGGTI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 922;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
30.4%; Score 1407.5; DB 20; Length 922;
Best Local Similarity 34.9%; Pred. No. 1.6e-112;
Matches 319; Conservative 133; Mismatches 280; Indele 183;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             New sugar transferase gene and enzyme - useful for catalysing transfer of an alpha-1 right arrow 3 bond to a sugar receptor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Acremonium sp. S4G13; glucose transfer; sugar transferase
                                                                                                                                                                                                             LPLOQSALTISRARRIAFHLLVALAEDGTASGYLFLDDGDS
                                                                                                                                                                                                                                 An enzyme with sugar transferase activity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Claim 1; Pages 13-17; 20pp; Japanese.
                                                                                                                                                                                                                                                                                                                                          922
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                                                                                                                                                                                                                                                                                                                                          AAW88044 standard; Protein;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   256 YIPVKSSEADASQDYISLSHGVFLRNSHGLEILLRRSQKLIWRTLGGGIDLTFYSGPAPAD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    59 DVQRLAVYASLETDSRLRVRI----TDADHPRWE-VPQDIIPRPAPGDVLHDAPPASSAP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            114 LOGRVLSPAGSDLVLTVHASP-FRFTVSRRSTGDTLFDT-APGLVFRDKYLEVTSALPAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   -----GTAHGVLLLSSNGMDVLYGGSYVTYKVIGGVLDFYFFAGPNPLA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         384 ODIFLKR-NGTNFVGNVWPGDVYFPDFMHPAAAEFWAREISLFRRTIPVDGLWIDMNEIS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ---LDDPPYRINNDGTGRPINNKTVRPLAVHYGGVTEYEEHN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                496 SFCVGSCGTGNLTLNPAHPSFLLPGEPGDIIYDYPEAFNITNATEAASASAGASSQAAAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RASLYGLGEHTKSSFRLRHNDSFTLWNADIGASYVDVNLYGSHPFYMDVR-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                       DNA encoding truncated variants of Aspergillus glucosyltransferase is claimed. Deletion from the N- or C-terminal reduces Grase activity of the protein. Specifically, glucoamylase with reduced Grase activity can be prepared. The full-length Grase structural gene was isolated as a 4.3kb Sph1 fragment from chromosomal DNA of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 243; Indels 133;
                                                                                                                                                                                                                         Glucoamylase prepn. with reduced glucosyl-transferase activity using microorganism transformed using plasmids including DNA fragments having deletion of N-end or C-end of Aspergilus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DB 14; Length 985;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          30.5%; Score 1410.5; DB 14
37.3%; Pred. No. 9.6e-113;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Matches 306; Conservative 139; Mismatches
                                                                                                                                                                                                                                                                                                                      Disclosure; Page 6-9; 11pp; Japanese.
                                                                           92JP-0101761
                                      92JP-0101761
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                                                                                                              (AMAN ) AMANO PHARM KK (UOZU/) UOZUMI T.
                                                                                                                                                                                                                                                                                 glucosyl-transferase
                                                                                                                                                                     WPI; 1993-364284/46.
N-PSDB; AAQ50982.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                     gene was iso]
A.niger #499.
                                      27-MAR-1992;
                                                                           27-MAR-1992;
19-0CT-1993
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Ishii Y;

Takahashi Y, Nagata T,

Asai S,

NIHON SCHOOL JURIDICAL PERSON

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The present invention describes a method for examining ischaemic conditions, comprising measuring the expression levels of particular genes (I) in a test sample or determining the expression profile of a gene group in the sample comprising genes selected from (I). The method is useful for examining the ischaemic condition (e.g. compression to ischaemia, occlusive ischaemia or vasospastic ischaemia) by measuring expression levels of particular genes (ABI99202 to ABI9912, encoding the protein sequences in ABB57020 to ABB57314) or by determining the expression profile of a gene group comprising these genes are undicator when screening for ischaemic condition-improving drugs or therapeutics for ischaemic diseases. ABI99913 and ABI99914

The protein requence of ischaemic condition-improving drugs or therapeutics for ischaemic condition related sequence, which are used in the exemplification of the present invention.
                                                                                                                                                            Examining the ischemic condition (e.g. occlusive ischemia) by measuring expression levels of particular genes defined in the specification or by determining the expression profile of a gene group comprising these
                                                                                                                                                                                                                                Claim 2; Page 1154-1158; 2690pp; English
              18-MAY-2001; 2001WO-JP04192
                                       18-MAY-2000; 2000JP-0145977
                                                                                                                       WPI; 2002-034733/04
                                                                                                                                    N-PSDB; ABI99468
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                                                                                             Ishikawa K,
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LG-----AHNDPMRLESVGYIRTFWNQDSYGVPNGANLYGSHPVYIDHRETGT-HG 216
                            VLLLSSNGMDVLY-----GGSYVTYKVIGGVLDFYFFAGPNPLAVVDQYTQLIARPAPMP 283
                                                                               YWSFGFHQCRYGYLNVSDLERVVARYAKARIPLEVMWTDIDYMDGFKDFTLDRVNFTAAE 343
                                                                                                393 VIVFPDWFAENIIQYWNNEFALFFDADEGVDIDGLWIDMNEPSNF----PCNFPCDNPYE 448
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                                                    VLFLNSNGMDVLIDEDEEGGKYLEYNTLGGVLDFYFFVGDSPSKAVEEYGEIAGRPPMQP
                                                                                                                                    LRPFVDRLHRNAQKYVLILDPGIRVDPIDATYGTFVRGMQQDIFLKR-NGTNFVGNVWPG
                                                                                                                                                                                        DVYFPDFMHPAAAEFWAREISLF---RRTIPVDGLWIDMNEISNFYNPEPMNALDDPPYR
                                                                                                                                                                                                                                                                        449 AAKGFPPTPPPVREPPRELPGFACVLQPEGTECEDGETAGSSKRDGSFGQPGLVTRQPGF
                                                                                                                                                                                                                                                                                                   ----INNKTVRPLAVH
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                                                                                                       73
                                                                                                                                           RLRVRITDADHPRWEVPQDIIPRPAPGDVLHDAPPASSAPLQGRVLSPAGSDLVLTVHAS
                                                                                                                                                                                                                                                                                                                  PFRFTVSRRSTGDTLFDT--APGLVFRDKYLEVTSALPAGRASLYGLGEHTKSSFRLRHN
                                                                                                                                                                                                                                                                                                                                                    217 PFGVIVRRKLGGRVLLNTTVAP-LFFADGFLQLSTSLPA--QHITGLGEHLSPLMLSTDW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            274 ARITLWNRDTPPSQ-GTNLYGSHPFYLALEDGGLAHGVFLLNSNAMDVILQPSPALTWRS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             311 KARIPLEVMWTDIDYMDGFKDFTLDRVNFTAABLRPFVDRLHRNAQKYVLILDPGIRVDP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          371 IDATYGTFVRGMQQDIFL-KRNGTNFVGNVWPGDVYFPDFMHPAAABFWAREISLFRRTI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            430 PVDGLWIDMNEISNPYNPE----PMNALDDPPYRINNDGTGRPINNKTVRPLAVHYGGVT
Length 953
                                                                                                                                                                                                                                                                RLHFKIKDPASKRYEVPLE-TPR-----VLSQAP----SPLYSVEFS-
30.3%; Score 1403; DB 23; 38.1%; Pred. No. 4.1e-112;
                         Best Local Similarity 38.1%; Pred. No. 4.1e-112;
Matches 327; Conservative 122; Mismatches 323;
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> Mouse ischaemic condition related protein sequence SEQ ID NO:422 Mouse, ischaemia, compressive ischaemia, occlusive ischaemia, vasospastic ischaemia, ischaemic condition, ischaemic disease

WO200188188-A2 Mus musculus

22-NOV-2001

(first entry)

07-MAR-2002

ABB57174;

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SETAQQAMRKAFALRYALLPYLYTLFHRAHVRGDTVARPLFLEFREDPSTWSVDRQLLMG 747
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                                                                                                                           RGVLVSPVLEPGPTTVDAYFPAGRWYRLYDYSL-------AVATRTGKHV 707
                                                                                                                                                 748 PALLITPVLEPGKTEVTGYFPKGTWYNMQVVSVDSLGTLPSPSSASSFRSAVQSK-GQWL 806
                                                                                                                                                                        767
                                                                                                                                                                                                                    EYGRRSDWSMVRFNYKIPNN------KGAIKVKSEVVHNSYAQSRTLVISKVVLM 816
                                                                                                                                                                                                                                   AVLEHGAYTLVTFSAK--NNTIVNKLVRVTKEGAELOLKEVTVLGVATAPTQVLSNGIPV 924
628 VPDILQFNLLGVPLVGADICGFIGDTSEELCVRWTQLGAFYPFWRNHNDLNSVPQEPYRF
                                                                                                                                                                        RLPAPADTVNVHLTGGT1LPLQQSALTTSRARRTAFHLLVALAEDGTASGYLFLDDGDSP
                                                                                                                                                                                      INTMLSFGLFGMPMIGADICGFNGNTTEELCGRWIQLGAFYPFSRDHSAIFTVRRELYLW
                                                                               PSVAASG-RKALGLRYQLLPYFYTLMYEAHMTGAPIARPLFFSYPHDVATYGVDRQFLLG
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                                                                                                                                                                                                                                                                                                                                                                                                                                        protein
                                                                                                                                                                                                                                                                                                                                                                                                                                      fungal; enhancer element; promoter; recombinant
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327 DGFKDFTLDRVNFTAAELRPFVDRLHRNAQKYVLILDPGIRV-DPIDAT--YGTFVRGMQ 383
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LQQSALTTSRARRTAFHLLVALAEDGTASGYLFLDDGDS--PEYGRRSDWSMVRFNYKIP 785
                                                                                                   114 LOGRVLSPAGSDLVLTVHASP-FRFTVSRRSTGDTLFDT-APGLVFRDKYLEVTSALPAG 171
                                                                                                                                                                                                                                                                                                                                                                                                                                     557
                                                                  ----APGT----AHGVLLLSSNGMDVLYGGSYVTYKVIGGVLDFYFFAGPNPLA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                             ------LDDPPYRINNDGTGRPINNKTVRPLAVHYGGVTEYEHNL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   558 SSTTTSAPYLRTTPTPGVRNVDHPPYVINHVQPGHDLSVHAISPNSTHSDGVQEYDVHSL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FGLFGMPM1GAD1CGFNGNTTEBLCGRW1QLGAFYPFSRDHSA1FTVRRELYLWPSVAAS
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                                                 59 DVQRLAVYASLETDSRLRVRIT----DADHPRWEV-PQDIIPRPAPGDVLHDAPPASSAP
                                                                                                                                                      RASLYGLGEHTKSSFRLRHNDSFTLWNADIGASYVDVNLYGSHPFYMDVR------
                         157;
 DB 18; Length 985
           Best Local Similarity 34.1%; Pred. No. 2.3e-107;
Matches 312; Conservative 158; Mismatches 289; Indels
29.1%; Score 1348.5; 34.1%; Pred. No. 2.3e
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RESULT 12 AAW74090 ID AAW7

Aspergillus oryzae contains two novel enhancer elements: one (designated "enhancer-B") corresponds to the consensus sequence CGGNNATTA and the other (designated "enhancer-C") is of sequence CCGNNATTA and the other (designated "enhancer-C") is of sequence CCAATCAGCGT. By inserting at least one of the enhancer elements into a promoter region which is functional in fungi, the activity of the promoter is enhanced Using such improved promoters, a gene of interest can be expressed efficiently in transformed fungi. The present sequence is encoded by the agdA gene.

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985

Sequence

AAW74090 standard; Protein; 1827 AA.

us-10-043-418-1.rag

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532 PDILDKLMYSKTICMDAVQNMG-KQYDVHSLYGYSMALATEQAVQKVFPNKRSFILTRST 590
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            238 IYGIGEQVHK--RFRHDLSWKTWPIFTRDQLPGDNNNNLYGHQTFFMCIEDTSGKSFGVF 295
                                                                                                     290 HQCRYGYLMVSDLERVVARYAKARIPLEVMMTDIDYMDGFKDFTLDRVNFTAAELRPFVD 349
                                                                                                                         356 QLSRWNYKSLDVVKEVVKRNREAGIPFDTQVTDIDYMEDKKDFTYDQVAFNG--LPQFVQ 413
                                                                                                                                                                       RLHRNAQKYVLILDPGIRVD - PIDATYGTFVRGMQQDIFLKRN - -GINFVGNVWPGDVY 405
                                                                                                                                                                                             414 DLHDHGQKYVILLDPAISIGRRANGTTYATYERGNTQHVWINESDGSTPIIGEVWPGLTV 473
                                                                                                                                                                                                                                                               NDGTGRPINNKTVRPLAVHYGGVTEYBEHNLFGLLEARATGRGVLR-DTGRRPFVLSRST 520
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DCTASGYLFLDDGDSPEYGRRSDWSMVRFNYKIPNNKGAIKVKSEVVHNSYAQSRTLVIS 811
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                                                                                                                                                                                                                                        FPDFMHPAAAEFWAREISLFRRTIPVDGLWIDMNEISNFYNPEP----MNALDDPPYRIN 461
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LLSSNGMDV-LYGGSYVTYKVIGGVLDFYFFAGPNPLAVVDQYTQLIARPAPMPYWSFGF
                                                                                                                                                                                                                                                                                                                                                                                                                                              QLGAFYPFSRDHSA----IFTVRRELYLWPSVAASGRKALGLRYQLLPYFYTLMYE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               This sequence is the human hSI protein. The invention relates to purified proteins (I) that bind specifically to at least one of the gastro-intestinal (GI) tract receptors human intestinal opeptide-associated transporter (HPTI), hEPETI, D2H and human beptide-associated transporter (HPTI), hEPETI, D2H and human concerisomaltase complex (hSI). (I) provide active transport of therapeutic agents through human and animal GI tissue (into the blood) for in vivo delivery, particularly for treatment or prevention of hypertension, diabetes, osteoporosis, haemophilia, anaemia, cancer, insulin or leuprolide, but many other suitable therapeutic agents are disclosed, including genes or inhibitory nucleic acid, imaging agents and antibodies (I) are: (I) to death of specified receptors in a sample (II) are: (I) to death of (II) tract. Other uses of (II) are: (I) to death of (II) tract. Other uses of (II) are used to that bind (II). Immunogenic analogues or derivatives of (II) are used to raise antibodies and in immunoassays. The antibodies are used to locate, detect and measure (II), e.g. for imaging monitoring treatment, tissue analysis etc., also for peptide purification and immobilisation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    23;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           175 LYGLGEHTKSSFRLRHNDSFTLW---NADIGASYVDVNLYGSHPFYMDVR-APGTAHGVL 230
                                                                                                                                    D2H; hPEPT1; human; GI tract receptor; sucrose-isomaltase complex; intestinal peptide-associated transporter; hypertension; diabetes; osteoporosis; haemophilia; anaemia; cancer; migraine; angina pectoris; therapeutic agent delivery; therapy; probe.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        | : : | : | : | : | : | | : | DINSVLETTQNQTPNRFRFKITDPNNRRYEVPHQYVKEFTGPTVSDTLYD-------
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                                                                                                                     Gastro-intestinal transport receptor; binding protein; hSI; HPTI;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                antibodies, used to deliver therapeutic or diagnostic agents to, through, the gastrointestinal tract, e.g. insulin or leuprolide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                New proteins that bind specifically to receptors in the gastro-intestinal tract and related nucleic acid - chimaeras and antibodies, used to deliver therapeutic or diagnostic agents to,
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J;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  28.7%; Score 1329.5; DB 2 36.4%; Pred. No. 2.7e-105;
                                                                                                                                                                                                                                                                                                                                                                                                                                              Cagney GM,
Singleton
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                                                                                                                                                                                                                                                                                                                             98WO-US10088
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Patterson CA,
                                                                                   Human hSI protein sequence.
                                                   (first entry)
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307; Conservat
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                                                   04-MAY-1999
                                                                                                                                                                                                                                                          409851325-A2
                                                                                                                                                                                                                                                                                                                                                            .5-MAY-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                            Alvarez VL,
Omahony DJ,
                                                                                                                                                                                                                                                                                          19-NOV-1998
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The invention relates to isolated polynucleotide (I) and polypeptide (II) sequences. (I) is useful as hybridisation probes, polymerase chain reaction (PCR) primers, oligomers, and for chromosome and gene mapping, and in recombinant production of (II). The polynucleotides are also used in diagnostics as expressed sequence tags for identifying expressed genes. (I) is useful in gene therapy techniques to restore normal activity of (II) or to treat disease states involving (II). (II) is useful for generating antibodies against it, detecting or quantitating a polypeptide in tissue, as molecular weight markers and as a food supplement. (II) and its binding partners are useful in medical imaging of sites expressing (II). (I) and (II) are useful for treating dischers involving aberrant protein expression or biological activity. The polypeptide and polynucleotide sequences have applications in diagnostics, forensics, gene mapping, identification of mutations
                         |||: | : |||: | : | :: | :|| AHVFGETVARPVIHEFYEDTNSWIEDTBFLMGPALLITPVIKQGADTVSAYIPDAIW--- 762
                                                                                                                AHMTGAPIARPLFFSYPHDVATYGVDRQFLLGRGVLVSPVLEPGPTTVDAYFPAGRWYRL
                                                                                      YDY-SLAVATRIGKHVRLPAPADTVNVHLIGGIILPLQQSALTISRARRIAFHLLVALAE
                                                                                                                                                                               752 DGTASGYLFLDDGDSPEYGRRSDWSMVRFNYKIPNNKGAIKVKSEVVHNSYAQSRTLVIS
                                                                                                                                                                                                                                                                     812 KVVLMGHRSPAAPKKLTVHVNSAEVEASSSAGTRYON--AGGLGGVAHIGGLSLVVGEEF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         New isolated polynucleotide and encoded polypeptides, useful in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits and to assess
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human; chromosome mapping; gene mapping; gene therapy; forensic; food supplement; medical imaging; diagnostic; genetic disorder.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Novel human diagnostic protein #14985
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ABG14994 standard; Protein; 1829 AA.
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2000US-0649167.
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TVKILG-
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23-AUG-2000;
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                                                                                                                                                                                                                                                                                                                                                                                                                                              metastatic colorectal cancer or primary and/or metastatic sconach or oesophageal cancer cells, also to confirm identification of such cells. These cancers can be treated by administration of an SI ligand and (optionally conjugated) cytostatic agent or radioimaged by administering a conjugate of the SI ligand and detectable agent. The present sequence
                                                                                                                                                                          In vitro screening for specific gastrointestinal cancer cells, useful for diagnosis, by detecting expression of the markers SI, CDX1 or CDX2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              59 DVQRLAVYASLETDSRLRVRITDADHPRWEVPQDIIPR---PAPGDVLHDAPPASSAPLQ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       238 IYGIGEQVHK--RFRHDLSWKTWPIFTRDQLPGDNNNNLYGHQTFFMCIEDISGKSFGVF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              296 LMNSNAMEIFIQPTPIVTYRVTGGILDFYILLGDTPEQVVQQYQQLVGLPAMPAYWNLGF
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                                                                                                                                                                                                                                                                                                                invention relates to in vitro screening of metastatic colorectal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       28.7%; Score 1329.5; DB 22; Length 1827; 36.4%; Pred. No. 2.7e-105;
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                                                                                                                                                                                                                                                                 Disclosure; Page 114-119; 119pp; English.
                     (UYJE-) UNIV JEFFERSON THOMAS.
                                                               Waldman SA, Park J,
                                                                                                           WPI; 2001-611641/70
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              represents human SI
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                                                                                                                                                                                                                                                                                                                                                                    240 IYGIGEQVHK--RFRHDLSWKTWPIFTRDQLPGDNNNNLYGHQTFFMCIEDTSGKSFGVF 297
responsible for genetic disorders or other traits to assess biodiversity
                                                            printed
from WIPO
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                                                                                                                                                                                                                                                                                                                                                                                                    LLSSNGMDV-LYGGSYVTYKVIGGVLDFYFFAGPNPLAVVDQYTQLIARPAPMPYWSFGF
            and to produce other types of data and products dependent on DNA and amino acid sequences. ABG00010-ABG30377 represent novel human diagnostic amino acid sequences of the invention.

Note: The sequence data for this patent did not appear in the printed specification, but was obtained in electronic format directly from WI at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                     Gaps
                                                                                                                                                      DB 22; Length 1829;
                                                                                                                                                                                                                                   tch 28.7%; Score 1329.5; DB 22 al Similarity 36.4%; Pred. No. 2.7e-105; 307; Conservative 144; Mismatches 309;
                                                                                                                         1829 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The present sequence represents Endomyces fibuliger (also called Saccharomycopsis fibuligera) glucoamylase GLAZ. The invention describes the recombinant GLAZ enzyme, which is useful for hydrolysing carbohydrate-containing materials, especially materials containing rice carbohydrates. The glucoamylase is used to produce glucose and alcohol from starch containing raw materials. GLAZ is useful for hydrolysing carbohydrate containing materials e.g. mixtures of a source of proteins and a source of carbohydrates, especially a mixture of leguminous plant or of a cooked oleaginous plant and of a cooked or roasted cereal source e.g. a mixture of soya or cooked beans and of cooked or roasted wheat or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        78 VITTAKGLIGILKINEATNIYGYDFDYLNLSV--EYQSDDRLNVHIEPVDTDNVFILPES
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                                                                                                                                                                                                                                                                                                                Endomyces fibuliger; glucoamylase; GLA2; hydrolysis; carbohydrate;
glucose; alcohol; starch; leguminous plant; cooked; oleaginous plant;
roasted; cereal; soya; wheat; rice.
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                                                                                                                                                                                                                                                       Endomyces fibuliger glucoamylase GLA2 protein.
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28.7%; Soc
Best Local Similarity 36.1%; Pre
Matches 296; Conservative 133;
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Search completed: October 27, 2003, 10:25:23 Job time: 54.3131 secs

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091gc6 oryza sativ
09avc3 physcomitre
09zp26 arabidopsis
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09lec9 solanum tub
09zp04 tropaeolum
09lzt7 arabidopsis
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0911y2 hordeum vul
08vwv9 pinus pinas
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O8iwe7 homo sapien
                                                    October 27, 2003, 10:19:13 ; Search time 62:5261 Seconds (without alignments) 3772:184 Million cell updates/sec
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GenCore version 5.1.6 (c) 1993 - 2003 Compugen Ltd.
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O22444
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Q9AVC3
Q9ZP26
Q9S7Y7
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ALIGNMENTS

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Arabidopsis thaliana (Mouse-ear cress).
Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, eudicotyledons, core eudicots, Rosidae,
eurosids II, Brassicales, Brassicaceae, Arabidopsis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
Shinn P., Chen H., Cheuk R., Kim C.J., Koesema E., Meyers M.C.,
Banh J., Bowser L., Carninci P., Dale J.M., Goldsmith A.D.,
Hayashizaki Y., Ishida J., Jiang P.X., Jones T., Kamiya A.,
Karlin-Neumann G., Kawai J., Lam B., Lee J.M., Lin J., Liu S.X.,
Miranda M., Narusaka M., Nguyen M., Onodera C.S., Palm C.J.,
Pham P.K., Quach H.L., Sakurai T., Satou M., Seki M., Southwick A.,
Tang C.C., Toriumi M., Yamada K., Yamamura Y., Yu G., Yu S.,
Shinozaki K., Davis R.W., Theologis A., Ecker J.R.;
                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.

Bevan M., Hilbert H., Braun M., Holzer B., Brandt A., Duesterhoeft, Hilbert T., Newes H.W., Rudd S., Lemcke K., Mayer K.F.X.; Submitted (APR-2000) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Cheuk R., Chen H., Kim C.J., Shinn P., Bowser L., Carninci P., Chan M.M., Chang C.H., Dale J.M., Hayashizaki Y., Hsuan V.W.,
                                                                                                                                                                                                                                                                                                                                                                                                                        EU Arabidopsis sequencing project;
Submitted (APR-2000) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Submitted (AUG-2001) to the EMBL/GenBank/DDBJ databases.
                                                                        01-0CT-2000 (TrEMBLrel. 15, Created)
01-0CT-2000 (TrEMBLrel. 15, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
Alpha-glucosidase 1 (ATSg11720/T22P2Z_110).
                                       902 AA
                                       PRT;
                                       PRELIMINARY;
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842 VMDKITILGLKRRVKIKEYTVQKDAGAIKVKGLGRRTSSHNQGGFFVSV-ISDLRQLVGQ 900
                                                                                  LDOYTKLIGRPAPMPYWAFGFHQCRWGYRDVNEIBTVVDKYAEARIPLEVMWTDIDYMDA 363
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       12 PTLAVVLPLVLCMVVEGATTSKNDNQGEAIGYGYGVKNAKVDNSTGKSLTALLQLIRNSP
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MEDLINE-9845620; PubMed-9411456;
MEDLINE-9845620; PubMed-9411456;
MONTOCO J.D., Hall B.D., Gough C.M., Stephen A.L.;
"Nucleotide sequence of an alpha-glucosidase gene (Accession Marolatole sequence of an alpha-glucosidase gene (Accession Pho14806) from Arabidopsis thaliana (PGR97-141).";
Plant Physiol. 115:863-863(1997).
EMBL, AFO14806; ARB82656.1;
InterPro: IPR000322; Glyco hydro_31.
Pran: PF01055; Glyco hydro_31; 1.
PROSITE; PS00129; GLYCOSYL_HYDROL_F31_1; 1.
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Matches 515; Conservative 146; Mismatches 220; Indels
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Last annotation update)
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A Ishida J., Jones T., Kamiya A., Karlin-Neumann G., Kawai J., Lam B.,
Lee J.M., Lin J., Miranda M., Narusaka M., Nguyen M., Palm C.J.,
Quach H.L., Sakurai T., Satou M., Seki M., Southwick A., Tang C.C.,
T. Tarbinai M., Wallender E.K., Wong C., Wu H.C., Yamada K., Yu G.,
Yuan S., Shinozaki K., Davis R.W., Theologis A., Ecker J.R.;
T. Arabidopsis ORF clones.";
Submitted (NOV-2002) to the EMBL/GenBank/DDBJ databases.
EMBL, AL163814; CAB87690.1;
EMBL, AL163814; CAB87690.1;
EMBL, BY00222; AANY2233.1;
EMBL, BY00222; AANY2233.1;
EMBL, BY00222; AANY2233.1;
EMBL; PRO0222; AANY2233.1;
EMBL; PRO0229; Glyco hydro 31.
PROSITE; PS001099; GLYCOSYL, HYDROL, F31.2;
PROSITE; PS001707; GLYCOSYL, HYDROL, F31.2;
PROSITE; PS001707; GLYCOSYL, HYDROL, F31.2;
EMBLG PS01705 AA, 101118 MW, DB56817DAA000B3B CRC64;
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VVLPLVLCMVVEGATTSKNDNQGEAIGYGYQVRNAKVDNSTGKSLTALLQLIRNSPVYGP 75
                        YLQLSSSLPAQQAHLYGLGEHTKPTFQLAHNQILTLWNADIASFNRDLNLYGSHPFYMDV
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                                                                            DIHFLSPTASFEEDDTLRIRFTDANNRRWEIPNEVLPRPPPPP---SPPPLSSLQHLPKP
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Pinus pinaster (Maritime pine).
Eukaryota: Viridiplantae: Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Coniferopsida; Coniferales; Pinaceae; Pinus.
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Last sequence update)
Last annotation update)
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                  GNPYLGSVWPGPVYYPDFLDPAARSFWVDEIKRFRDILPIDGIWIDMNEASNFITSAPTP
                                                                                            GSTLDNPPYKINNSGGRVPINSKTIPATAMHYGNVTEYNAHNLYGFLESQATREALVRPA
                                                                                                                GKRPFILSRSTFVSSGKYTAHWTGDNAAKWEDLAYSIPGILNFGLFGIPWVGADICGFSH
                                                                                                                                                                                                                                                                      VSLSNYTSSVSVSAGTYVSLSAPPDHINVHIHEGNIVAMQGEAMTTQAARSTPFHLLVVM
                                                                                                                                                                                                                                                                                                                                                                                                                               FDLFNYSFAVGGDSGKHVRLDTPADHVNVHVREGSIVAMQGBALTTRDARKTPYQLLVVA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            VMDXITILGLKRRVKIKEYTVQKDAGAIKVKGLGRRTSSHNQGGFFVSV-ISDLRQLVGQ
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"Purification, enzymatic characterization, and nucleotide sequence of a high-isoelectric-point alpha-glucosidase from barley malt.";
Plant Physiol. 123:55-286 (2000).
EMBL, AF18226, AAF76254.1;
InterPro; IPR000322; GJyco.hydro.31.
InterPro; IPR002052; N6 Mtase.
PROSITE; PS00129; GLYCOSYL HYDROL F31.1;
PROSITE; PS00109; GLYCOSYL HYDROL F31.2; 1.
SEQUENCE 879 AA; 96558 MW; AF9235ECE7D15B44 CRC64;
                                        GEPYLGEVWPGKVYFPDFLNPAAATFWSNEIKWFQEILPLDGGLWIDMNELSNPITSPLSS
                                                                                                                                                                                                                                                                                                                            MYDANLRGSPIARPLSFTFPDDVATYGISSQFLIGRGIMVSPVLQPGSSIVNAYSPRGNW
                                                                                                                                                                                                                                                  STTEELCCRWIQLGAFYPFSRDHSARDTTHQELYLWESVAASARTVLGLRYELLPYYYTL
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01-0CT-2000 (TrEMBLrel. 15, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
Migh pI alpha-glucosidase.
AGL97.
Hordeum vulgare (Barley).
Bukaxyota, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooideae; Triticeae; Hordeum.
NCBL TaxID=4513;
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Best Local Similarity 53.6%; Pred. No. 2.4e-180;
Matches 480; Conservative 149; Mismatches 235;
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STRAIN-cv. Igri;
MEDLINE-20267959; PubMed=10806244;
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894 KFEMRL 899
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QGEAMTTQAARSTPFHLLVVMSDHVAST----GELFLDNGIEMDIGGPGGKWTLVRFFA 817
                                     754 QRGGMTTTVARMTPFTLIIAFPLGFQSTGGKAKGHLFLDSGEDVDMKIAEGKSTYVDFSA 813
                                                                                                       814 ESDGKKVRLVSQVESGSYGLSQGWVVEKLMILGLSKSHLSSQIAFQLDGKPFTSSSFTYS 873
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  317 MPYWAFGFHQCRWGYRDVNEIETVVDKYABARIPLEVMWTDIDYMDAFKDFTLDPVHFPL 376
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          296 MPYWARGFHQCRWGYKNLSVVEGVVEGYRNAQIPLDVIWNDDDHMDAAXDFTLDPVNYPR 355
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       257 MVGSTHGVFLLNSNGMDVEYTGDRITYKVIGGIIDLYIFAGRTPEMVLDQYTKLIGRPAP
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Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
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                                                                                                                                                                                                                                                                                                                                                     01-0cT-2000 (TrEMBLrel. 15, Created)
01-0cT-2000 (TrEMBLrel. 15, Last sequence update)
01-0cT-2002 (TrEMBLrel. 22, Last annotation update)
BST AU092739 (C53221) corresponds to a region of the predicted
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                                                                               ESGINNLTISSEVVNRGYAMSQRWVMDKITILGLKRRVKIKEYTVQKD-
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al Similarity 44.1%; Score 2058.5; DB 10; Length
al Similarity 44.1%; Pred. No. 8.4e-148;
407; Conservative 164; Mismatches 277; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
STRANIE-CV. Nipponbare;
Sasaki T., Mateumoro T., Yamamoto K.;
"Oryza sativa nipponbare(GA3) genomic DNA, chromosome 1,
clone:POSO4H10.",
Submitted (JUN-2000) to the EMBL/GenBank/DDBJ databases.
EMBL; AP002526; BAA99366.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gramene; Q9LGC6; -.
InterPro; IPR000322; Glyco hydro_31.
Pfam; PF01055; Glyco_hydro_31, PF0 Pfam; PF01055; Glyco_hydro_31, F31, 1; 1.
PROSITE; PS001229; GlycoSYL HYDROL F31, 1; 1.
SEQUENCE 929 AA; 102550 MW; S36EID0B9D7F97BF CRC64;
                                                                                                                                                                                           VKGLGRRTSSHNQGGFFVSVISDLRQLVGQAFKL 904
                                                                                                                                                                                                                                                                                                                  PRELIMINARY;
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Oryza sativa (Rice)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            138 PTTTVLSHPHSDLAFTL------FHTTPFGFTIYRKSTHDVLFDATPIPSNPTTF 186
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          217
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  HPFYMDVRSSPMVGSTHGVFLLNSNGMDVEYTGDRITYKVIGGIIDLYIFAGRTPEMVLD 305
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        QYTKLIGRPAPMPYWAFGFHQCRWGYRDVNEIETVVDKYAEARIPLEVMWTDIDYMDAFK 365
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PYLGSVWPGPVYYPDFLDPAARSFWVDEIKRFRDILPIDGIWIDMNEASNFIT---SAPT 482
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ----PGSTL------DNPPYKINNSGGRVPINSKTIPATAMHYGNVTEYN 522
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      574
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 VSPVLQPGSSIVNAYSPRGNWVSLSNYTSSVSVSAGTYVSLSAPPDHINVHIHEGNIVAM 762
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       62
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             78 HFLSFTASFEEDDTLRIRFTDANNRRWEIPNEVLPRPPPPSPPPSSLOHLPKPIPONO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    -----AKSAFEFSKFAGGELIVSFISNPFGFAIKRKSNGDVLFNSS-----YGN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LIYKDQYLQLSSSLPAQQAHLYGLGEHTKPT-FQLAHNQILTLWNADIASFNRDLNLYGS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DFTLDPVHFPLDKMQQFVTKLHRNGQRYVPILDPGINTNKSYGTFIRGMQSNVFIKRNGN
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                                                                                                                                                                                                                                                                                                                                                                                                                                         18 LPLVLCMVVEGATTSKNDNQGEAIGYGYQVKNAKVDNSTGKSLTALLQLIRNSPVYGPDI
                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                    81;
                                                                                                                                                                                                                                                                                                                                                        45.1%; Score 2191.5; DB 10; Length 910; 47.6%; Pred. No. 5.9e-158;
                                                                                                     and
                                                  TISSUE=Etiolated hypocotyl;
Sanchez M., Gianzo C., Sampedro J., Revilla G., Zarra I.;
Changes in alpha-xylosidase gene expression during intact induced growth of pine hypocotyls,";
Submitted (NOV-2001) to the EMBL/GenBank/DDBJ databases.
REMBL; AF48201; AAL40352.1;
InterPro; IPR001322; Glyco_hydro_31.
RILE**Pro; IPR001032; Hill basic.
Rema; PF01055; Glyco_hydro_31; 1.
RPROSITE; PS00129; GLYCOSYL,HYDROL_F31_2; 1.
RPROSITE; PS00707; GLYCOSYL,HYDROL_F31_2; 1.
RPROSITE; PS00703; GLYCOSYL,HYDROL_F31_2; 1.
SROGITE; PS00703; HILH 1; 1.
SEQUENCE 910 AA; 100609 MW; C4B75C7306CC16F9 CRC64;
                                                                                                     intact
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                                     SEQUENCE FROM N.A.
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73 YGPDIHFLSFTASFEEDDTLRIRFTDANNRRWEIPNEVLPRPPPPPPPPPSSLGHLPKP 132
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                     61 YGPDISPLRMIARYDSDDRLHVHITDSIHARWEVPQDIIPRPDSS-----SLVTHVKG- 113
                                                                                                                                        DFTLDPVHFPLDKMQQFVTKLHRNGQRYVPILDPGINTN-KSYGTFIRGMQSNVFIKRN- 423
                                                                                                                                                                                                                                                                                                                                                                                                                                         RGIMVSPVLQPGSSIVNAYSPRGNWVSLSNYTSSVSVSAGTYVSLSAPPDHINVHIHEGN 758
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          708 RSVLISPIVAEGLTSVNAYFPKGTWYNLFDF--SKIVSTGERRMLPAFADSINVHVSEGQ 765
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       HPFYMDVRSSPMVGSTHGVFLLNSNGMDVEYTGDRITYKVIGGIIDLYIFAGRTPEMVLD 305
                                                                                                                                                                                                                                            QYTKLIGRPAPMPYWAFGFHQCRWGYRDVNEIBTVVDKYAEARIPLEVMWTDIDYMDAFK 365
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SIPTMLNFGLFGMPMIGADICGFAESTTEELCCRWIQLGAFYPFSRDHSARDTTHQELYL 638
                                                                                                                                                                                                                                                                                                                                                                                          408 GNNYLAQVWPGPVYFPDFLHPKASSWWTQEIADFFDKVPFDGLWIDMNEASNPCTGSACS
                                                                                                                                                                                                                                                                                                                                                                                                                        WESVAASARTVLGLRYELLPYYYTLMYDANLRGSPIARPLSFTFPDDVATYGISSQFLIG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        IVANOGEAMITIQAARSTPFHLLVVMS-DHVAS-TGELFLDNGIEMDIGGPGGKWILVRFF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 817 AESGINNLTISSEVVNRGYAMSQRWVMDKITILGL------KRRVKIKBYTVQKD
                                                               133 IPQNQPTTTVLSHPHSDLAFTLFHTT-PFGFTIYRKSTHDVLFDATP---IPSNPTTF--
                                                                                                                       187 LIYKDQYLQLSSSLPAQQAHLYGLGEHTKPT-FQLAHNQILTLWNADIASFNRDLNLYGS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 519 TEYNAHNLYGFLESQATRBALVRPATRGPFLLSRSTFAGSGKYTAHWTGDNAARWDDLQY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
Alpha-xylosidase precursor (Fragment).
XYL1
XYL1
Arabidopsis thaliana (Mouse-ear cress).
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               200
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRELIMINARY;
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                                                                                                                                                                                                                                                                                                                   SEVVNRGYAMSQRWVMDKITILGLKRRVKIKEYTVQKDAGAIKVKGLGRRTSSHNQGGFF 887
YYPDFLDPAARSFWVDEIKRFRDILPIDGIWIDMNEASNFITS------APTPGSTL 487
                                                            ------DNPPYKINNSGGRVPINSKTIPATAMHYGNVTEYNAHNLYGFLE 531
                                                                                                                     SQATREALVRPATRGPFLLSRSTFAGSGKYTAHWTGDNAARWDDLQYSIPTMLNFGLFGM 591
                                                                                                                                                                              PMIGADICGFAESTTEELCCRWIQLGAFYPFSRDHSARDTTHQELYLWESVAASARTVLG 651
                                                                                                                                                                                                                                                                                                                                                            AARSTPFHLLVVM---SDHVASTGELFLDNGIEMDIGGPGGKWTLVRFFAESGINNLTIS 827
                                                                                                                                                                                                                                                                                                                                                                                                                                                    -----EGTGRDLAVHVDGANA 874
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      42.2%; Score 2050.5; DB 10; Length 916; 44.9%; Pred. No. 3.3e-147; arive 163; Mismatches 273; Indels 65;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Physcomitrella patens subsp. patens.
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Bryophyta;
Bryopsida; Funariidae; Funariales; Funariaceae; Physcomitrella.
NCBI_TaxID=145481;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Hiwatashi Y., Nishiyama T., Hasebe M.;

Hiwatashi Y., Nishiyama T., Hasebe M.;

Hiwatashi Y., Nishiyama T., Hasebe M.;

"Escablishment of gene- and enhancer-trap systems of the mosimated that the strength of gene- and enhancer-trap systems of the mosimated (MAR-2001) to the EMBL/GenBank/DDBJ databases.

R EMBL, ABOS7452; BAB39467.1; -

R InterPro; IPR001064; Crystallin.

R InterPro; IPR001032; Glyco-hydro-31.

R PROSITE; PS00225; GRYSTALLIN BETAGAMA, 1.

R PROSITE; PS00129; GLYCOSYL HYDROL F31.1; 1.

R PROSITE; PS00109; GLYCOSYL HYDROL F31.1; 1.

R PROSITE; PS00109; GLYCOSYL HYDROL F31.2; 1.

C SEQUENCE 916 AA; 102282 MW; AACE2AC6E440DBB3 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-JUN-2001 (TrEMBLrel. 17, Created)
01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
Putative alpha-glucosidase.
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TTQAARSTPFHLLVVM---SDHVASTGELFLDNG--IEMDIGGPGGKWTLVRFFAESGIN 822
                      EQGKTEVEALFPPGSWYHMFDMTQAVVSKNGKRVTLPAPLNFVNVHLYQNTILPTQQGGL 754
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Σ H
                                                                                        323 NLTISSEVVNRGYAMSQRWVMDKITILGLKRRVKIKEYTVQKDAGAIKVK------GL
                                                                                                                                                                                                                                                                                                                                                                                                                ol-mar-2000 (TrEMBLrel. 13, Last sequence update)
ol-MR-2003 (TrEMBLrel. 23, Last annotation update)
Alpha-xylosidase precursor (ATIG68560/F24J5_10).
XYLI OR F24J5_20.
Arabidopsis thaliana (Mouse-ear cress).
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Gagnoliophyta; eudicocyledons; core eudicots. Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
[1]
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Kim C.J., Chen H., Cheuk R., Shinn P., BowBer L., Carninci P., Chan G.J., Chen H., Dale J.M., Hayashizaki Y., Hsuan V.M., Chang C.H., Dale J.M., Hayashizaki Y., Hsuan V.M., Lin J., Jones T., Karlin-Neumann G., Kawai J., Lam B., Lee J.M., Lin J., Miranda M., Narusaka M., Nguyen M., Onodera C.S., Palm C.J., Quach H.L., Sakurai T., Sarcu M., Seki M., Southwick A., Shinozaki K., Dariumi M., Wong C.C., Wu H.C., Yamada K., Yu G., Yuan S., Shinozaki K., Davis R.W., Theologis A., Bcker J.R.; Submitted (DEC-2002) to the EMBL/GenBank/DDBJ databases.

EMBL, AC008075; AAD49987.1; -.
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STATASTON COlumbia.
STRATASTON COlumbia.
STRATASTON COlumbia.
Lee J.M., Li J., Gonzalez A., Liu A., Liu K., Vaysberg M., Sakano H.,
Lee J.M., Li J., Gonzalez A., Liu A., Liu K., Vaysberg M., Sakano H.,
Chino C., Chiou J., Altafi H., Araujo R., Brooks S.,
Buehler E., Chao Q., Com L., Conway A.B., Dunn P., Hansen N.,
Howng B., Huizar L., Khan S., Kim C., Palm C., Rowley D., Shinn P.,
Walker M., Davis R.W., Ecker J.R., Federspial N.A., Theologis A.;
"The sequence of BAC F24J5 from Arabidopsis thaliana chromosome 1.";
Submitted (AUG-1999) to the EMBL/GenBank/DDBJ databases.
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STRAIN=cv. Columbia;
Sampedro J., Sieiro C., Villa T.G., Revilla G., Zarra I.;
Sampedro J., Sieiro C., Villa T.G., Revilla G., Zarra I.;
"Cloning and expression pattern of an alpha-xylosidase gene
Arabidopsis thaliana.";
Submitted (APR-1999) to the EMBL/GenBank/DDBJ databases.
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Submitted (SEP-2001) to the EMBL/GenBank/DDBJ databases.
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  PRELIMINARY;
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                                                       SECUENCE FROM N.A.
SETALINE-V. COlumbia; TISSUE-Seedling hypocotyl;
MEDLINE-21295583; PubMed-11402218;
Sampedro J., Sieiro C., Revilla G., Gonzalez-Villa T., Zarra I.;
Sampedro J., Sieiro C., Revilla G., Gonzalez-Villa T., Zarra I.;
"Cloning and Expression Pattern of a Gene Encoding an alpha-Xylosidase
Active against Xyloglucan Oligosaccharides from Arabidopsis.";
Plant Physiol. 126:910-920(2001).
EMBL, AR097481, AAD05559.1;
InterPro; IPR000322; Glyco_hydro_31.
Pfam; PP01055; Glyco_hydro_31.1.
PROSITE; PS00129; GLYCOSYL_HYDROL_F31_1: 1.
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LRNVGGKAYAHAVLLLNSNGMDVFYRGDSLTYKVIGGVFDFYFIAGPSPLNVVDQYTQLI
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                                                                                                                                                                                                                                                                                                                                                                                                                       ch 42.1%; Score 2045; DB 10; Length 907; Il Similarity 43.8%; Pred. No. 8.7e-147; 409; Conservative 166; Mismatches 282; Indels 76;
                                                                                                                                                                                                                                                                                                                                     <1 19 POTENTIAL.
116 907 ALPHA-XYLOSIDASE.
907 AA; 101647 MW; 58ABBD235366C588 CRC64;</pre>
eurosids II; Brassicales; Brassicaceae; Arabidopsis.
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907
                      NCBI_TaxID=3702
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101 NRRWEI PNEVLPRPPPPPPPPPLSSLOHLPKPIPONOPITIVLSHPHSDLAFILFHTTPP 160
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STRAIN=cv. Record; TISSUE=Tuberising stolon tip;
MEDLINE=2136228; Pubmed=11465591;
Taylor M.A., Ross H.A., McRae D., Wright F., Viola R., Davies H.V.;
"COpy-DNA cloning and characterisation of a potato alpha-glucosidase: expression in Escherichia coli and effects of down-regulation in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               41 IGYGYQVKNAKVDNSTGKSLTALLQLIRNSPVYGPDIHFLSFTASFEEDDTLRIRFTDAN
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Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Asteridae; lamids; Solanales; Solanaceae; Solanum.
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Last annotation update)
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                                                                           transgenic potato.";
Planta 213:258-264(2001).
EMBL; AJ277244; CAB96077.1; -.
Interpro; IPR000322; Glyco.hydro_31.
Pram; PP01055; Glyco.hydro_31, 1.
PROSITE; PS00129; GLYCOSYL_HYDROL_F31_1; 1.
Glycosidase; Hydrolase.
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                                             GRRTSSHNQGGFFVSVISDLR---QLVGQAFKL
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01-0CT-2000 (TrEMBLrel. 15, Last
01-MAR-2002 (TrEMBLrel. 20, Last
Alpha-glucosidase (EC 3.2.1.20).
                                                                                                                                                                                                                                              PRELIMINARY;
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LRNVGGKAYAHAVLLLNSNGMDVFYRGDSLTYKVIGGVFDFYFIAGFSPLNVVDQYTQLI 282
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APTPG-----STLDNPPYKINNSGGRVPINSKTIPATAMHYGNVTEYNAHNLY 527
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      YGPDIHFLSFTASFEEDDTLRIRFTDANNRRWEIPNEVLPRPPPPPSPPLSSLOHLPKP 132
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        YLQLSSSLPAQQAHLYGLGEHTKPT-FQLAHNQILTLWNADIASFNRDLNLYGSHPFYMD 251
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                                                                                                                                                                                                                                                                                                                                                                                                                   13 TLAVVLPLVLCMVVEGATTSKNDNQGEALGYGYQVKNAKVDNSTGKSLTALLQLIRNSPV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  133 IPQNQPTTTVLSHPHSDLAFTLFHTTPFGFTIYRKSTHDVLFDATPIPSNPTTFLIYKDQ
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                                                                                                                                                                                                                                                                                                                                                             16;
                                                                                                                                                                                                                                                                                                       Length
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                                                                                                                                                                                                               124 915 ALPHA-XYLOSIDASE.
915 AA; 102398 MW; 28F9610DBD7EA657 CRC64;
                                                                                                                                                                                                                                                                                                 Query Match 42.1%; Score 2045; DB 10;
Best Local Similarity 43.8%; Pred. No. 8.8e-147;
Matches 409; Conservative 166; Mismatches 282;
EMBL, AX057482, AAL09716.1; -.
EMBL, BT002675, AAC11591.1; -.
InterPro; IPR000322; Glyco_hydro_31.
PR051TE, PS00129; GLYCOSYL_HYDROL_F31_1; 1.
Signal.
1 27 POTENTIAL.
                                                                                                                                                                                                               CHAIN
SEQUENCE
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PAPMPYWAFGFHQCRWGYRDVNEIETVVDKYAEARIPLEVMWTDIDYMDAFKDFTLDPVH 373
                                                                                                                                                                                                                                                                      GPVYYPDFLDPAARSFWVDEIKRFRDILPIDGIWIDMNEASNFI-----TSAPT-- 482
                                                                                                                                                                                                                                                                                                                                                                                                                          530 LESQATREALVRPATRGPFLLSRSTFAGSGKYTAHWTGDNAARWDDLQYSIPTMLNFGLF 589
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SQTVATHKALQGLEGKRPFILTRSTFVGSGHYAAHWTGDNQGTWENLRYSISTMLNFGIF 603
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LGLRYELLPYYYTLMYDANLRGSPIARPLSFTFPDDVATYGISSQFLIGRGIMVSPVLQP 709
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                         ONOPITIVLSHPHSDLAFILFHTTPFGFTIYRKSTHDVLFDATPIPSNPTTFLIYKDQYL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       QAARSTPFHLLVVM----SDHVASTGELFLDNG--IEMDIGGPGGKWTLVRFFAESGINN
                                                                                               QLSSSLPAQQAHLYGLGEHTKP-TFQLAHNQILTLWNADIASFNRDLNLYGSHPFYMDVR
                                                                                                                           SSPMVGSTHGVPLLNSNGMDVBYTGDRITYKVIGGIIDLYIPAGRTPEMVLDQYTKLIGR
                                                                                                                                                                                             PPLDKMQQFVTKLHRNGQRYVPILDPGINTNKSYGTFIRGMQSNVFIKRNGNPYLGSVWP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           - PG------STLDNPPYKINNSGRVPINSKTIPATAMHYGNVTBYNAHNLYGF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GPGWICCLDCKNITKTRWDEPPYKINATGVQAPIGFKTIATSCTHYNGVLEYDAHSIYGF
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Arabidopsis thaliana (Mouse-ear cress).
Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Eukaryota; Viridiplantae; Streptophyta; Eukaryota; Core eudicots; Rosidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mewes H.W.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A. Jordelmann R., Voss H., Unseld M., Mev Jordan N., Bangert S., Wiedelmann R., Voss H., Unseld M., Mev Rudd S., Lemcke K., Mayer K.F.X., Quetier F., Salanoubat M.; Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Spermatophyta, Magnoliophyta, eudicotyledons, core e
eurosids II, Brassicales, Brassicaceae, Arabidopsis.
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01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-OCT-2002 (TrEMBLrel. 21, Last annotation updat Hypothetical 95.9 kDa protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 855
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NCBI_TaxID=3702;
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                                                                                                                                                                                                             IARPLSFTFPDDVATYGISSQFLIGRGIMVSPVLQPGSSIVNAYSPRGNWVSLSNYTSSV 733
                                                                                                                                                                                                                                                IVRPLFFTFPNIPELYELSTQFLVGSNVMVSPVLEKAKTKVSALFPPGTWYSLFDMTQVI 740
                                                                                                                                                                                                                                                                                     789
                                                                                                                                                                                                                                                                                                           VIKEPHYRSLDAPLHVVNVHLYQNIILPMQRGGMLIKEARMTPFIIIVAFPLGASEGVAK 800
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                                                                                                                                                                                                                                                                                                                                                                                                                                    ILGLKRRVKIKEYTVQKDAGAIK-VKGLGRRTSSH-----NQGGFFVSVISDLRQL--- 897
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         VLGLNGIG--GAFDILVDGSKVEDTSKLEFETEEHKFIDKLEEGGHKKSMMLDIKGLELP 915
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STRAIN=cv. tall climbing mixed; TISSUE-Cotyledon;
Crombie H.J., Chengappa S., Jarman C., Sidebottom C., Reid G.;
"Molecular characterisation of a xyloqlucan oligosaccharide-acting
alpha-D-xylosidase from the cotyledons of nasturtium (Tropaeolum majus
VGSGHYAAHWIGDNKGTWEDLKYSISTVLNFGIFGVPMVGSDICGFYPAAPPLEELCNRW
                                                                                                                                                          734 SVSAGTYVSLSAPPDHINVHIHEGNIVAMQGEAMTTQAARSTPFHLLVVM----SDHVAS
                                                                                                                                                                                                                                                                                                                                                            TGELFLDNG--IEMDIGGPGGKWTLVRFFAESGINNLTISSEVVNRGYAMSQRWVMDKIT
                                                                                                                                                                                                                                                                                                                                                                                     -GNLFLDDDELPEMKLG--NGKSTYMDFHATTSNGTVKIWSEVQESKYALDKGWYIEKVT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Tropaeolum majus (Common nasturtium).
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
eurosids II; Brassicales; Tropaeolaceae; Tropaeolum.
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                                                            AGSGKYTAHWTGDNAARWDDLQYSIPTMLNFGLFGMPMIGADICGF--AESTTEELCCRW
                                                                                                                                     I QLGAFYPFSRDHSARDTTHQELYLWESVAASARTVLGLRYELLPYYYTLMYDANLRGSP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           40.5%; Score 1969.5; DB 10; Lengt llarity 44.2%; Pred. No. 5.2e-141; Conservative 154; Mismatches 284; Indels
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935 ALPHA-D-XYLOSIDASE.
104937 MW; 22DE6901E9CE19BD CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Submitted (AUG-1999) to the EMBL/GenBank/DDBJ databases
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01-WAY-1999 (TrEMBLrel. 10, Created)
01-WAY-2000 (TrEMBLrel. 13, Last sequence update)
01-UNN-2001 (TrEMBLrel. 17, Last annotation update)
Alpha-D-xylosidase precursor.
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InterPro; IPR000322; Glyco_hydro_31.
Pfam; PF01055; Glyco_hydro_31; 1.
PROSTTE; PS00129; GLYCOSYL_HYDROL_F31_1; 1.
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25
935 AA;
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Best Local (
Matches 39:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     R-VTKRAENPIYSLE----ISQD----ISQD-------PFGVLLRRQGTGTV
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                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Kunita R., Nakabayashi O., Wu J.Y., Hagiwara Y., Mizutani M., Pennybacker M., Chen Y.T., Kikuchi T., "Molecular cloning of acid alpha-glucosidase cDNA of Japanese quail (corurnix coturnix japonica) and the lack of its mRNA in acid maltas deficient quails.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 32.0%; Score 1553.5; DB 13; Length 932; Best Local Similarity 40.2%; Pred. No. 2.7e-109; Matches 352; Conservative 129; Mismatches 286; Indels 109;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       "Genomic sequenses of ggaal and ggaa2.";
Submitted (MAR-2002) to the EMBL/GenBank/DDBJ databases.
EMBL, AB000967; BAA25884.1;
EMBL, AB001289; BAC15595.1;
HSSP; P04155; 1PS2.
InterPro: IPR000322; Glyco hydro_31.
InterPro: IPR000519; P_trefoil.
Pfam; PF00088; trefoil; 1.
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                                                                                                                                                                                                                                                                         Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                  Coturnix coturnix japonica (Japanese quail).
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Biochim. Biophys. Acta 1362:269-278(1997)
                                                                                                                                                                                                                                                      Created)
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MEDLINE=98201735; PubMed=9540858;
                                                                                                                                                                                                                                     01-AUG-1998 (TrEMBLrel. 07, C:
01-AUG-1998 (TrEMBLrel. 07, Le
01-MAR-2003 (TrEMBLrel. 23, Le
Acid alpha glucosidase.
GAAI OR GAAI.
                                                                                                                                                                                                         PRELIMINARY;
                                                                                      KDFNI 835
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                                              900 QAFKL 904
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|KLFLDDDELPEMKLG--NGKSTYIDFYASVGNESVKIWSQVKGGGFALSQGLVIEKVIV 770
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                                                                                                                                                                                                                                                                                                                                                                                                                                 GPDIHFLSFTASFEEDDTLRIRFTDANNRRWEIPNEVLPRPPPPPPPPPSSLQHLPKPI 133
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                                                                                                                                                                                                                                                                                                                                                                  LSLLVAIILCF-----SSLQCSNAIGKGYRLISMEKSPDDG-SFIGYLQVKQSNKIY
                                                                                                                                                                                                                                                                                                                                                                                                                                                             134 PONOPITIVLSHPHSDLAFTLFHTTPFGFTIYRKSTHDVLFDATPIPSNPTTF--LIYKD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RKSPVTVQEISGPELILIFTV---DPFSPAVRRSNGETIFNTS---SSDESFGEMVFKD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     371 PVHFPLDKMOQFVTKLHRNGQRYVPILDPGINTNKSYGTFIRGMQSNVFIKRNGNPYLGS
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                                                                                                                                                                                                                                                 Length 855;
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38.0%; Score 1849; DB 10; Length E
Best Local Similarity 41.8%; Pred. No. 6.9e-132;
Matches 378; Conservative 165; Mismatches 274; Indels
                                     EU Arabidopsis sequencing project;
Submitted (APR-2000) to the EMBL/GenBank/DDBJ databases.
BMBL, AL162459; CAB82818.1;
InterPro; IRR000322; Glyco hydro 31.
PROMITE, PSO0129; GLYCOSYL_HYDROL_F31_1; 1.
BYDOCHAEL PROFILE POTOLED FOR EMBLY BYDOLD 
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                       SEQUENCE FROM N.A.
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794 FLDNGIEMDIGGPGGKWTLVRFFAESGINNLTISS--EVVNRGYAMSORWVMDKITILG- 850
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                                                                                               164 IYRKSTHDVLFDATPIPSNPTTFLIYKDQYLQLSSSLPAQQAHLYGLGEHTKPTFQLAHN 223
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01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
Similar to glucosidase, alpha, acid.
SAA.
Mus musculus (Mouse).
Bikaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia; Butheria, Rodentia, Sciurognathi; Muridae; Murinae, Mus.
113 TaxID=10090;
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MEDINEE-22354683; PubMed=12466851;
The FANTOM Consortium.
The FANTOM Consortium.
The RIKEN Genome Exploration Research Group Phase I & II Team;
"Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs.";
Nature 420:563-573 (2002).
EMBL; AK088481; BAC40382.1; -.
397 DAQWNDIDYMOGYRDFTFDPQKFA--SLPSLVEDLHKHGQHYVIILDPGISSTSPRGSYW
                                                                                                         IDMNEASNFITSAP--TPGSTLDNPPYK---INNSGGRVPINSKTIPATAMHYGNVTEYN
                                                                                                                                                                                             569 LHNLYGLKEAEATASALIRIRGKRPFVISRSTFPSQCRYSGHWLGDNRSQWKDMYYSIPG
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                                                                       "FIRGMOSNVFIK-RNGNPYLGSVWPGPVYYPDFLDPAARSFWVDEIKRFRDILPIDGIW
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
NCBI_TaxID=10090;
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Last annotation update)
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491 TEFHAQVPFDGMMIDMNEPSNPVRGSVDGCPDNSLENPPYLPGVVGG--TLRAATICASS 548
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                                         911 ATAPTOVLSNGIPVSNFTYSPDNKSLAI 938
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                                                                                                                                                                                                                 PRELIMINARY;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              136 YRLENL---SSTESGYTA--TLTRTSPTFFPXDVLTLQLEVLMGTDSRLHFKIKDPASKR 190
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                YKVIGGIIDLYIFAGRIPEMVLDQYIKLIGRPAPMPYWAFGFHQCRWGYRDVNEIETVVD 342
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GINT---NKSYGTFIRGMOSNVFI-KRNGNPYLGSVWPGPVYYPDFLDPAARSFWVDEIK 455
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                505 EFHAQVPFDGMMLDMNEPSNFVRGSQQCPNNELENPPYVPGVVGG--ILQAATICASS- 561
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         HYGNVTEYNAHNLYGFLESQATREALVRPATRG--PFLLSRSTFAGSGKYTAHWTGDNAA 571
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  IYRKSTHDVLFDATPIPSNPTTFLIYKDQYLQLSSSLPAQQAHLYGLGEHTKPTFQLAHN 223
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                                                                                                                                                                                                                                                                                                                                                                                                                                                        Indels 106;
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                                                                                                                                                                                                    SMART; SMOOODS, PD, 1.
PROSITE; PS00129; GLYCOSYL, HYDROL, F31_1; 1.
PROSITE; PS00707; GLYCOSYL, HYDROL, F31_2; 1.
PROSITE; PS007025; PTERFOLI; 1.
SEQUENCE 953 AA; 106157 MW; 32086D7354A5FF91 CRC64;
Submitted (JUL-2001) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                            Query Match 30.5%; Score 1484; DB 11; Best Local Similarity 38.1%; Pred. No. 5.5e-104; Matches 331; Conservative 131; Mismatches 300;
                   EMBL, BC010210, AAH10210.1; -...
MGD; MGI:95609; Gaa.
InterPro; IPR0000327; Glyco hydro_31.
InterPro; IPR000519; Ptrefoil.
Pfam; PF01055; Glyco hydro_31; 1.
Pfam; PF00088; trefoil; 1.
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104 WEIPNEVLPRPPPPPSPPPLSSLQHLPKPIPQNQPTTTVLSHPHSDLAFTL----FHTTP 159
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                                                                                                                                                                                                                                     MEDLINE=2018872; Pubmed=10723725;
MEDLINE=2018872; Pubmed=10723725;
Dennis J.A., Moran C., Healy P.J.;
Dennis J.A., Moran C., Healy P.J.;
The bovine alpha-glucosidase gene: coding region, genomic structure, and mutations that cause bovine generalized glycogenosis.";
and mutations that cause bovine generalized glycogenosis.";
Mamm. Genome 11.206-212(2000).
BEBBL; AF171666; AAF81636.1; -.
BEBL; AF171665; AAF81636.1; -.
BEBL; AF171665; AAF81636.1; -.
BEBL; AF171665; AAF81631.1.
BEBL; AF171665; AAF81631.1.
BEBL; AF17165; Glyco hydro_31.
BIT EFPRO; IPRO00519; P.Trefoil.
BEBL; PRO0088; trefoil.
BEBL; PRO0129; GLYCOSYL HYDROL F31.1; 1.
BRAART: SM00018; PD; 1.
BRASTTE; PS000129; GLYCOSYL HYDROL F31.2; 1.
BROSTTE; PS00025; P.TREFOIL.
BRESTIE; PS00025; P.TREFOIL.
BRESTIE; PS0025; P.TREFOIL.
BRESTIE; PS0025; P.TREFOIL.
BRESTIE; PS0025; P.TREFOIL.
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Bos taurus (Bovine).
Wakaryota, Metazoa; Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Cetartiodactyla, Ruminantia, Pecora, Bovoidea,
Bovidae, Bovinae, Bos.
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513 MHYGNVTEYNAHNLYGFLESQATREALVRPATRGPFLLSRSTFAGSGKYTAHWTGDNAAR 572
                549 -HQFLSTHYDLHNLYGLTEALASHRALVKARGMRPFVISRSTFAGHGRYSGHMTGDVWSN 607
                                                   WDDLQYSIPTMLNFGLFGMPMIGADICGFAESTTEELCCRWIQLGAFYPFSRDHSARDTT 632
                                                                  633 HQELYLWESVAASA-RTVLGLRYELLPYYYTLMYDANLRGSPIARPLSFTFPDDVATYGI 691
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                                                                                                                                                           692 SSQFLIGRGIMVSPVLQPGSSIVNAYSPRGNWVSLSNY-----TSSVSVSAG 738
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728 DRQLLWGEALLITPVLEAEKVEVTGYPPQGTWYDLQTVPMEAFGSLPPPAPLTSVIHSKG 787
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Search completed: October 27, 2003, 10:30:57 Job time : 67.5261 secs

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1 MERSKLPRYICPTLAVVLPL.....RQLVGQAFKLELEFEGATRV
GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
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AGLU HORVU
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IYAG HOWAN
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MGA HUWAN
AGLU SCHPO
SUIS RABIT
AGLU SPROG
AMYG DEBOC
YAJI SCHPO
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Gapop 10.0 , Gapext 0.5
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063273 rattus norv 061626 mus musculu 059185 borrelia bu P52143 escherichia 099719 schizosacch 016478 homo sapien P13944 gallus gall 092143 rattus norv P23559 clostridium P43467 pediococcus 0990b5 bacteriopha P30920 bacillus ci			ltase).	ophyta; Tracheophyta; core eudicots; e; Beta.	CQUENCE. :i H., Honma M., Chiba S.; encoding alpha-glucosidase from		i H., Honma M., e of active site in	L, non-reducing 1,4- D-glucose. SYL HYDROLASES.	uced through a collaboration a and the EMBL outstation are no restrictions on its its content is in no way Jeage by and for commercial p://www.isb-sib.ch/announce,	S (POTENTIAL)) (POTENTIAL) (POTENTIAL)
979 1 GLKS_RAT 979 1 GLKS_MOUSE 806 1 LON_BORBU 1569 1 YPJA_ECOLI 2358 1 MOKD_SCHPO 3124 1 CALS_HIDAAN 3124 1 CALS_HIDAAN 3124 1 CALS_HICK 776 1 SM4F_RAT 986 1 CUNZ_CLOSR 733 1 AGAI PEDPE 1103 1 VG37_BPARI 718 1 CDGT_BACCI	ALIGNMENTS	STANDARD; PRI; 913 AA.	. 36, Created) . 36, Last sequence update) . 39, Last annotation update) e precursor (EC 3.2.1.20) (Ma)	beta Vulgaris (sugar beet). Eukaryota; Viridiplantae; Streptophyta; Embryophyta; 1 Spermatophyta; Magnoliophyta; eudicotyledons; core euc Caryophyllidae; Caryophyllales; Chenopodiaceae; Beta. NCBI_TaxID=161934;	PARTIAL SE 1=9178565; Ito H., Moi	them. 61:875-880(19 E OF 464-472. 1=7766184;	ui H., Kimura A., Ito H., Mori cation and amino acid sequence	Tr sugar beet alpha-glucosidase.; If sugar beet alpha-glucosidase.; If sugar beet alpha-glucosidase.; If Elosci. Bloched Blochem. 59:459-461(1995). If ELONCTION: HIGH ACTIVITY: POR ALPHA-GLUCAN. Inked D-glucose residues with release of D-glucose. Inked D-glucose residues with release of D-glucose. If PHR: THE N-TERMINUS IS BLOCKED. IF PTM: THE N-TERMINUS IS BLOCKED. IF SIMILARITY: BELONGS TO FAMILY 31 OF GLYCOSYL HYDROLASES.	This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its modified by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).	BAA20343.1; 105463. 100322; Glyco hydro_31. 129; Glyco hydro_31; 1. 129; Glyco SyL HydroL F31_2; 1. 1707; GLYCOSYL HYDROL F31_2; 1. 1708; Glycoprotein; Signal. 1808; Glycoprotein; Signal. 1809; Glycoprotein; Signal. 1809; Glycoprotein; Signal. 1809; A69; N-LINKED (GLCNAC.) 1809; A69; N-LINKED (GLCNAC.) 1809; A95; N-LINKED (GLCNAC.)
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                              STRAIN=CV. Dash;
MEDLINE=97238484; PubMed=9132069;
Sugimoto M., Furui S., Suzuki Y.;
"Molecular cloning and characterization of a cDNA encoding alpha-
glucosidase from spinach.";
Plant Mol. Biol. 33.765-768(1997).
-!- FUNCTION: ALPHA-GLUCOSIDASE I AND II HAVE HIGH ACTIVITY TOWARDS
MALTO-OLIGOSACCHARIDES AND STARCH, WHILE FORM III AND IV HAVE HIGH
                                                               15-JUL-1998 (Rel. 36, Created)
15-JUL-1998 (Rel. 36, Last sequence update)
15-JUL-1998 (Rel. 36, Last sequence update)
Alpha-glucosidase precursor (EC 3.2.1.20) (Maltase).
Spinacia oleracea (Spinach).
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Caryophyllidae; Caryophyllales; Chenopodiaceae; Spinacia.
NCBL TaxID=3562;
                                                                                                                                                                                                                                                                                                                                                                                                                                                    -!- CATALYTIC ACTIVITY: Hydrolysis of terminal, non-reducing 1,4-linked D-glucose residues with release of D-glucose.
-!- PTM: POUR DIFFERENT FORMS (I-IV) MAY BE PRODUCED BY POST-TRANSLATIONAL MODIFICATION.
-!- SIMILARITY: BELONGS TO FAMILY 31 OF GLYCOSYL HYDROLASES.
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N-LINKED GLCUNAC...) (
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ALPHA-GLUCOSIDASE
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PIR; T09143; T09143.
InterPro; IRR000322; Glyco hydro_31.
Pfam; PF01055; Glyco hydro_31; 1.
PROSTTE; PS00129; GLYCOSYL HYDROL F31.1; 1.
PROSITE; PS00707; GLYCOSYL HYDROL F31.2; 1.
Hydrolase; Glycosidase; Glycoprotein; Signal.
                                                             903 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EMVLDQYTKLIGRPAPMPYWAFGFHQCRWGYRDVNEIETVVDKYAEARIPLEVMWTDIDY 360
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                   N-LINKED (GLCNAC. . .) (POTENTIAL)
N-LINKED (GLCNAC. . .) (POTENTIAL)
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   N-LINKED (GLCNAC. . .) (POTENTIAL)
                                                                                        Length 913;
                                                                                    Query Match 99.9%; Score 4858; DB 1; Length 9 Best Local Similarity 100.0%; Pred. No. 2.5e-317; Matches 913; Conservative 0; Mismatches 0; Indels
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                                             WVLDQYTKLIGRPAPMPYWAFGFHQCRWGYRDVNEIETVVDKYAEARIPLEVMWTDIDYM
                                                                        298 QUVEQFTRVIGRPAFMPYWAFGFQQCRYGYHDVYELQSVVAGYAKAKIPLEVMMTDIDYM
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                                                                                                                                       418 RNGKPYLGSVWPGPVYPPDFLKPSALTFWTDEIKRFLNLLPVDGLWIDMNEISNFISSPP
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).

EMEL; U12450; AAB02985.1; PIR; S65057; S65057.
InterPro; IPR000322; Glyco hydro_31.
Pfam; PF01055; Glyco hydro_31; 1.
PROSITE; PS00129; GLYCOSYL HYDROL F31_1; 1.
R PROSITE; PS00707; GLYCOSYL HYDROL F31_2; 1.
Hydrolase; Glycosidase; Glycoprotein; Signal.
23 POTENTIAL.

ALPHA-GLUCOSIDASE

ACT SITE CARBOHYD

CHAIN

CARBOHYD CARBOHYD

putative alpha-glucosidase gene from barley.";
Plant Mol. Biol. 30:229-241(1996).
-:- CATALYTIC ACTIVITY: Hydrolysis of terminal, non-reducing 1,4linked D-glucose residues with release of D-glucose.
-:- TISSUE SPECIFICITY: HIGH LEVELS SEEN IN THE ALEURONE AND SCUTELLUM
--- TISSUE SPECIFICITY: HIGH LEVELS SEEN IN THE ALEURONE AND SCUTELLUM
--- DEVELOPMENTAL STAGE: LEVELS INCREASE STEADLLY THROUGHOUT
--- IMBIBITION REACHING MAXIMOM LEVELS AT DAY 7. DURING GENMINATION,
--- LEVELS INCREASE FROM DAY 2, REACH MAXIMUM LEVELS AT DAY 3 AND

DECLINE AFTER DAY 5. INDUCTION: BY GIBBERELLIN A3 (GA). SIMILARITY: BELONGS TO FAMILY 31 OF GLYCOSYL HYDROLASES.

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                                                                                                                                                                                                                                                                                                                                                                         48.7%; Score 2370; DB 1;
51.2%; Pred. No. 7.5e-151;
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AGLU HORVU STANDARD; PRT; 877 AA.

Q43763;
15-JUL-1998 (Rel. 36, Last sequence update)
15-JUL-1998 (Rel. 36, Last sequence update)
15-JUL-1998 (Rel. 36, Last annotation update)
Alpha-glucosidase precursor (EC 3.2.1.20) (Maltase).
Hordeum vulgare (Barley).
Bukaryota, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnollophyta; Liliopsida; Poales; Pooceae; Pooideae;

STRAIN=CV. Morex; TISSUE-Aleurone; MEDLINE=96178863; PubMed=8616248; Tibbot B.K., Skadsen R.W.; "Molecular cloning and characterization of a gibberellin-inducible;

SEQUENCE FROM N.A. NCBI_TaxID=4513;

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        -:- CATALYTIC ACTIVITY: Hydrolysis of terminal, non-reducing linked D-glucose residues with release of D-glucose.
-:- SIMILARITY: BELONGS TO FAMILY 31 OF GLYCOSYL HYDROLASES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FUNCTION: Hydrolyzes not only malto-oligosaccharides but
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LOVY-1997 (Rel. 35, Last sequence update)
15-SEP-2003 (Rel. 42, Last annotation update)
Alpha-glucosidase precursor (EC 3.2.1.20) (Maltase)
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Pfam; PF01055; Glyco hydro 31; 1.
PROSITE; PS00129; GLYCOSYL_HYDROL_F31_1; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sugimoto M., Suzuki Y.;
"Molecular cloning, sequencing, and expre
alpha-glucosidase from Mucor javanicus.";
J. Blochem. 119:500-505(1996).
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WEDLINE=96271012; PubMed=8830045;
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500707; GLYCOSYL HYDROL F31 2; FALSE NEG Glycogidase; Glycoprotein; Signal.
                                                                                                                         POTENTIAL.
ALPHA-GLUCOSIDASE
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type II (GSDII).
Hum. Mol. Genet.
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SEQUENCE FROM N.A., AND PARTIAL SEQUENCE OF 70-89; 123-145; 204-215; 230-249; 332-345; 349-370; 394-409; 480-513; 520-545; 703-719; 726-731 AND 795-803.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
MEDLINE=91097465; PubMed=2268276;
Hoefsloot L.H., Hoogeveen-Westerveld M., Reuser A.J.J., Costra B.A.;
"Characterization of the human lysosomal alpha-glucosidase gene.";
Biochem. J. 272:493-497(1990).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE=95327152; PubMed=7603530;
Reuser A.J.J., Kroos M.A., Hermans M.M.P., Bijvoet A.G.A.,
Verbeet M.P., van Diggelen O.P., Kleijer W.J., van der Ploeg A.T.;
"Glycogenosis type II (acid maltase deficiency).";
Muscle Nerve 3:S61-S69(1995).
                                                                                                                                                      P10253; Q14351; Q16302;
Ol-WAR-1989 (Rel. 10, Created)
Ol-FEB-1991 (Rel. 17, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Lysosomal alpha-glucosidase precursor (EC 3.2.1.20) (Acid maltase).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE=90262651; PubMed=2111708; Marthiuk F., Merhorn R.; Martiniuk F., Mehler M., Tzall S., Meredith G., Hirschhorn R.; Sequence of the cDNA and 5'-flanking region for human acid alphaglucosidase, detection of an intron in the 5' untranslated leader glucosidase, definition of 18-bp polymorphisms, and differences with previous cDNA and amino acid sequences.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human lysosomal alpha-glucosidase: functional characterization of
                                                                                                                                                                                                                                                                                      Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                                                                                                                                                                              TISSUE=Placenta, Testis, and Urine;
MEDLINE=89005058; PubMed=3044072;
Hoefsloot L.H., Hoogeven-Westerveld M., Kroos M.A., van Beeumen .
Reuser A.J.J., Costra B.A.;
"Primary structure and processing of lysosomal alpha-glucosidase;
homology with the intestinal sucrase-isomaltase complex.";
EMBO J. 7:1697-1704(1988).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Submitted (JUN-1990) to the EMBL/GenBank/DDBJ databases
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                                                                                                                                         952 AA
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                                                                                                                                           PRT;
               STGELFLDNGIEMDIGGPGG 808
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                                                                                                                                         STANDARD;
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MEDLINE=90365036; PubMed=2203258;
Martiniuk F., Bodkin M., Tzall S., Hirschhorn R.;
"Identification of the base-pair substitution responsible for a human acid alpha glucosidase allele with lower 'affinity' for glycogen (GAA and transient gene expression in deficient cells.";
Am. J. Hum. Genet. 47:440-445(1990). Hermans M.M.P., de Graaff E., Kroos M.A., Wisselaar H.A., Oostra B.A., MEDLINE=93168115; PubMed=8094613; Hermans M.M.P., de Graaff E., Kroos M.A., Wisselaar H.A., Willemson R., Oostra B.A., Reuser A.J.J.; The conservative substitution Asp-645-->Glu in lysosomal alpha-The conservative substitution Asp-645-->Glu in lysosomal alpha-glucosidase affects transport and phosphorylation of the enzyme in an adult patient with glycogen-storage disease type II."; Biochem. J. 289:687-693(1993). MEDLINE=92096118; PubMed=1684505; Martiniuk F., Mehler M., Bodkin M., Tzall S., Hirschhorn K., Zhong N., "Identification of a missense mutation in an adult-onset patient with glycogenosis type II expressing only one allele.";
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MEDLINE-95072571; PubMed=7981676;
Huie M.L., Chen A.S., Brooks S.S., Grix A., Hirschhorn R.;
Had en M.L., a newly identified C647W missense mutation and a deletion of exon 18 in infantile onset glycogen storage disease MEDLINE=94004908; PubMed=8401535; Arcoss M.A., de Graaff E., Oostra B.A., Reuser A.J.J M.P., Kroos M.A., de Graaff E., oostra B.A., Reuser A.J.J M.Po mutations affecting the transport and maturation of lysosomal alpha-glucosidase in an adult case of glycogen storage disease type MEDLINE=95170739; PubMed=7866409; Huie M.L., Hirschhorn R., Chen A.S., Martiniuk F., Zhong N.; "Mutation at the catalytic site (MS19V) in glycogen storage disease MEDLINE-91353580; PubMed=1652892; Zhong N., Martiniuk F., Taall S., Hirschhorn R.; Zhong N., Martiniuk F., Taall S., Hirschhorn R.; Identification of a missense mutation in one allele of a patient with Pompe disease, and use of endonuclease digestion of PCR-amplified RNA to demonstrate lack of mRNA expression from the Reuser A.J.J.; "Identification of a point mutation in the human lysosomal alphaglucosidase gene causing infantile glycogenosis type II."; Biochem. Biophys. Res. Commun. 179:919-926(1991). VARIANT GSD-II GLU-645, AND VARIANTS ILE-816 AND ILE-927 VARIANT GSD-II GLU-645, AND VARIANTS ILE-816 AND ILE-927 VARIANTS GSD-II ARG-643 AND TRP-725. second allele."; Am. J. Hum. Genet. 49:635-645(1991) 11 (GSD11)."; Mol. Genet. 3:1081-1087(1994) VARIANT GSD-II LYS-521. MEDLINE=91379015; PubMed=1898413; VARIANTS ILE-816 AND ILE-927 Hum. Mutat. 2:268-273(1993). Mutat. 4:291-293(1994) VARIANT GSD-II THR-318. VARIANT GSD-II VAL-519. (Pompe disease) Hirschhorn R.;

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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
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01-NOV-1997 (Rel. 35, Last sequence update)
30-MAY-2000 (Rel. 39, Last annotation update)
Lysosomal alpha-glucosidase precursor (EC 3.2.1.20) (Acid
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STRANT-BALBA/c; TISSUE-Liver;
Ding J.H., Yang B.Z., Reuser A.J.J., Roe C.R.;
Submitted (SEP-1996) to the EMBL/GenBank/DDBJ databases.
  173 METENRLHFTIKDPANRRYEVPLET-PR-VHSRAPSPLYSVE
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MEDLINE=98205625; Dubmdc=9535769;
Huie M.L., Tsujino S., Bencks S.S., Engel A., Elias E., Bonthron D.T.,
Bessley C., Shanske S., Dimauro S., Goto Y.I., Hirschhorn R.;
"Glycogen storage disease type II: identification of four novel
missense mutations (D645N, G6488, R672M, R672Q) and two
insertions/deletions in the acid alpha-glucosidase locus of patients
                                                                                                                                                                                                                                                  VARIANTS GSD-II ARG-299; LYS-903 DEL AND VARIANTS HIS-199; ARG-223 AND
                         MEDLINE=95187163; PubMed=7881422;
Hermain M.W. T., de Graaff E., Kroos M.A., Mohkamsing S., Eussen B.J.,
Joosse M., Willemsen R., Kleijer W.J., Oostra B.A., Reuser A.J.J.;
"The effect of a single base pair deletion (deita T525) and a C1634T
missense mutation (Pro5451cu) on the expression of lysosomal alpha-
glucosidase in patients with glycogen storage disease type II.";
Hum. Mol. Genet. 3:2213-2218(1994).
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Boerkoel C.F., Exelbert R., Nicastri C., Nichols R.C., Miller F.W., Plotz P.H., Raben N.;
"Leaky splicing mutation in the acid maltase gene is associated with delayed onset of glycogenosis type II.";
Am. J. Hum. Genet. 56:887-897(1995).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   "Acid alpha-glucosidase deficiency: identification and expression
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       "Glycogen storage disease type II: genetic and biochemical analys of novel mutations in infantile patients from Turkish ancestry.";
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MEDILIBE-98180719; PubMed=9521422;
Hermans M.M.P., Kroos M.A., Smeitink J.A.M., van der Ploeg A.T.,
Kleijer W.J., Reuser A.J.J.;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      VARIANT GSD-II VAL-529.
MEDLINE=96431166; PubMed=8834250;
TSUNCOda H., Obshima T., Tohyama J., Sasaki M., Sakuragawa N.,
Martiniuk F.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Best Local Similarity 37.2%; Pred. No. 9.8e-90;
Matches 330; Conservative 135; Mismatches 313; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             a missense mutation (S529V) in a Japanese adult phenotype.
Hum. Genet. 97:496-499(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE OF 631-680 FROM N.A., AND VARIANT GSD-II HIS-645.
MEDLINE=95209708; PubMed=7695647;
Lin C.-Y.,
Lin C.-Y.,
Lidentification of a de novo point mutation resulting in iform of Pompe's disease.";
Blochem. Blophys. Res. Commun. 208:886-893(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE=99202470; PubMed=10189220;
Raben N., Lee E., Lee L., Hirschhorn R., Plotz P.H.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Biochem. Biophys. Res. Commun. 244:921-927(1998)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    VARIANT GSD-II GLY-VAL-PRO-VAL-SER-ASN-925 INS
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VARIANT GSD-II LEU-545
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    104 WEIPNEVLPRPPPPPPPPLSSLOHLPKPIPQNOPITTVLSHPHSDLAFTLFHTTPFGFT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           136 YRLENL---SSTESGYTA--TLTRTSPTFFPKDVLTLQLEVLMETDSRLHFKIKDPASKR
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ESSENTIAL FOR THE DEGRADATION OF GLYGOGEN TO GLUCOSE
                                                  CATALYTIC ACTIVITY: Hydrolysis of terminal, non-reducing 1,4-linked D-glucose residues with release of D-glucose. SUBCELLULAR LOCATION: Lysosomal.
SIMILARITY: Contains 1 P-type (trefoil) domain.
SIMILARITY: BELONGS TO FAMILY 31 OF GLYCOSYL HYDROLASES.
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InterPro; IRR000322; Glyco hydro_31.
InterPro; IRR000322; Glyco hydro_31.
InterPro; IRR00519; P trefoil.
Pfam; PF01058; trefoil; 1.
SMART; SM0018; PD; 1.
PROSITE; PS00025; P TREFOIL; 1.
PROSITE; PS007029; GLYCOSYL HYDROL F31 1; 1.
PROSITE; PS00707; GLYCOSYL HYDROL F31 2; 1.
Hydrolase; Glycosidase; Glycoprotein; Lysosome; Signal.
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Pred. No. 3.1e-89;
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its way non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
|:: || : || : || : || : || 445 AISSAGPAGSYRPYDEGLRRGVFITNETGQPLIGKVCPGTTAFPDFTNPETLDWWQDMVS 504
                                                                                                                   456 RPRDILPIDGIWIDMNBASNFITSAP--TPGSTLDNPPYKINNSGGRVPINSKTIPATAM 513
                                                                                                                                                                 632 THQELYLWESVAASA-RTVLGLRYELLPYYYTLMYDANLRGSPIARPLSFTFPDDVATYG 690
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               800 Q-SKGQWLTLEAPLDTINVHLREGYIIPLQGPSLTTTESRKQPMALAVALTASGEADGEL 858
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Wed. Wycol. 37:357-36 (1999)

-!- CATALYTIC ACTIVITY: Hydrolysis of terminal 1,4-linked alpha-D-
glucose residues successively from non-reducing ends of the chains
with release of beta-D-glucose.
-!- SUBCELUNIAR LOCATION: CELL WALL ASSOCIATED.
-!- SUBCELUNIAR: BELONGS TO FAMILY 31 OF GLYCOSYL HYDROLASES.
                                                                                                                                                                                                                                                                                                                                                572 RWDDLQYSIPTMLNFGLFGMPMIGADICGFAESTTBELCCRWIQLGAFYPFSRDHSARDT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ISSQFLIGRGIMVSPVLQPGSSIVNAYSPRGNWV-------SLSNYTSSV
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15-JUL-1999 (Rel. 38, Last sequence update)
26-FEB-2003 (Rel. 41, Last annotation update)
Glucoamylase 1 precursor (EC 3.2.1.3) (Glucan 1,4-alpha-glucosidase)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
Saccharomycetales; mitosporic Saccharomycetales; Candida.
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Sturtevant J., Dixon F., Wadsworth E., Latge J.-P., Zhao X.-J.,
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EAL--VRPATRGPFLLSRSTFAGSGKYTAHWTGDNAARWDDLQYSIPTMLNFGLFGMPMI 594
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                   InterPro, IPR000322, Glyco hydro 31.
Pfam. PF01055; Glyco hydro 31.1.
PROSITE: PS00129; GLYCOSL HYDROL F31.1: 1.
PROSITE: PS00179; GLYCOSYL HYDROL F31.2: 1.
Hydrolase; Glycosidase; Polysaccharide degradation; Glycoprotein;
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Conservative 155; Mismatches 337; Indels 143;
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"Tyrosine sulfation, a post-translational modification of microvillar enzymes in the small intestinal enterocyte.";
EMBO J. 6:2891-2896(1987).
-!- FUNCTION: MAY SERVE AS AN ALTERNATE PATHWAY FOR STARCH DIGESTION WHEN LUMINAL ALPHA-AMYLASE ACTIVITY IS REDUCED BECAUSE OF IMMATURITY OR MALNUTHION. MAY PLAY A UNIQUE ROLE IN THE DIGESTION OF MALLED DIETARY OLIGOSACCHARIDES USED IN FOOD GADICGFAESTTEELCCRWIQLGAFYPFSRDHSARDTTHQELYLWESVAASARTVLGLRY TISSUE=Small intestine mucosa;
MEDLINE=89066802; PubMed=3143729;
Naim H.Y., Sterchi E.E., Lentze M.J.;
"Structure, biosynthesis, and glycosylation of human small intestinal malease-glucoamylase.";
J. Biol. Chem. 263:19709-19717(1988). SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.
TISSUB-Small intestine;
MEDINE-98112863; PubMed=9446624;
Michols B.L., Eldering J.A., Avery S.E., Hahn D., Quaroni A.,
Sterchi E.E.;
"Human small intestinal maltase-glucoamylase cDNA cloning. Homology Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi, Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo. 28-FEB-2003 (Rel. 41, Last sequence update)
28-FEB-2003 (Rel. 41, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Maltase-glucoamylase, intestinal [Includes: Maltase (BC 3.2.1.20)
Glucosidase); Glucoamylase (BC 3.2.1.3) (Glucan 1,4-alpha-MGAM OR MGA OR MGAML. REVISIONS TO 776; 1049; 1100; 1541; 1612 AND 1811. Nichols B.L., Eldering J.A., Avery S.E., Hahn D., Quaroni A., Sterchi E.E.; Submitted (DEC-2001) to the EMBL/GenBank/DDBJ databases

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283 --PIFNRDTTPNGNGTNLYGAQTPFLCLEDAS--GLSFGVFLMNSNAMEVVLQPAPAITY 338
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 339 RIIGGILDFYVFLGNTPEQVVQEYLELIGRPALPSYWALGFHLSRYEYGTLDNMREVVER 398
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                   CATALYTIC ACTIVITY: Hydrolysis of terminal, non-reducing 1,4-
linked D-glucose residues with release of D-glucose.
CATALYTIC ACTIVITY: Hydrolysis of terminal 1,4-linked alpha-D-
glucose residues successively from non-reducing ends of the chains
subunit: hornomer.
SUBCELDULAR LOCATION: Type II membrane protein. Brush border.
TISSUE SPECIFICITY: EXPRESSED IN SMALL INTESTINE, GRANULOCYTE, AND
TINDEY BUT NOT IN SALIVARY GLAND OR PANCREAS.
PTM: N- AND O-GLYCOSYLATED.
PTM: DOES NOT UNDERGO INTRACELLULAR OR EXTRACELLULAR PROTEOLYTIC
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SIGNAL-ANCHOR (TYPE-II MEMBRANE PROTEIN)
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DR InterPro; IPR000322; Glyco.hydro_31.

DR InterPro; IPR000519; P.trefoil.

DR Ffam; PP00088; trefoil.

DR SWART; SM0018; PD; 2.

DR SWART; SM0018; PD; 2.

DR ROSITE; PS00225; P.TREFOIL; 1.

Whitifunctional enzyme; Transmembrane; Glycoprotein; Hydrolase; Glycosidase; Repeat; Signal-anchor; Sulfation.

T INIT MET 0 CYTOPLASMIC (POTENTIAL).

T TRANSMEM 13 33 CTANY COTENTIAL).
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SIMILARITY: BELONGS TO FAMILY 31 OF GLYCOSYL HYDROLASES.
SIMILARITY: Contains 2 P-type (trefoil) domains.
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RA MEDINE=21848401; PubMed=11859360;
RA MOOD V., Gwilliam R., Rajandream M.A., Lyne M., Lyne R., Stewart A., Squiros J., Pearl N., Hayles J., Baker S., Basham D., Bowaman S., Brown D., Brown D., Baker S., Chillingworth T., Churcher C.M., Brooks K., Brown D., Brown B., Chillingworth T., Churcher C.M., R. Brooks K., Brown D., Brown B., Chillingworth T., Churcher C.M., Gantles S., Goble A., Hamin N., Harris D., Hidalgo J., Hodgson G., Andres M., Hornsby T., Howratth S., Huckle E.J., Hunt S., McLean J., RA Holroy S., Noule S., Mungall K., Murphy L., Niblett D., Odell C., RA Mooney P., Moule S., Mungall K., Murphy L., Niblett D., Odell C., RA Mooney P., Moule S., Saunders D., Squares S., Stevens K., Skelton J., Simmonds M., Squares D., Squares S., Stevens K., Skelton J., Simmonds M., Squares R., Squares S., Stevens K., Skelton J., Workwert G., Aert R., Robben J., Grymonprez B., Moodward J., Volkaert G., Aert R., Robben J., Grymonprez B., Rabel C., Fuchs M., Fritzc C., Holzer E., Moestl D., Hilbert H., Meller-Auer S., Rabel C., Fuchs M., Fritzc C., Holzer E., Moestl D., Hilbert H., Reinhardt R., Pohl T.M., R. Eder P., Zimmermann W., Wedler H., Wambutt R., Purnelle B., A. Lucas M., Rochet M., Gaillardin C., Lallada V.A., Garzon A., Thode G., R. Andra R., Cruzdo L., Jamenz J., Sanchez M., Gaillardin C., Sanchez M., Gallardo L., Jamenz J., Sanchez M., Garzon A., Thode S., Amstrong J., Forsburg S.L., Revuetlta J.L., Lowe T., McCombie W.R., Paulsen I., Potashkin J., Rurer 415:871-880(2002).

R. Nature 415:871-880(2002).

R. Nature 415:871-880(2002).

R. Nature 415:871-880(2002).

R. Tinke Genome sequence of Schizosaccharomyces pombe.";

R. The genome sequence of Schizosaccharomyces pombe.";

R. The genome sequence of Schizosaccharomyces pombe.";

R. The genome sequence residues with release of D-glucose.

C. Chirke J. Subcellular Locar Leader W. Hurst S. D. Educose.

C. Chirke J. Subcellular R. Locar L. Sanches J. D. Hurst J. D. Westellular R. D. Westellular R. D. Westellular R. D. We
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A., SEQUENCE OF 25-36; 175-194; 375-395 AND 427-451, AND MITAGENESIS OF ASP-481; GLU-484 AND ASP-647.
MEDLINE=21195240; PUDMed=11298744;
OKUYama M., OKUNO A., Shimizu N., Mori H., Kimura A., Chiba S.;
"Carboxyl group of residue Asp647 as possible proton donor in catalytic reaction of alpha-glucosidase from Schizosaccharomyces
                                                                                                                                                                                       16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
16-SEP-2003 (Rel. 42, Last annotation update)
Alpha-glucosidase precursor (EC 3.2.1.20) (Maltase).
AGL OR SPAPB24D3.10C.
                                                                                                                                                                                                                                                                                                                                                          Eukaryota, Fungi, Ascomycota, Schizosaccharomycetes, Schizosaccharomycetales, Schizosaccharomycetaceae;
915 KHNGVPSQTSPTVTYDSNLKVAIITDIDLLLGEAYTVE 952
                                                                                                                                                                                                                                                                                                                                   Schizosaccharomyces pombe (Fission yeast)
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                                                                                                                                         STANDARD;
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EMBL; AL590582; CAC36906.1; -. EMBL; AB045751; BAB43946.1; -.

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161 GFTIYRKSTHDVLFDATPIPSNPTTFLIYKDQYLQLSSSLPAQQAHLYGLGEHTKPTFQL 220
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28.0%; Score 1360.5; DB 1; Length 969;
Best Local Similarity 33.2%; Pred. No. 3.1e-83;
Matches 316; Conservative 154; Mismatches 320; Indels 163;
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220 P -> A (IN REF. 1).

507 T -> V (IN REF. 1).

566 D -> N (IN REF. 1).

108666 MM; F3122EZCFAS51C25 CRC64;
InterPro; IPR000322; Glyco hydro 31.
Pfam: PF01055; Glyco hydro 31; 1.
PROSITE; PS00109; GLYCOSYL HYDROL F31 1; 1.
PROSITE; PS00107; GLYCOSYL HYDROL F31 2; FALSE NEG.
Hydrolase; Glycosidase; Glycoprotein; Signal.
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Eukaryota; Metazoa: Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
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Sucrase-isomaltase, intestinal [Contains: Sucrase (EC 3.2.1.48); Isomaltase (EC 3.2.1.10)].
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Hunziker W., Spiess M., Semenza G., Lodish H.F.;
The sucrase-isomaltase complex: primary structure, membrane-
orientation, and evolution of a stalked, intrinsic brush border
                                                                                                                   DFLDPAARSFWVDEIKRF ---- RDILPIDGIWIDMNBASNFITS --
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                                                      in some oligosaccharides produced from starch and glycogen by alpha-amylase, and in isomaltose.

SUBUNIT: THE RESULTING SCHASEA NO ISOMALTASE SUBUNITS STAY ASSOCIATED WITH ONE ANOTHER IN A COMPLEX BY NON-COVALENT LINKAGES. SUBCELLULAR LOCATION: Type II membrane protein. Brush border. PAM: THE PRECURSOR IS PROTEOLYTICALLY CLEAVED WHEN EXPOSED TO PAM: OLGYCOSYLATED.

PTM: NLFATED (BY SIMILARITY).

MISCELLANEOUS: THERE IS A HIGH DEGREE OF HOMOLOGY BETWEEN THE ISOMALTASE AND SUCRASE PORTIONS (41 % OF AMINO ACID IDENTITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (TYPE-II MEMBRANE PROTEIN)
                                  alpha-D-glucosidase-type action.
CATALYTIC ACTIVITY: Hydrolysis of 1,6-alpha-D-glucosidic linkages
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           CARBOHYDRATE DIGESTION. CATALYTIC ACTIVITY: Hydrolysis of sucrose and maltose by an
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PROSTIE: PS00125; PTREFOLL; 1.
PROSTIE: PS00129; GIYCOSYL_HYDROL_F31_1; 2.
PROSTIE; PS00107; GLYCOSYL_HYDROL_F31_2; 2.
Multifunctional enzyme; Transmembrane; Glycoprotein; Hydrolase; Glycosidase; Repeat; Signal-anchor; Sulfation.
INIT_MET
                                                                                                                                                                                                     DUPLICATION.
SIMILARITY: Contains 1 P-type (trefoil) domain.
SIMILARITY: BELONGS TO FAMILY 31 OF GLYCOSYL HYDROLASES
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FUNCTION: PLAYS AN IMPORTANT ROLE IN THE FINAL STAGE
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InterPro; IPR000322; Glyco hydro_31.
InterPro; IPR000519; P_trefoil.
Pfam; PF01055; Glyco hydro_31; 2.
Pfam; PF00088; trefoil; 2.
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                                                                                                                                                                                                                                                                                                                                                                                                               Nakamura A., Nishimura I., Yokoyama A., Lee D.-G., Hidaka M., Masaki H., Kimura A., Chiba S., Uozumi T., "Cloning and sequencing of an alpha-glucosidase gene from Aspergillus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Kimura A., Takata M., Sakai O., Matsui H., Takai N., Takayanagi T.,
Nishimua I., Uozumi T., Chiba S.,
"Complete amino acid sequence of crystalline alpha-glucosidase from
Aspergillus niger.";
Blotechnol. Biochem. 56:1368-1370(1992).
-!- FUNCTION: Hydrolyzes malto-oligosaccharides, but has a low
activity toward soluble starch.
-!- CATALYTIC ACTIVITY: Hydrolysis of terminal, non-reducing 1,4-
linked D-glucose residues with release of D-glucose.
-!- SIMILARITY: BELONGS TO FAMILY 31 OF GLYCOSYL HYDROLASES.
                                                                                                                                                                                                                                                                            Sukaryota, Fungi, Ascomycota, Pezizomycotina, Burotiomycetes,
Eurotiales, Trichocomaceae, mitosporic Trichocomaceae, Aspergillus.
NCBL TaxID=5061;
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15-UUL-1998 (Rel. 36, Created)
15-UUL-1998 (Rel. 36, Last sequence update)
15-SEP-2003 (Rel. 42, Last annotation update)
Alpha-glucosidase precursor (EC 3.2.1.20) (Maltase)
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InterPro; IPR000322; Glyco_hydro_31.
Pfam; PF01055; Glyco_hydro_31; 1.
PROSITE; PS00129; GLYCOSYL, HYDROL_F31_1; 1.
PROSITE; PS00107; GLYCOSYL_HYDROL_F31_2; 1.
Hydrolase; Glycosidase; Glycoprotein; Signal.
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J. Biotechnol. 53:75-84(1997).
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MEDLINE=97308536; PubMed=9165762;
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  (POTENTIAL).
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                                                                                                                                                                                                Matches 320; Conservative 157; Mismatches 313; Indels 121;
                                                                                                                                                             DB 1; Length 1826;
                                                                                                                      MW; 6840D03955A45BE5 CRC64;
  (GLCNAC. . . )
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                                                                                                                                                             27.9%; Score 1355.5; DB 35.1%; Pred. No. 1.6e-82;
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its mose by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                          882 GTASGQLYLDDG------ESIYPNATLHVDFTASRSSLRSSAQGRWK 922
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             "Striking structural and functional similarities suggest that intesting structural and functional similarities suggest that intestinal sucrase-isomaltase, human lysosomal alpha-glucosidase and Schwanniomyces occidentalis glucoamylase are derived from a common ancestral gene.",
FEBS Lett. 294:109-112(1991).
-!- FUNCTION: THIS GLUCOAMYLASE HAS A SPECIFICITY TOWARD BOTH ALPHA-1,4 AND ALPHA-1,6 LINKAGES.
-!- CATALYTIC ACTIVITY: Hydrolygis of terminal 1,4-linked alpha-D-glucose residues successively from non-reducing ends of the chains with release of beta-D-glucose.
-!- SIMILARITY: BELONGS TO FAMILY 31 OF GLYCOSYL HYDROLASES.
         728 NYT-SSVSVSAGTYVSLSAPPDHINVHIHEGNIVAMQGEAMTTQAARSTPFHLLVVMSDH
                                 823 -YIQAAVDAKPGVNTTISAPLGHIPVYVRGGNILPMQEPALTTREARQTPWALLAALGSN
                                                                                                787 VASTGELFLDNGIEMDIGGPGCKWTLVRFFAESGINNLTISSE-VVNRGYAMSO---RW-
                                                                                                                                                                                                                                                                                                                                                               P22861; 092336;
01-AUG-1991 (Rel. 19, Created)
01-AUG-1991 (Rel. 34, Last sequence update)
15-JUL-1998 (Rel. 36, Last annotation update)
Glucoamylase 1 precursor (EC 3.2.1.3) (Glucan 1,4-alpha-glucosidase)
(1,4-alpha-D-glucan glucohydrolase)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.
STRAIN=ATCC 26076;
MEDLINE=91071592; PubMed=1979298;
Dohmen R.J., Strasser A.W.M., Dahlems U.M., Hollenberg C.P.;
"Cloning of the Schwanniomyces occidentalis glucoamylase gene (GAMI.) and its expression in Saccharomyces cerevisiae.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                InterProj IPR000322; Glyco_hydro_31.
Pfam; PF01055; Glyco_hydro_31; 1.
PROSITE; PS00129; GLYCOSYL_HYDROL_F31_1; 1.
PROSITE; PS001707; GLYCOSYL_HYDROL_F31_2; 1.
Hydrolase; Glycosidase; Polysacchāridē degradation; Glycoprotein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Debaryomyces occidentalis (Yeast) (Schwanniomyces occidentalis).
Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
Saccharomycetales; Saccharomycetaceae; Debaryomyces.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SIMILARITY TO OTHER FAMILY 31 MEMBERS.
MEDINDE=22077121; PubMed=1743281;
MIN H.Y., Niermann T., Kleinhans U., Hollenberg C.P.,
Strasser A.W.M.;
                                                                                                                                                                                       ---VMDKITILGLKRRVKIKEYTVQKDAGAIKVKG 873
                                                                                                                                                                                                                                  -----VNKEPSAVTLNG 946
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AVDFWANELVIWSKKVAFDGVWYDMSEVSSFCVGSCGTGNLTLNPAHPSFLLPGEPGDII 526
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                                                                                                                                                                                                                                                                                                  Query Match 27.6%; Score 1339.5; DB 1; Length 985; Best Local Similarity 32.6%; Pred. No. 8.1e-82; Matches 324; Conservative 156; Mismatches 306; Indels 209; Gaps
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R. Nature 415:811-88012002)

R. Data M. Stroker M. Barrell B.G., Nurse P.;

R. Nature 415:811-88012002)
900 KADQ--PLANYILGVGHKPKSVKFENANVDFTYKK--STVFVTGLDKYT---KDGAF 950
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PIR; T38598; T38598.

InterPro; SRC30D11.01c; -.

InterPro; IPR000322; Glyco hydro_31.

Pfam; PF01055; Glyco hydro_31; 1.

PROSITE; PS00129; GLYCOSYL HYDROL F31 1; FALSE NEG.

PROSITE; PS00707; GLYCOSYL HYDROL F31 2; 1.

Hypothetical protein; Hydrolase; Glycosidase; Glycoprotein; Signal. I 24

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01-CT-1996 (Rel. 34, Last sequence update)
01-COT-1996 (Rel. 34, Last sequence update)
10-CT-1996 (Rel. 34, Last annotation update)
10-CT-1996 (Rel. 34, Last annotation update)
10-CT-1996 (Rel. 31, Last annotation update)
10-CT-1996 (Rel. 31, 19-CT-19)
10-CT-1996 (Rel. 31, 19-CT
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   583 NGKPEFSINYPPYALDTDTETHDLAQFGVSPNATMHGNTLRYNLFNTYGYSESKISFEAL 642
                                       --VRPATRGPFLLSRSTPAGSGKYTAHWTGDNAARWDDLQYSIPTMLNFGLFGMPMIGAD 597
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Eurotiales, Trichocomaceae, mitosporic Trichocomaceae, Aspergillus.
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Nucleotide sequence and expression of alpha-glucosidase-encoding
gene (agdA) from Aspergillus oryzae.";

Biosci. Biotechnol. Biochem. 59:1516-1521(1995).

-!- FUNCTION: Hydrolyzes malto-oligosaccharides, but has a low
activity toward soluble starch.

-!- CATALYTIC ACTIVITY: Hydrolysis of terminal, non-reducing 1,4-
linked D-glucose residues with release of D-glucose..-
-!- INDUCTION: By maltose.
-!- SIMILARITY: BELONGS TO FAMILY 31 OF GLYCOSYL HYDROLASES.
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IS-JUL-1998 (Rel. 36, Last sequence update)
IS-SEP-2003 (Rel. 42, Last annotation update)
Alpha-glucosidase precursor (EC 3.2.1.20) (Maltase) (AGL)
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Biochem. J. 285:915-923(1992)
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31.8%; Pred. No. 1.2e-79;
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RGIMVSPVLQPGSSIVNAYSP---RG----NWVSLSNYTSSVSVSAGTYVSLSAPPDHIN
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--- SUBUNIT: THE RESULTING SUCKASE AND ISOMALTASE SUBUNITS STAY
ASSOCIATED WITH ONE ANOTHER IN A COMPLEX BY NON-COVALENT LINKAGES.
--- SUBCELLULAR LOCATION: Type II membrane protein. Brush border.
--- PITH: THE PRECURSOR IS PROTEOLYTICALLY CLEAVED WHEN EXPOSED TO
PANCREATIC PROTEASES IN THE INTESTINAL LUMEN.
                                                                                                                                                                       VHIHEGNIVAMQGEAMTTQAARSTPFHLLVVMSDHVASTGELFLDNGIEMDIGGPGGKWT
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--- CATALYTIC ACTIVITY: Hydrolysis of sucrose and maltose by an alpha-D-glucosidase-type action.
--- CATALYTIC ACTIVITY: Hydrolysis of 1,6-alpha-D-glucosidic linkages in some oligosaccharides produced from starch and glycogen by
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WEDLINE=96189940; PubMed=6609217;

Ouwendijk J., Woolenaar C.E.C., Peters W.J., Hollenberg C.P.,

Ginsel L.A., Fransen J.A.M., Naim H.Y.;

"Congenital sucrase-isomaltase deficiency; identification of a
glutamine to profile substitution that leads to a transport block sucrase-isomaltase in a pre-Golgi compartment.";

J. Clin. Invest. 97:633-641(1996).

-- FUNCTION: PRAYS AN IMPORTANT ROLE IN THE FINAL STAGE OF
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Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.
NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-JAN-1990 (Rel. 13, Created)
30-MAY-2000 (Rel. 39, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Sucrase-isomaltase, intestinal [Contains: Sucrase (EC 3.2.1.48);
Isomaltase (EC 3.2.1.10)].
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            "Isolation of a cDNA probe for a human jejunal brush-border hydrolase, sucrase-isomaltase, and assignment of the gene locus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE OF 1-677 FROM N.A.
MEDLINE=88112852; PubMed=2962903;
Green F., Edwards Y., Hauri H.-P., Povey S., Ho M.W., Pinto M.,
Swallow D.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 sucrase-isomaltase gene. Possible homology with a yeast
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103 RWEIPNEVLPRPPPPPPPPPSSLQHLPRPIPQNQPTTTVLSHPHSDLAFTLFHTTFFGF 162
                                                                                                                                                                                                                                                  223 NOILTLWNADIASFNRDL-----NLYGSHPFYMDVRSSPWVGSTHGVFLLNSNGMDVE 275
                                                                                                                                                                                                                                                                                                                                                                                                       276 YTGDRI-TYKVIGGIIDLYIFAGRIPEMVLDQYTKLIGRPAPMPYWAFGFHQCRWGYRDV 334
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      395 PILDPGINTNK----SYGTFIRGMQSNVFIKRN--GNPYLGSVWPGPVYYPDFLDPAAR 447
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             556 AGSGKYTAHWIGDNAARWDDLQYSIPIMLNFGLFGMPMIGADICGFAESITEELCCRWIQ 615
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                651 IGAFYPFSRNHNSDGYEHODPAFFGONSLLVKSSRQYLTIRYTLLPFLYTLFYKAHVFGE 710
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         673 PIARPLSFTFPDDVATYGISSQFLIGRGIMVSPVLQPGSSIVNAYSPRGNWVSLSNYTSS 732
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              163 TIYRKSTHDVLFDATPIPSNPTTFLIYKDQYLQLSSSLPAQQAHLYGLGEHTKPTFQLAH 222
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  305 IQPTPIVTYRVTGGILDFYILLGDTPEQVVQQYQQLVGLPAMPAYMNLGFQLSRWNYKSL 364
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NEIETVVDKYAEARIPLEVMWTDIDYMDAFKDPTLDPVHFPLDKMQQFVTKLHRNGQRYV 394
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      733 VSVS-AGTYVSLSAPPDHINVHIHEGNIVAMQGEAMTTQAARSTPFHLLVVMSDHVASTG 791
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                                                                                                                                          43 YGYQVKNAKVDNSTGKSLTALLQLIRNSPVYGPDIHFLSFTASFBEDDTLRIRFTDANNR
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                                                         26.8%; Score 1304; DB 1; Length 1826;
llarity 34.6%; Pred. No. 4.6e-79;
Conservative 157; Mismatches 316; Indels 114;
                    209272 MW; 3F7E4B66FDCF9C8E CRC64;
    MISSING (IN REF.
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                      1826 AA;
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                                                                                                                                                     This SWISS-FROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bloinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (see http://www.isb-sib.ch/announce) or send an email to license@lsb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SIGNAL-ANCHOR (TYPE-II MEMBRANE PROTEIN).
                                                                                                                                                                                                                                                                                                                          E WEBL; X63597; CA445140.1; -..

R EMBL; M22616; AA460551.1; ALT_SEQ.

R PIR; S36082; UUHU.

R Genew; HGNC:10856; SI.

R Gorew; HGNC:10856; SI.

R Gorew; HGNC:10856; SI.

R GO; GO:0005903; C:brush border; TAS.

R GO; GO:0005903; C:brush border; TAS.

R GO; GO:0005903; C:brush border; TAS.

R GO; GO:000329; Glgidi apparatus; TAS.

R InterPro; IPR000512; Glycoc hydro_31.

R InterPro; IPR000519; P trefoil.

R Fam; PF00088; trefoil.; P TREFOIL; I.

R PROSITE; PS00025; P TREFOIL; I.

R ROSITE; PS00129; GlYCOSYL HYDROL F31_2; I.

R PROSITE; PS00129; GlYCOSYL HYDROL F31_2; I.

R MULLifunctional enzyme; Transmembrane; Glycoprotein; Hydrolase; KW MULLifunctional enzyme; Transmembrane; Glycoprotein; Hydrolase; KW MULLifunctional enzyme; Signal-ambrane; Glycoprotein; BY SIMILARITY.

R INIT_MET 0 BY SIMILARITY.

FT CHAIN IIIT_MET 1 1826

R SUCRASE ISOMALTASE, INTESTINAL.
DISEASE: Defects in SI are the cause of disaccharide intolerance
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ot
                                     MISCELLANEOUS: THERE IS A HIGH DEGREE OF HOMOLOGY BETWEEN THE ISOMALTASE AND SUCRASE PORTIONS (41 % OF AMINO ACID IDENTITY) INDICATING THAT THIS PROTEIN IS EVOLVED BY PARTIAL GENE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              iD (GLCNAC. . .) (POTENTIAL).
(in disaccharide intolerance)
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                                                                                                                   -!- SIMILARITY: BELONGS TO FAMILY 31 OF GLYCOSYL HYDROLASES.
-!- SIMILARITY: Contains 1 P-type (trefoil) domain.
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BY SIMILARITY.
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SULFATION (POTENTIAL).
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GenCore version 5.1.6
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; Search time 23.8921 Seconds (without alignments) 3678.964 Million cell updates/sec US-10-043-418-2 4862 1 MERSKLPRYICPTLAVVLPL......RQLVGQAFKLELEFEGATRV 914 OM protein - protein search, using sw model October 27, 2003, 10:19:13 Perfect score: Sequence: Run on:

Total number of hits satisfying chosen parameters:

283308 seqs, 96168682 residues

Searched:

BLOSUM62 Gapop 10.0 , Gapext 0.5

Scoring table:

seq length: 0 seq length: 200000000 Minimum DB Maximum DB Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

PIR 76:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:* Database

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

alpha-glucosidase alpha-glucosidase alpha-glucosidase hypothetical prote alpha-glucosidase sucrose alpha-gluc glucan 1,4 alpha-g probable family 31 alpha-glucosidase sucrose alpha-gluc sucrose alpha-gluc alpha-glucosidase hypothetical prote hypothetical prote alpha-glucosidase hypothetical prote alpha-glucosidase hypothetical prote alpha-glucosidase alpha-glucosidase alpha-glucosidase alpha-glucosidase alpha-glucosidase alpha-glucosidase alpha-glucosidase alpha-glucosidase alpha-glucosidase probable alpha-glu alpha-glucosidase alpha-glucosidase hypothetical hypothetical hypothetical Description SUMMARIES JCS463 T09143 S68531 S68657 H96709 T47534 JC4624 A23609 A33945 JN0102 JC45217 UN0102 JC4517 UN0102 T10799 S19686 T15893 JC1200 AH1097 AG1460 S46105 AC2472 T22050 T22044 T32449 T16693 T22575 AE2402 T07391 Ouery Match Length DB 4858 3243.5 2719.5 2370 2045 1467 1467 1450.5 1355.5 1321.5 1321.5 1321.5 1321.5 1320.5 1320.5 1320.5 1320.5 1320.5 1320.5 1320.5 1320.5 1320.5 1320.5 1320.5 1320.5 1320.5 1320.5 1320.5 1320.5 1320.5 1320.5 1320.5 1320.5 1320.5 1320.5 1320.5 1320.5 1320.5 1320.5 1320.5 1320.5 1320.5 1320.5 1320.5 1320.5 1320.5 1320.5 1320.5 1320.5 1320.5 1320.5 1320.5 1320.5 1320.5 1320.5 1320.5 1320.5 1320.5 1320.5 1320.5 1320.5 1320.5 1320.5 1320.5 1320.5 1320.5 1320.5 1320.5 1320.5 1320.5 1320.5 1320.5 1320.5 1320.5 1320.5 1320.5 1320.5 1320.5 1320.5 1320.5 1320.5 1320.5 1320.5 1320.5 1320.5 1320.5 1320.5 1320.5 1320.5 1320.5 1320.5 1320.5 1320.5 1320.5 1320.5 1320.5 1320.5 1320.5 1320.5 1320.5 1320.5 1320.5 1320.5 1320.5 1320.5 1320.5 1320.5 1320.5 1320.5 1320.5 1320.5 1320.5 1320.5 1320.5 1320.5 1320.5 1320.5 1320.5 1320.5 1320.5 1320.5 1320.5 1320.5 1320.5 1320.5 1320.5 1320.5 1320.5 1320.5 1320.5 1320.5 1320.5 1320.5 1320.5 1320.5 1320.5 1320.5 1320.5 1320.5 1320.5 1320.5 1320.5 1320.5 1320.5 1320.5 1320.5 1320.5 1320.5 1320.5 1320.5 1320.5 1320.5 1320.5 1320.5 1320.5 1320.5 1320.5 1320.5 1320.5 1320.5 1320.5 1320.5 1320.5 1320.5 1320.5 1320.5 1320.5 1320.5 1320.5 1320.5 1320.5 1320.5 1320.5 1320.5 1320.5 1320.5 1320.5 1320.5 1320.5 1320.5 1320.5 1320.5 1320.5 1320.5 1320.5 1320.5 1320.5 1320.5 1320.5 1320.5 1320.5 1320.5 1320.5 1320.5 1320.5 1320.5 1320.5 1320.5 1320.5 1320.5 1320.5 1320.5 1320.5 1320.5 1320.5 1320.5 1320.5 1320.5 1320.5 1320.5 1320.5 1320.5 1320.5 1320.5 1320.5 1320.5 1320.5 1320.5 1320.5 1320.5 1320.5 1320.5 1320.5 1320.5 1320.5 1320.5 1320.5 1320.5 1320.5 1320.5 1320.5 1320.5 1320.5 1320.5 1320.5 1320.5 1320.5 1320.5 1320.5 1320.5 1320.5 1320.5 1320.5 1320.5 1320.5 1320.5 1320.5 1320.5 1320.5 1320.5 1320.5 1320.5 1320.5 1320.5 1320.5 1320.5 1320.5 1320.5 1320.5 1320.5 1320.5 1320.5 1320.5 1320.5 1320.5 1320.5 1320.5 1320.5 1320.5 1320.5 1320.5 1320.5 1320.5 1320.5 1320.5 1320.5 1320.5 1320.5 1320.5 1320.5 1320.5 1320.5 1320.5 1320.5 1320.5 1320.5 1320.5 1320.5 1320.5 1320.5 1320.5 1320.5 1320.5 1320.5 1320.5 1320.5 1320.5 1 Score Result No.

alpha-glucosidase	sucrose alpha-gluc	alpha-xylosidase -	hypothetical 88.1	hypothetical prote	hypothetical prote	alpha-xylosidase (probable glycosyl	hypothetical prote	glycosyl hydrolase	glucosidase BH0704	alpha-glucosidase	probable glucosida	probable glycosyl	hypothetical prote	sucrose alpha-gluc
H90486	S11386	A72394	B65167	D91195	B86042	D90483	A10968	A83888	B87347	H83737	H97033	AD0104	AD0507	G83906	A36690
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693	642	764	772	772	772	731	772	773	983	801	769	792	619	657	275
14.3	11.1	6.6	9.6	9.7	9.7	9.7	9.3	9.1	8.8	8.7	9.8	8.1	7.7	7.6	7.5
		2	'n	ß.	s.	470	453	444.5	428.5	424	418	392.5	373.5	368.5	367
969	541.5	481	479	473	473	•	•	44	42			39	37.	36	.,

ALIGNMENTS

RESULT 1 JCS463 alpha-glucosidase (EC 3.2.1.20) - sugar beet alpha-glucosidase (EC 3.2.1.20) - sugar beet Alternate names: alpha-D-glucoside glucohydrolase C;Species: Beta vulgaris var. altissima (sugar beet) C;Accession: JC5463; PC4330 R;Matsui, H.; Iwanami, S.; Ito, H.; Mori, H.; Honma, M.; Chiba, S. Biosci. Biotechnol. Biothem. 61, 817-880, 1997 A;Title: Cloning and sequencing of a cDNA encoding alpha-glucosidase from sugar beet. A;Reference number: JC5463; MUID:97321863; PMID:9178565 A;Accession: JC5463; MUID:97321863; PMID:9178565	MAT1> DDBJ:D89615; NID:g2217947; PIDN:BAA20343. ce: seed; cv. NK-152 otein ;310-365;507-541;810-840 <mat2> cs seed yme is a exo-glucohydrolase that catalyzes somal alpha-glucosidase; sucrase/isomaltas daee; hydrolase ucrase/isomaltase homology <sim></sim></mat2>	<pre>Query Match 99.9%; Score 4858; DB 2; Length 913; Best Local Similarity 100.0%; Pred. No. 0; Matches 913; Conservative 0; Mismatches 0; Indels 0; Gaps 0; Matches 911; Conservative 0; Mismatches 0; Indels 0; Gaps 0; I MERSKI.PRYICPTLAVVI.PLVI.CMVVEGATTSKNDNQCEAIGYGYQVKNAKVDNSTGKSL 60</pre>	TALLOLIRNSPVYGDDIHFLSFTASFEEDDTLRIRFTDANNRRWEIPNBVLPRPPPPPS	121 PPLOSECHERKIPONOPTITVESHPHSDLAFTEFHTIFGFT1IKASTHDVEDATFIF 180 	181 SNPTFLIYKDQYLQLSSSLPAQQAHLYGLGEHTKPTFQLAHNQILTLWNADIASFNRDL 240 	241 NLYGSHPEYMDVRSSPMVGSTHGVFLLNSNGMDVRYTGDRITYKVIGGIIDLYIFAGRTP 300 	301 EMVLDOYTKLIGREARMPYWAFGFHOCRWGYRDVNEIETVVDKYAEARIPLEVWWTDIDY 360
RESULT 1 JC5463 JC5463 NALpha-glucosidase ((NALternate names: () C;Species: Beta vul. C;Actes: Jr.Jun.1997 C;Actession: H.; Iwanal Blosci. Biotechnol. A;Title: Cloning an A;Reference number: A;Accession: JC5463 A;Accession: JC5463 A;Accession: JC5463 A;Accession: JC5463 A;Accession: JC5463 A;Accession: JC5463 A;Accession: JC5463 A;Accession: JC5463 A;Accession: JC5463 A;Accession: JC5463 A;Accession: JC5463 A;Accession: JC5463 A;Accession: JC5463 A;Accession: JC5463 A;Accession: JC5463 A;Accession: JC5463 A;Accession: JC5463 A;Accession: JC5463 A;Accession: JC5463 A;Accession: JC5463 A;Accession: JC5463 A;Accession: JC5463 A;Accession: JC5463 A;Accession: JC5463 A;Accession: JC5463 A;Accession: JC5463 A;Accession: JC5463 A;Accession: JC5463 A;Accession: JC5463 A;Accession: JC5463 A;Accession: JC5463 A;Accession: JC5463 A;Accession: JC5463 A;Accession: JC5463 A;Accession: JC5463 A;Accession: JC5463 A;Accession: JC5463 A;Accession: JC5463 A;Accession: JC5463 A;Accession: JC5463 A;Accession: JC5463 A;Accession: JC5463 A;Accession: JC5463 A;Accession: JC5463 A;Accession: JC5463 A;Accession: JC5463 A;Accession: JC5463 A;Accession: JC5463 A;Accession: JC5463 A;Accession: JC5463 A;Accession: JC5463 A;Accession: JC5463 A;Accession: JC5463 A;Accession: JC5463 A;Accession: JC5463 A;Accession: JC5463 A;Accession: JC5463 A;Accession: JC5463 A;Accession: JC5463 A;Accession: JC5463 A;Accession: JC5463 A;Accession: JC5463 A;Accession: JC5463 A;Accession: JC5463 A;Accession: JC5463 A;Accession: JC5463 A;Accession: JC5463 A;Accession: JC5463 A;Accession: JC5463 A;Accession: JC5463 A;Accession: JC5463 A;Accession: JC5463 A;Accession: JC5463 A;Accession: JC5463 A;Accession: JC5463 A;Accession: JC5463 A;Accession: JC5463 A;Accession: JC5463 A;Accession: JC5463 A;Accession: JC5463 A;Accession: JC5463 A;Accession: JC5463 A;Accession: JC5463 A;Accession: JC5463 A;Accession: JC5463 A;Accession: JC5463 A;Accession: JC5463 A;Accession: JC5463 A;Accession: JC5463 A;Accession: JC5463 A;Accession: JC5463 A;Accession: JC5463 A;Accession: J	A, Residues: 1-913 and A, Cross-references: A, Cross-references: A, Accession: PC4330 A, Molecule type: pr A, Residues: 234-261 A, Experimental sour C, Comment: This enc. C, Superfamily: 1yso C, Reywords: glycosi F;149-803/Domain: s	Query Matc Best Local Matches 9	6 6	12 12	18	24 4	30
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alpha-glucosidase 1 - Arabidopsis thaliana
N;Alternate names: protein T22P22.110
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 20-Apr-2000 #sequence_revision 20-Apr-2000 #text_change 21-Jul-2000
C;Accession: T48531
R;Bevan, M.; Hilbert, H.; Braun, M.; Holzer, E.; Brandt, A.; Duesterhoeft, A.; Bancro: submitted to the Protein Sequence Database, April 2000
A;Reference number: 224490
A;Accession: T48531
A;Accession: T48531
A;Accession: P48531
A;Accession: P48531
A;Accession: Bashainary
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A;Coross-references: EMBL:ALI63814
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                           SLSSLYRILLSSPITNRRKILLSHPNSDLIPSLINITPFGFTISRKSTHDVLFDATPDPT 177
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                                                                                                                                                                                        LYGSHPFYMDVRSSPMVGSTHGVFLLNSNGMDVEYTGDRITYKVIGGIIDLYIFAGRTPE 301
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  PLSSLQHLPKPIPQNQPTTTVLSHPHSDLAFTLFHTTPFGFTIYRKSTHDVLFDATPIPS
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                                                                                             NPTTFLIYKDQYLQLSSSLPAQQAHLYGLGEHTKPTFQLAHNQILTLWNADIASFNRDLN
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C;Species: Spinacia oleracea (spinach)
C;Species: Spinacia oleracea (spinach)
C;Date: 11-Jun-1999 #sequence_revision 11-Jun-1999 #text_change 21-Jul-2000
C;Accession: T09143
R;Sugimoto, M.; Furui, S.; Suzuki, Y.
R;Sugimoto, M.; Furui, S.; Suzuki, Y.
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C; Superfamily: lysosomal alpha-glucosidase; sucrase/isomaltase homology; trefoil homolog
C; Keywords: glycosidase; hydrolase
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                                                                                                                     KRNGNPYLGSVWPGPVYYPDFLDPAARSFWVDEIKRFRDILPIJGIWIDWREASNFITSA
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MDAFKDFTLDPVHFPLDKMQQFVTKLHRNGQRYVPILDPGINTNKSYGTFIRGMQSNVFI
                                                                                                                                                                                        PTPGSTLDNPPYKINNSGGRVPINSKTIPATAMHYGNVTEYNAHNLYGFLESQATREALV
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                                                                                          KRNGNPYLGSVWPGPVYYPDFLDPAARSFWVDEIKRFRDILPIDGIWIDMNEASNFITSA
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Best Local Similarity 67.3%; Pred. No. 2e-221;
Matches 610; Conservative 122; Mismatches 166; Indels
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A/Accession: S65057
A/Molecule type: mRNA
A/Recession: S65057
A/Molecule type: mRNA
A/Recession: S65058
A/Molecule type: mRNA
A/Tribot, B.K.; Skadeen, R.W.
Plant Mol. Biol. 30, 229-241, 1996
A/Trile: Molecular cloning and characterization of a gibberellin-inducible, putative in A/Trile: Molecular cloning and characterization of a gibberellin-inducible, putative in A/Trile: Molecular cloning and characterization of a gibberellin-inducible, putative in A/Trile: Molecular cloning and characterization of a gibberellin-inducible, putative in A/Trile: Molecular cloning and characterization of a gibberellin-inducible, putative in A/Trile: Molecular cloning and characterization of a gibberellin-inducible, putative in A/Trile: Molecular cloning and characterization of a gibberellin-inducible, putative in A/Trile: Molecular closide scidence not shown
A/Accession: S65058
A/Trile: Molecular cloning and characterization of a gibberellin-inducible, putative in A/Trile: Molecular closide scidence not shown
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                                                                                                                              alpha-glucosidase (EC 3.2.1.20) - barley
C;Species: Hordeum vulgare (barley)
C;Species: Hordeum vulgare (barley)
C;Dacession: S65057, S65058
R;Tibbot, B.K.; Skadsen, R.W.
submitted to the RMBL Data Library, March 1995
A;Description: Molecular cloning and characterization of a gibberellin-induc
A;Reference number: S65057
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  183 PTTPLIYKDQYLQLSSSLPAQQAHLYGLGEHTKPTFQLAHNQILTLWNADIASFNRDLNL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ---GLVFRDKYLEVTSALPAGRASLYGLGEHTKSSFRLRHNDSFTLWNADIGASYVDVNL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     16 VVLPLVLCMVVEGATTSKNDNQGEA---IGYGYQVKNA-KVDNST-GKSLTALLQLIRNS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 7 LLLCLCLCLCLFAPRLCSSKEEGPLAARTVLAVAVTMEGALRAEAATGGRSSTG-----
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     894 KFEMRL
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                                                                                                                                      C; Superfamily: lysosomal alpha-glucosidase; sucrase/isomaltase homology; trefoil homolog
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FKDFTLDPVHFPLDKMQQFVTKLHRNGQRYVPILDPGINTNKSYGTFIRGMQSNVFIKRN 423
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                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                       55.9%; Score 2719.5; DB 2; Length 902; 57.0%; Pred. No. 2.7e-184;
                                                                                                                                                                                                                                                    Indels
A; Experimental source: cultivar Columbia; BAC clone T22P22
                                                                                                                                                                                                                       Best Local Similarity 57.0%; Pred. No. 2./e-184;
Matches 516; Conservative 146; Mismatches 219;
                                        A;Map ________5
A;Introns: 78/2; 313/1; 390/1; 605/3; 747/1
A;Note: T22P22.110
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;Superfamily: lysosomal alpha-glucosidase; sucrase/isomaltase homology; trefoil homo
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C;Species: Arabidopsis thaliana (Mouse-ear cress)
C;Species: Arabidopsis thaliana (Mouse-ear cress)
C;Species: Arabidopsis thaliana (Mouse-ear cress)
C;Accession: T47534
R;Jordan, N.; Bangert, S.; Wiedelmann, R.; Voss, H.; Unseld, M.; Mewes, H.W.; Rudd, Submitted to the Protein Sequence Database, March 2000
A;Reference number: Z24468
A;Accession: T47534
A;Status: preliminary
A;Molecule type: DMR
A;Residues: 1-855 sJOR
A;Resperimental source: Cultivar Columbia; BAC clone F16L2
:|:
LRNVGGKAYAHAVLLLNSNGMDVFYRGDSLTYKVIGGVFDFYFIAGPSPLNVVDQYTQLI 282
                                                                GRPAPMPYWAFGFHQCRWGYRDVNEIETVVDKYAEARIPLEVMWTDIDYMDAFKDFTLDP 371
                                                                                          462
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                                                                                                                                                  VHFPLDKMOOFVTKLHRNGORYVPILDPGINTNKSYGTFIRGMOSNVFIKRNGNPYLGSV
                                                                                                                                                                                                                                    WPGPVYYPDFLDPAARSFWVDEIKRFRDILDPIDGIWIDMNEASNFIT-----S
                                                                                                                                                                                                                                                                              403 WPGPVYFPDFLNPKTVSWWGDEIKRFHDLVPIDGLWIDMNBVSNFCSGLCTIPEGKOCPS
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A;Introns: 69/3; 291/1; 427/3; 699/1
A;Note: F16L2.150
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C,Species: Arabidopsis thaliana (mouse-ear cress)
C,Species: Arabidopsis thaliana (mouse-ear cress)
C,Accession: H96709
R;Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alonso, Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, K.; ansen, N.F.; Hughes, B.; Huizar, L.
Nature 408, 816-820, 2000
A;Authors: Hunter, J.L.; Ji, N.; Liu, X.; Liu, X.K.; Liu, Z.A.; Luros, J.S.; Khaykin, E.; Kim, C.C., Li, J.H.; Li, Y.; Liu, X.; Liu, X.K.; Liu, Z.A.; Luros, J.S.; Maiti, R.; Marziali, Rizoney, T.; Rowley, D.; Sakano, H.
A;Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon, A;Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.
A;Reference number: A86141; MUID:21016719; PMID:11130712
                                                                                                          719
                                                                                                                                                  685
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                                                                                                                                                                                                                                                                              LVVMSDHVASTGELFLDNGIEMDIGGPGGKWTLVRFFAESGINN--LTISSEVVNRGYAM 837
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A,Molecule type: DNA
A,Residues: 1-915 <STO>
A,Cross-references: GB:AE005173; NID:g5734722; PIDN:AAD49987.1; GSPDB:GN00141
                                              566 GFNGNTTEELCGRWIQLGAFYPFSRDHSAIFTVRRELYLWPSVAASGRKALGLRYQLLPY
                                                                                                                              720 RGNWVSLSNYTSSVSVSAGTYVSLSAPPDHINVHIHEGNIVAMQGEAMTTQAARSTPFHL
                                                                                                                                                                                                                  13 TLAVVLPLVLCMVVEGATTSKNDNQGEAIGYGYQVKNAKVDNSTGKSLTALLQLIRNSPV
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                                                                                                        YYTLMYDANLRGSPIARPLSFTFPDDVATYGISSQFLIGRGIMVSPVLQPGSSIVNAYSP
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                      GFAESTTEELCCRWIQLGAFYPFSRDHSARDTTHQELYLWESVAASARTVLGLRYELLPY
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864 VVGEEFELKV 873
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JC4624
alpha glucosidase (EC 3.2.1.20) - Rhizomucor circinelloides f. circinelloides
cispecies: Rhizomucor circinelloides f. circinelloides
cispecies: Rhizomucor circinelloides f. circinelloides
cispecies: 10-May-1996 #sequence_revision 19-Jul-1996 #text_change 20-Jun-2000
cispeciesion: JC4624; PC4149
Els.Sugimoto, M.; Suzuki, Y.
J. Blochem. 119, 500-505, 1996
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idues: 203-214,492-495,612-623;715-731;742-751;769-778 <SUG2>
idues: 203-214,492-495,612-623;715-731;742-751;769-778 <SUG2>
idues: 203-214,492-495,612-623;715-731;742-751;769-778 <SUG2>
idues: 203-214,492-495;612-623,715-731;742-751;769-778 <SUG2>
idues: 203-404,704 is an exo-carbohydrase, and catalyzes the splitting of an alphaent: extramily: 1ysosomal alpha-glucosidase; sucrase/isomaltase homology; trefoil homowords: 31ycoprocein; 31ycosidase; hydrolase
words: 31ycoprocein; 31ycosidase; hydrolase
%SOS/Domain: sucrase/isomaltase homology <SIM>
%SOS/Domain: sucrase/isomaltase homology <SIM>
%Active site: Asp #status predicted
                                         of a cDNA encoding alpha-gluco:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ---LNLYGSHPPYMDVRSSPMVGSTHGVFLLNSNGMDVEYTGDRITYKVIGGIIDLYIFA 296
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             297 GRT--PEMVLDQYTKLIGRPAPMPYWAFGFHQCRWGYRDVNEIETVVDKYAEARIPLEVM 354
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         QSNVPIKR-NGNPYLGSVWPGPVYYPDFLDPAARSFWVDEIKRFRDILPIDGIWIDMNEA 473
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                                                                                                                                                                                                                                 idues: 1-864 <SUG1>
ss-references: DDBJ:D67034; NID:g1498134; PIDN:BAA11053.1; PID:g1498135
ession: PC4149
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        9 YICPTLAVVLPLVLCMVVEGATTSKNDNGGRAIGYGYGVQVKNAKVDNSTGKSLTAL-LOLI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PSNPTTFLIYKDQYLQLSSSLPAQQAHLYGLGEHTKPTFQLAHNQILTLWNADIASFNRD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ry Match 30.0%; Score 1460.5; DB 2; Length 864; t Local Similarity 36.4%; Pred. No. 4.1e-95; ches 313; Conservative 151; Mismatches 281; Indels 115;
le: Molecular cloning, sequencing, and expression c
erence number: JC4624; MUID:96271012; PMID:8830045
ession: JC4624
                                                                                                                                                                                                  scule type: mRNA
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A;Gene: GDB:GAA
A;Cross-references: GDB:119965; OMIM:232300
A;Gene: GDB:GAA
A;Cross-references: GDB:119965; OMIM:232300
A;Gene: GDB:GAA
A;Cross-references: GDB:119965; OMIM:232300
A;Introns: 182/3: 231/2: 286/3; 319/1; 359/1; 398/3; 442/3; 479/3; 517/3; 546/1; 585/A;Introns: 182/3: 231/2: 286/3; 319/1; 359/1; 398/3; 442/3; 479/3; 517/3; 546/1; 585/A;Introns: 182/3: 231/2: 286/4; and GAA 4 are common alleles in the normal population
C;Function:
A;Note: GAA 1, GAA 2, and GAA 4 are common alleles in the normal population
A;Description: also has BC 3.1.2.3 activity; hydrolyzes alpha 1, 4 and alpha 1, 6 glyco
C;Fuperfamily: lysosomal alpha-glucosidase; bucrase/isomaltase homology complexed is glycoprotein; glycosidase; hydrolase; lycosomal storage disease; lysosome
C;Fuperfamily: lysosomal alpha-glucosidase; hydrolase; lycosomal storage disease; lysosome
F;82-130/Domain: trefoil homology care.
F;20-130/Domain: trefoil homology care.
F;20-130/Domain: trefoil homology care.
F;20-100,103-127/Disulfide bonds: #status predicted
F;122-123/Cleavage site: Met-Gly (unidentified proteinase) #status experimental
F;20-204/Cleavage site: Arg-Ala (unidentified proteinase) #status experimental
F;300,470,492,652,882,925/Binding site: carbohydrate (Asn) (covalent) #status predict
;Comment: In common with other lysosomal enzymes, posttranslational processing inclu processing at both amino and carboxyl ends.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   659 VRWTQLGAFYPFMRNHNSLLSLPQBPYSFSBPAQQAMRXALTLRYALLPHLYTLFHQAHV 718
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               32 SKNDNQGEAIGYGY----QVKNAKVDNSTGKSLTALLQLIRNSPVYGP-DIHFLSFTAS
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A; Residues: 1-126, 'VLL', 130-198, 'R', 200-222, 'H', 224-371, 'L', 373-401, 'R', 403-412, 'TSRSTRN
A; Cross-references: EMBL:Y00839
A; Accession: 518847
A; Molecule type: protein
A; Molecule type: protein
A; Residues: 70-89;123-126, 'VLL', 130-145;204-215;230-249;332-345;349-370;394-4C1, 'R', 403-R; Lin, C.Y; Shieh, J.J.
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A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 631-644, H', 646-680 «RES>
A;Cross-references: GB:S76893; NID:g912786; PIDN:AAB33842.1; PID:g912787
A;Note: homozygous mutation of Asp-645 to His causes an infantile form of Pompe's diseas
B;Puller, M,; van der Ploeg, A., Reuser, A.J.J.; Anson, D.S.; Hopwood, J.J.
Bur. J Biochem. 234, 903-909, 1995
A;Title: Isolation and characterisation of a recombinant, precursor form of lysosomal act A;Reference number: S63526; MUID:96163476; PMID:8575451
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A; Title: Identification of the base-pair substitution responsible for a human acid alpha
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       R;Hoefsloot, L.H.; Hoogeveen-Westerveld, M.; Kroos, M.A.; van Beeumen, J.; Reuser, A.J.;
BMD J. 7, 1697-1704, 1988
A;Title: Primary structure and processing of lysosomal alpha-glucosidase; homology with
A;Reference number: S00831; MUID:89005058; PMID:3049072
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Pompe
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A; Molecule type: DNA
A; Molecule type: DNA
A; Nolecule type: MAN
A; Note: Order of exons in Figure 2 is incorrect
A; Note: order of exons in Figure 2 is incorrect
B; Martiniuk, F.; Mehler, M.; Tzall, S.; Meredith, G.; Hirschhorn, R.
DNA Cell Biol. 9, 85-94, 1990
A; Title: Sequence of the CDNA and 5'-flanking region for human acid alpha-glucosidase, a with previous CDNA and amino acid sequences.
A; Reference number: A32609; MUID:90262651; PMID:2111708
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               structural gene for human acid
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A;Title: Identification of a de novo point mutation resulting in infantile form of
A;Reference number: 152309; MUID:95209708; PXID:7695647
                                    SVSAGT-----YVSLSAPPDHINVHIHEGNIVAMQGEAMTTQAARSTPFHLLVVWSCHVA 788
                                                                                                  731 TVDNKSNKKVKTVTĽDAPLTHÍPIHÍRGÁAÍIPTKTPKYTVGETFATPYNLVIALDKKGQ 790
                                                                                                                                                                                                                                                                                                                                                                                             alpha-glucosidase (BC 3.2.1.20) precursor, lysosomal - human N.Alternate names: acid alpha-glucosidase; acid maltase; maltase-glucoamylase C.Species: Home sapiens (man)
C.Date: 21-May-1990 Msequence_revision 05-Apr-1995 #text_change 18-Jun-1999 C.Accession: A40577; A32609; A35698; S00831; S18847; I52309; S63526 R.Martiniuk, F.; Bodkin, M.; Tzall, S.; Hirschhorn, R. A.Title: Isolation and partial characterization of the structural gene for hum A.Reference number: A40577; MUID:91229688; PMID:1674202
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A;Cross-references: GB:M34424; NID:g182907; PIDN:AAA52506.1; PID:g182908
R;Martiniuk, F.; Bodkin, M.; Tzall, S.; Hirschhorn, R.
Am. J. Hum. Genet. 47, 440-445, 1990
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A,Contents: partial sequence of GAA 2 allelic form
A,Accession: A35698
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A,Residues: 1-90,'N',92-129 <MA3>
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A, Residues: 68-74,'X',76-79,'X',81 <FUL>
                                                                                                                                                                                                                                    791 ASGRLYIDDGESLEVKSSSG 810
                                                                                                                                                                       STGELFLDNGIEMDIGGPGG
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A; Residues: 1-952 < MA2>
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LMGEALLITPVLQAGKAEVTGYFPLGTWYDL 775 QY 103 RWEIPNBVLPRPPPPRSPPPRSPPPLSSLQHLPKPIPQNQPTTTVLSHPHSDLAFTLFHTTP -GTYVSLSAPPDHINVHIHEGNIVAMQGEAMTTQ 770 Db 169 RYEVPHQFYTEFAGPAATETLYDVQVTENPTENPTENPTENPTEN	834 QY 163	830 Db 202	871 Db 252	TYSPDTKVLDI 937 QY 276 YTGDRI-TYKVIGGIIDLYIFAGRTPEMVLDQYTKLIGRPAPMPYWAFGFHQCRWGYRDV	Qy	ct_change 24-May-1996 Qy 395 PILDDGINTNKSYGTFIRGMQSNVPIKRNGNPYLGSVWPGPVYYPDFLDPAAR	ure, membrane-orientation, and ev Oy 448 SFWVDEIKRERDILPIDGIWIDMNEASNFITSAPTPGSTLDNPPYKINNSGGRVP :	Cy 503INSKTIPATAMEFYGNVTEYNAHNLYGFLESQATREALVRPATRGPFLLSRSTFAG	ase-isoma Qy 558	Qy 618	nal seque DD 654 Oy 675	and 0-11	ucosi	0y 795	y rolase; π	111) #status experimental <150> : : :: :: :: :: :: ::	906 ÅÖ	Db 932 DQTFLESEKIT	9/Binding	C.Species: Schizoaaccharomyces pombe C.Species: O9-Jun-2000 #sequence_revision 09-Jun-2000 #text_ C.Accession: T50267 C.Accession: C.Accession: R.Hunt, C.; Aves, S.; McDougall, R.C.; Rajandream, M.A.;	
AGETVARPLFLEFPKDSSTWTVDHQLLWGEALLITPVLQAGKAEVTGYFPLGTWYDL TSSVSVSAGTYVSLSAPPDHINVHIHEGNIVAMQGEAM	LGSLPPPPAAPREPAIHS	771 AARSTPFHLLVVMSDHVASTGELFLDNGIEMDIGGPGGKWTLVRFFAESGINNLTISSEV :	831 VNRGYAMSQRWVMDKITILGLKRRVXIKEYTVQKDAGAIKV	890 VRVTSEGAGLQLQKVTVLGVATAPQQVLSNGVPVSNFTYSPDTKVLDI snr o	resour ; 723945 sucrose alpha-glucosidase (EC 3.2.1.48) / oligo-1,6-glu N/Alternate names: small intestinal sucrase/isomaltase	<pre>C:Species: Oryctolagus cuniculus (domestic rabbit) C;Date: 03-Mar-1994 #sequence_revision 03-Mar-1994 #text_change 24-May-1996 C;Accession: A23945; B25987; A2916 C;Accession: A23945; B25987; A2916</pre> R;Hunziker, W.; Spiess, M.; Semenza, G.; Lodish, H.F.	il 46, 227-234, 1986 Title: The sucraer-isomaltase complex: primary structs Reference number: A23945; MUID:86245068; PMID:3755079 Accession: A23945	Actions Cype: many Residues: 1-1827 «HUN» Spostroem, H.; Noren, O.; Christiansen, L.A.; Wacker BS Lett. 148, 321-325, 1982	Title: N-terminal sequences of pig intestinal sucrase Reference number: A25987; MUD:83105704; PMID:7152027 Accession: B25987	Residues: 2-32, fxxxx, 36-38,1008, N', 1010-1014, E' <sj. 183-188,="" 1978="" 96,="" archor="" brunner,="" bydronybic="" frank,="" g.;="" h.;="" integrinal="" iss="" j.;="" jauser,="" lett.="" of="" semen:="" small="" successive.<="" td="" the="" title:="" wacker,=""><td>TITLE: The mydrophobic anchor of small-incestinal suc- Reference number: A29163; MUID:79086207; PMID:729784 Accession: A29163</td><td>Molecule type: protein Residues: 2,'VAV',6-32,'XXX',36-38 <fra> Comment: Carbohydrate analysis of the mature enzyme c</fra></td><td>Complex: the two product chains remain associated afti- Function: 41SX> Description: oligo-1,6-glucosidase catalyzes the hydr</td><td>Pathway: carbohydrate digestion Function: <suc> Description: sucrose alpha-glucosidase catalyzes the</suc></td><td>.Pachway: carbonydrate digestion .Superfamily: sucrase/isomaltase; sucrase/isomaltase homology; trefoil homology .Keywords: carbohydrate digestion; duplication; glycoprotein; glycosidase; hydrolase;</td><td><pre>;2-100//Product: Oligo-1,6-glucosidase (isomaltase cha ;13-32/Domain: membrane associated #status predicted <' .43-65/Region earing/threoning-rich</pre></td><td>;189-840/Domain: grefoil homology <trf1> ;189-840/Domain: gucrase/isomaltase homology <sim></sim></trf1></td><td>F:931-977/Domain: trefoil homology <trf2> F:1088-1827/Product: sucrose alpha-qlucosidase (sucrase - 1.060-1717/Product: sucrase-signmaliase homology <tm2)< td=""><td>7:10-2-1/31/Domain: Bucrase/, Somairase nomo.197 <>:Inc. 7:12/Binding site: carbohydrate (Thr) (covalent) #statu. 7:19,455,455,896,904,1235,1303,1325,1340,1354,1368,1403 7:1007-1008/Cleavage site: Arg-Ile (trypsin) #status pr</td><td>Query Match 27.9%; Score 1355.5; DB 1; Bedt Local Similarity 35.1%; Pred. No. 3.8e-87; Matches 320; Conservative 157; Mismatches 313;</td><td>Qy 43 YGYQVRNAKVDNSTGKSLTALLQLIRNSPVYGPDIHFLSFTASFEEDDTLRIRFTDANNR</td></tm2)<></trf2></td></sj.>	TITLE: The mydrophobic anchor of small-incestinal suc- Reference number: A29163; MUID:79086207; PMID:729784 Accession: A29163	Molecule type: protein Residues: 2,'VAV',6-32,'XXX',36-38 <fra> Comment: Carbohydrate analysis of the mature enzyme c</fra>	Complex: the two product chains remain associated afti- Function: 41SX> Description: oligo-1,6-glucosidase catalyzes the hydr	Pathway: carbohydrate digestion Function: <suc> Description: sucrose alpha-glucosidase catalyzes the</suc>	.Pachway: carbonydrate digestion .Superfamily: sucrase/isomaltase; sucrase/isomaltase homology; trefoil homology .Keywords: carbohydrate digestion; duplication; glycoprotein; glycosidase; hydrolase;	<pre>;2-100//Product: Oligo-1,6-glucosidase (isomaltase cha ;13-32/Domain: membrane associated #status predicted <' .43-65/Region earing/threoning-rich</pre>	;189-840/Domain: grefoil homology <trf1> ;189-840/Domain: gucrase/isomaltase homology <sim></sim></trf1>	F:931-977/Domain: trefoil homology <trf2> F:1088-1827/Product: sucrose alpha-qlucosidase (sucrase - 1.060-1717/Product: sucrase-signmaliase homology <tm2)< td=""><td>7:10-2-1/31/Domain: Bucrase/, Somairase nomo.197 <>:Inc. 7:12/Binding site: carbohydrate (Thr) (covalent) #statu. 7:19,455,455,896,904,1235,1303,1325,1340,1354,1368,1403 7:1007-1008/Cleavage site: Arg-Ile (trypsin) #status pr</td><td>Query Match 27.9%; Score 1355.5; DB 1; Bedt Local Similarity 35.1%; Pred. No. 3.8e-87; Matches 320; Conservative 157; Mismatches 313;</td><td>Qy 43 YGYQVRNAKVDNSTGKSLTALLQLIRNSPVYGPDIHFLSFTASFEEDDTLRIRFTDANNR</td></tm2)<></trf2>	7:10-2-1/31/Domain: Bucrase/, Somairase nomo.197 <>:Inc. 7:12/Binding site: carbohydrate (Thr) (covalent) #statu. 7:19,455,455,896,904,1235,1303,1325,1340,1354,1368,1403 7:1007-1008/Cleavage site: Arg-Ile (trypsin) #status pr	Query Match 27.9%; Score 1355.5; DB 1; Bedt Local Similarity 35.1%; Pred. No. 3.8e-87; Matches 320; Conservative 157; Mismatches 313;	Qy 43 YGYQVRNAKVDNSTGKSLTALLQLIRNSPVYGPDIHFLSFTASFEEDDTLRIRFTDANNR

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Glucan 1,4-alpha-glucosidase (EC 3.2.1.3) GAM1 precursor - yeast (Schwanniomyces occinican 1,4-alpha-glucosidase (EC 3.2.1.3) GAM1 precursor - yeast (Schwanniomyces occidentalis C; percise: Schwanniomyces occidentalis C; pate: 10-Mar.1994 #sequence_revision 05-Apr.1995 #text_change 18-Jun-1999 C; Accession: JN0102 #sequence_revision 05-Apr.1995 #text_change 18-Jun-1999 C; Accession: JN0102 #sequence_revision 05-Apr.1995 #text_change 18-Jun-1999 R; Dobmen, R. J.; Strasser, A.W.M.; Dahlems, U.M.; Hollenberg, C.P. Gene 95, 111-121, 1990 A; Title: Cloning of the Schwanniomyces occidentalis glucoamylase gene (GAM1) and its A; Accession: JN0102 A; MUID:91071592; PMID:1979298 A; Accession: JN0102 A; MUID:91071592; PMID:1979298 A; Accession: JN0102 A; MUID:91071592; PMID:1979298 A; Accession: JN0102 A; MUID:91071592; PMID:1979298 A; Accession: JN0102 A; MUID:91071592; PMID:1979298 A; Accession: JN0102 A; MUID:91071592; PMID:1979298 A; Accession: JN0102 A; MUID:91071592; PMID:1979298 A; Accession: JN0102 A; MUID:91071592; PMID:1979298 A; Accession: JN0102 A; MUID:91071592; PMID:1979298 A; Accession: JN0102 A; Accession: JN0102 A; Accession: JN0102 A; Accession: JN0102 A; Accession: JN0102 A; Accession: JN0102 A; Accession: JN0102 A; Accession: JN0102 A; Accession: JN0102 A; Accession: JN0102 A; Accession: JN0102 A; Accession: JN0102 A; Accession: JN0102 A; Accession: JN0102 A; Accession: JN0102 A; Accession: JN0102 A; Accession: JN0102 A; Accession: JN0102 A; Accession: JN0102 A; Accession: JN0102 A; Accession: JN0102 A; Accession: JN0102 A; Accession: JN0102 A; Accession: JN0102 A; Accession: JN0102 A; Accession: JN0102 A; Accession: JN0102 A; Accession: JN0102 A; Accession: JN0102 A; Accession: JN0102 A; Accession: JN0102 A; Accession: JN0102 A; Accession: JN0102 A; Accession: JN0102 A; Accession: JN0102 A; Accession: JN0102 A; Accession: JN0102 A; Accession: JN0102 A; Accession: JN0102 A; Accession: JN0102 A; Accession: JN0102 A; Accession: JN0102 A; Accession: JN0102 A; Accession: JN0102 A; Accession: JN0102 A; Acce
61 NDSAVDANAAAKGYDLVNV---TNTPRGLTGILKLKEATNIYGYDFDYLNLTVEYQADTR 117
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                  A,Cross-references: EMBL:AL133522, PIDN:CAB63549.1; GSPDB:GN00066; SPDB:SPAC922.02c
A,Experimental source: strain 972h(-); cosmid c922
C,Genetics:
A,Gene: SPAC1039.11c; SPDB:SPAC922.02c
A,Map position: 1
C;Superfamily: Schwanniomyces glucan 1,4-alpha-glucosidase GAM1; sucrase/isomaltase homc
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     372 VHFPLDKMQOFVTKLHRNGQRYVPILDPGINT----NKS---YGTFIRGMQSNVFIKRNG 424
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                                                                                                                                                                        Query Match
27.3*; Score 1327; LL.,
Best Local Similarity 32.0*; Pred. No. 1.1e-85;
Matches 313; Conservative 164; Mismatches 307; Indels 194;
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		RESULT 13 JC4217 JC4217 JC59cies: Aspergillus oryzae C;Species: Biochem. 59, 1516-1521, 1995 A;Title: Nucleotide sequence and expression of alpha-glucosidase-encoding gene (agdA) A;Reference number: JC4217, MUID:96032211; PMID:7549103 A;Residues: 1-985 <min> A;Residues: 1-985 <min></min></min>
Qy 489NPPYKINNSGGRVPINSKTIPATAMHYGNVTEYNAHNLYGFLESGATREALVRPA 543 Db 555 NINYPPYAIYNMQGDSDLATHAVSPNATHADGTVEYDIHNLYGYLGGATREALVRPA 644 Cy 544 TRGFPLLSRSTFAGGGKYTAHWTGDNARWDDLOYSIPTMLNFGLFGMPHGADICGFAE 603 Db 615 KR-PFMISRSTFPRAGKWTGHWGGDNTADWAYAFSIPQAFSMGIAGLPFFGADVGFNG 673 Qy 604 STTEELCCRWIQLGAFYPSRDHSARDTTHQELYLWESVAASARTVLGLRYELLPYYYTL 663	RESULT 12 T3858 Probable family 31 glycosyl hydrolase (alpha glucosidase) precursor - fission yeast (Sch Cispecies: Schizosaccharomyces pombe Cibate: 20-Oct-2000 #sequence_revision 20-Oct-2000 #text_change 20-Oct-2000 CiAccession: T38589; Sc5559; T38911 R.Pearson, D.; Churcher, C.M.; Barrell, B.G.; Rajandream, M.A.; Walsh, S.V. A; Reference number: Z21801 A; Recession: T38598 A; Molecule type: DNA A; Residues: 1-385 < PRA A; Cross_references: EMBL: Z67961; PIDN: CAA91887.1; GSPDB: GN00066; SPDB: SPAC30D11.01c A; Reference number: S62559 A; Residues: 1-384 < PRE> A; Cross_references: EMBL: Z67961 A; Residues: 1-384 < PRE> A; Cross_reference number: S62559 A; Residues: 1-384 < PRE> A; Residues: 1-384 < PRE> A; Residues: 1-384 < PRE> A; Residues: 1-384 < PRE> A; Residues: 1-384 < PRE> A; Residues: 1-384 < PRE> A; Residues: 221811 A; Residues: 221811 A; Residues: 221811 A; Residues: 221817 A; Residues: 221817 A; Residues: 221817 A; Residues: BBL: Z69728; PIDN: CAA93572.1; GSPDB: GN00066; SPDB: SPAC56F8.01 A; Cross_references: EMBL: Z69728; PIDN: CAA93572.1; GSPDB: GN00066; SPDB: SPAC56F8.01	C;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Gene SPDB:SPAC30D11.01c; SPDB:SPAC5678.01 A;Map position: 1L C;Superfamily: Schwanniomyces glucan 1,4-alpha-glucosidase GAM1; sucrase/isomaltase homology (fragment) C;Superfamily: Schwanniomyces glucan 1,4-alpha-glucosidase GAM1; sucrase/isomaltase homology (fragment) C;Superfamily: Schwanniomyces glucan 1,4-alpha-glucosidase GAM1; sucrase/isomaltase homology (fragment) C;Superfamily: Schwanniomyces glucan 1,4-alpha-glucosidase GAM1; sucrase/isomaltase homology (fragment) C;Superfamily: Schwanniomyces glucan 1,4-alpha-glucosidase GAM1; sucrase/isomaltase homology (fragment) C;Superfamily: Schwanniomyces glucan 1,4-alpha-glucosidase GAM1; sucrase/isomaltase homology (fragment) C;Superfamily: Schwanniomyces glucan 1,4-alpha-glucosidase GAM1; sucrase/isomaltase homology (fragment) C;Superfamily: Schwanniomyces glucan 1,4-alpha-glucosidase GAM1; sucrase/isomaltase homology (fragment) C;Superfamily: Schwanniomyces glucan 1,4-alpha-glucosidase GAM1; sucrase/isomaltase homology (fragment) C;Superfamily: Schwanniomyces glucan 1,4-alpha-glucosidase GAM1; sucrase/isomaltase homology (fragment) C;Superfamily: Schwanniomyces glucan 1,4-alpha-glucosidase GAM1; sucrase/isomaltase homology (fragment) C;Superfamily: Schwannicase/isomaltase homology (fragment) C;Superfamil

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Fi189-840/Domain: sucrase/isomaltase homology <SIM>
Fi189-840/Domain: sucrase/isomaltase homology <SIM>
Fi1008-1827/Product: sucrose alpha qlucosidase (sucrase chain) #status experimental <
Fi1065-1734/Domain: sucrase/isomaltase homology <SIM2>
Fi12/Binding site: carbohydrate (Ser) (covalent) #status absent
Fi99-437,455,823,855,904,226,1235,1303,1340,1354,1403,1535,1572,1675,1748,1763,1815/F
Fi1007-1008/Cleavage site: Arg-Ile (trypsin) #status predicted
          LVRFFAESGINNLTISSEVVNRGYAMSQRW----VMDKITILGLKRR----VKIKEYTVQK 864
                                                                                                                                                                    ----YPEDTLSVDFLASRSTLRASARG-TWKEANPLANVTVLGVTEKPSSVTLNGETLSS 951
                                                                                                                                                                                                                                                  D-----AGAIKVKGLGRRTS 879
                                                                                                                                                                                                                                                                                                             952 DSVKYNATSHVLHVGGLOXHTA 973
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                                                                                                                                                                 A; Introns: 234/2; 371/2; 428/2
C; Superfamily: Schwanniomyces glucan 1,4-alpha-glucosidase GAM1; sucrase/isomaltase home
C; Seywords: glycoprotein; glycosidase; hydrolase
F; 152-898/Domain: sucrase/isomaltase homology sSIM>
F; 152-898/Domain: sucrase/isomaltase homology sSIM>
F; 126, 145, 255, 349, 424, 508, 536, 539, 602, 624, 661, 835, 881, 929, 957/Binding site: carbohydrate
A;Cross-references: DDBJ:D45179; NID:g1054564; PIDN:BAA08125.1; PID:g1054565 C:Comment: This enzyme catalyzes the liberation of alpha-glucose from the non-reducing portant enzyme in the food industry as the isomalto-oligosaccharides.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SGPTQAEVTKOYOLSTVGLPAMQQYNTLGFHQCRWGYNNWSEPEDVLANFERFEIPLEYL 370
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FTASFEEDDTLRIR----FTDANNRRWEI-PNEVLPRPPPPPPSPPLSSLQHLPKPIPQN 136
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     QPTTTVLSHPHSDLAFTLFHTTPFGFTIYRKSTHDVLFDATPIPSNPTTFLIYKDQYLQL 196
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SSSLPAQQAHLYGLGEHTKPTFQLAHNQILTLMNADIASFNRDLNLYGSHPFYMDVR--- 253
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AGRIPEMVLDQY-TKLIGRPAPMPYWAFGFHQCRWGYRDVNEIETVVDKYAEARIPLEVM 354
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WIDIDYMDAFKDFTLDPVHFPLDKMQQFVTKLHRNGQRYVPILDPGI------NTNKSYG 408
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     81
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    -----ASVPQSDFVVSWSNEPSFNFKVIRKATGDVLF-----NTKGSTLVYENOFIEF 193
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  752 VHIHEGNIVAMQGEAMTIQAARSTPFHLLVVMSDHVASTGELFLDNGIEMDIGGPGGKWT 811
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 28 GATTSKNDNQGEAIGY----GYQVKNAKVDNSTGKSLTALLQLIRN-SPVYGPDIHFLS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         -----SSPMVGSTHGVFLLNSNGMDVEYTGDRITYKVIGGIIDLYIF
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                                                                                                                                                                                                                                                                                                                                                                                                            Ouery Match 26.9%; Score 1307; DB 2; Length 985;
Best Local Similarity 31.8%; Pred. No. 3.8e-84;
Matches 312; Conservative 165; Mismatches 321; Indels 184; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LTVEYQAKDRLNIQIVPTYFDASNASWYILSEELVPRP-
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                                                                                                            C,Genetics:
A,Gene: agdA
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A; Title: Cloning and sequencing of a full-length rat sucrase-isomaltase-encoding CDNA A; Reference number: 217155; MUID:95121929; PMID:7821806
A; Accession: T10799
A; Accession: T10799: MRNA
A; Accession: T10799: MRNA
A; Molecule type: MRNA
A; Molecul
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                                                                                                                                           HGYNVODM----TITSIGVEAKLARIPSPILFGNDINSVLFTTONOTPNRFRFKITDPNNR
                                                                                                                                                                                       RWEI PNEVLPRPPPPPPPPPLSSLQHLPKPI PQNQPTTTVLSHPHSDLAFTLFHTTPPGF
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                                                                                                    YGYOVKNAKVDNSTGKSLTALLQLIRNSPVYGPDIHFLSFTASFEEDDTLRIRFTDANNR
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                    Length 1827;
                                                                                                                                                                                                                                RYEVPHQYVKEFTGPTVSDTLYDVK-----VAQN-----
               Query Match 26.8%; Score 1304; DB 1; Best Local Similarity 34.6%; Pred. No. 1.7e-83; Matches 311; Conservative 157; Mismatches 316;
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373 GSLDTVSEVVRRNREAGIPYDAQVTDIDYMEDHKEFTYDRVKF--NGLPEFAQDLHNHG- 429 444 445 AARSFWVDEIKRFRDILPIDGIWIDMNEASNFITSA-------P-TPGSTLDN 489 490 QTIEWWANECNLPHQQVEYDGLMIDMNEVSSPIQGSLNLKGVLLIVLNYPPPFTPG-ILDK 548 546 909 665 DANLRGSPIARPLSFTFPDDVATYGISSQPLIGRGIMVSPVLQPGSSIVNAYSPRGNWVS 725 DVEYTGDR-ITYKVIGGIIDLYIFAGRIPEMVLDQYIKLIGRPAPMPYWAFGFHQCRWGY 331 RDVNEIETVVDKYAEARIPLEVMWTDIDYMDAFKDFTLDPVHFPLDKWQQFVTKLHRNGQ 391 549 VMY-----SKTLCMDAVOHWGK--QYDVHSLYGYSMAIATEQAVERVFPNKRS 594 - FILTRSTFGGSGRHANHWLGDNTASWEQMEWSITGMLEFGIFGMPLVGATSCGFLADTT 653 726 LSNYTSSVSVS-AGTYVSLSAPPDHINVHIHEGNIVAMQGEAMTTQAARSTPFHLLVVMS 784 RYVPILDPGINTNK-----SYGTFIRGMQSNVPIKRNG--NPYLGSVWPGPVYYDDFLDP PPYKINNSGGRVPINSKTIPATAM-HYGNVTEYNAHNLYGFLESQATREALVR--PATRG 547 PFLLSRSTFAGSGKYTAHWTGDNAARWDDLQYSIPTMLNFGLFGMPMIGADICGFAESTT EBLCCRWIQLGAFYPFSRDHSARDTTHQE-LYLWESVAASARTVLGLRYELLPYYYTLMY -----•• 999 711 654

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(EC 3.2.1.10)

21-Jul-2000

sucrose alpha-glucosidase (EC 3.2.1.48) / oligo-1,6-glucosidase C;Species: Rattus norvegicus (Norway rat) C;Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change: C;Accession: 110799 C;Accession: 110799 R;Chandrasena, G.; Osterholm, D.E.; Sunitha, I.; Henning, S.J.

RESULT 15

T10799

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770 --DYSTGIKRPWRKERINMYLPGDKIGLHLRGGYIIPTQEPDVTTTASRKNPLGLIVALD 827
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844		882
EVVNRGYAMSQRWVMD		CTHSSYAEGTSLAFK
SGINNLTISS	:: - -	/SN-NELVLN
KWTLVRFFAE	:: ::	KMYILYTFSV
DHVASTGELFLDNGIEMDIGGPGG		DNQAAKGELFWDDGESKDSIEK
785		828

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⁸⁴⁵ KITILGLKRRVK 856 | :|||: 883 TIKVLGLREDVR 894

Search completed: October 27, 2003, 10:22:06 Job time : 28.8921 secs

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Sequence 2, Appli
Sequence 3, Appli
Sequence 1, Appli
Sequence 125, Appli
Sequence 42, Appli
Sequence 44, Appli
Sequence 121, Appl
Sequence 121, Appl
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1393.955 Million cell updates/sec
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                                                                                                                                     October 27, 2003, 10:20:43 ; Search time 109.802 Seconds
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| US-10-043-418-3
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| US-10-032-189-125
| US-10-032-189-42
| US-10-032-189-42
| US-10-032-189-44
| US-10-032-189-123
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Maximum Match 100%
Listing first 45 summaries
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Gapop 10.0 , Gapext 0.5
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Maximum DB seq length: 2000000000
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744 15.3 565 15 US-10-102-806-557 Sequence 557, App	14.3 693 12 US-10-228-063-5 Sequence	14.3 712 12 US-10-228-063-27 Seguence	14.3 718 12 US-10-228-063-26 Sequence 26,	14.3 718 12 US-10-228-063-36	12.4 788 15 US-10-156-761-14497 Seguence 1449	11.9 235 9 US-09-734-569-132 Sequence 132,	10.5 1070 10 US-09-280-197-6 Sequence 6,	10 US-09-423-126-4 Sequence	.5 10.3 1066 10 US-09-280-197-5 Sequence 5,	1 1066 10 US-09-423-126-3 Sequence 3,	8.5 642 15 US-10-156-761-10107 Sequence 101	7.4 188 9 US-09-734.569-134 Sequence 13	. 1092 10 US-09-423-126-5 Sequence 5,	6.9 570 10 US-09-423-126-6 Sequence	6.5 1088 10 US-09-280-197-1 Sequence 1,	6.5 1088 10 US-09-423-126-1 Sequence 1,	6.4 1091 10 US-09-280-197-2 Sequence 2,	6.4 1091 10 US-09-423-126-2 Sequence 2,	6.2 199 9 US-09-734-569-130 Sequence 130,	2.6 317 10 US-09-280-197-9 Sequence 9,	2.4 740 12 US-10-032-585-7673 Sequence	2.4 785 11 US-09-733-643-2 Sequence	682 9 US-09-798-791-2 Sequence 2, Ag	2.3 1569 12 US-10-287-274-312	2.3 2301 11 US-09-822-871-4 Sequence	2.3 980 12 US-10-320-351-9 Sequence	2.3 630 15 US-10-081-872-202	2.2 1044 10 US-09-960-226-3 Sequence	200 000 000 000 000 000
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ALIGNMENTS

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61 TALLQLIRNSPVYGPDIHFLSFTASFERDDTLRIRFTDANNRRWEIPNEVLPRPPPPPPP 120
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   Sequence 2, Application US/10043418;
Publication No. US20020184662A1;
GENERAL INFORMATION:
APPLICANT: Henson, Cynthia A.
APPLICANT: Henson, Cynthia A.
APPLICANT: Mualin, Elizabeth H.
APPLICANT: Mualin, Elizabeth H.
APPLICANT: Mualin, Biliabeth H.
APPLICANT: Mualin, Biliabeth H.
CURRENT PRINCE 196296.97466;
CURRENT PRILING DATE: 2002-06-25
PRIOR FILING DATE: 2002-06-25
PRIOR FILING DATE: 2001-01-0
NUMBER OF SEG ID NOS: 7
SOFTWARE: Patentin Ver. 2.1
SEG ID NOS: 7
                                                                                                                                                                                                                                                                                                                                                                                                                                       0; Mismatches
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Pred. No. 0;
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Best Local Similarity
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ORGANISM: Sugar beet
US-10-043-418-2
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          SNPTTFLIXKDQYLQLSSSLPAQQAHLYGLEHTXPTFQLAHNQILTLMNADIASFNRDL
                                        NLYGSHPFYMDVRSSPMVGSTHGVFLLNSNGMDVEYTGDRITYKVIGGIIDLYIFAGRTP
                                                  KRNGNPYLGSVWPGPVYYPDFLDPAARSFWVDEIKRFRDILPIDGIWIDMNEASNFITSA
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Publication No. US20020184662A1
GENERAL INFORMATION:
APPLICANT: Henson: Cynthia A.
APPLICANT: Henson: Cynthia A.
APPLICANT: Muslin, Elizabeth H.
APPLICANT: Clark, Suzanne E.
ITLE OF INVENTION: Modified barley alpha-glucosidase
FILE REFERENCE: 960296.99486
CURRENT APPLICATION NUMBER: US/10/043,418
CURRENT APPLICATION NUMBER: 60260.787
FRIOR FILING DATE: 2001-01-10
NUMBER OF SEQ ID NOS: 7
SOFTWARE: PARCHAIN VER 2.21
SEQ ID NO 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AFKLELEFEGATRV 914
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ORGANISM: Spinach
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                                                     Gaps
     DB 14; Length 903;
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Query Match 66.7%; Score 3243.5; DB 14; Lengt Best Local Similarity 67.3%; Pred. No. 7.5e-275; Matches 610; Conservative 122; Mismatches 166; Indels
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71 PVYGPDIHFLSFTASFEEDDTLRIRFTDANNRRWEIPNEVLPRP------PPPPSPPP 122
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88.7%; Score 2370; DB 14; Length 8
Best Local Similarity 51.2%; Pred. No. 2.5e-198;
Matches 466; Conservative 147; Mismatches 235; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Honon, Cynthia A.
APPLICANT: Muslin, Elizabeth H.
APPLICANT: Clark, Suzanne E.
ITILE OF INVENTION: Modified barley alpha-glucosidase
FILE REFERENCE: 960296.97486
CURRENT APPLICATION NUMBER: US/10/043,418
CURRENT FILING DATE: 2002-06-25
PRIOR APPLICATION NUMBER: 60/260,787
PRIOR FILING DATE: 2001-01-10
NUMBER OF SEQ ID NOS: 7
SOFTWARE: Patentin Ver: 2.1
SEQ ID NO 1
                                                                                                                                                                                                                                                                                                                                                            Sequence 1, Application US/10043418; Publication No. US20020184662A1; GENERAL INFORMATION:
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ORGANISM: Barley
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Best Local S
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LIYKDQYLQLSSSLPAQQAHLYGLGEHTKPTFQLAHNQILTLWNADIASFNRDLNLYGSH 246
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                                                      APPLICANT: Husson, Cynthia A.
APPLICANT: Muslin, Elizabeth H.
APPLICANT: Muslin, Elizabeth H.
APPLICANT: Clark, Suzame E.
TITLE OF INVENTION: Modified barley alpha-glucosidase
FILE REFERENCE: 960296.97486
CURRENT APPLICATION NUMBER: 05/10/043,418
CURRENT FILING DATE: 2002-66-25
PRIOR APPLICATION NUMBER: 60/260,787
PRIOR APPLICATION NUMBER: 60/260,787
SOFTWARE: Patentin Ver. 2.1
SOFTWARE: Patentin Ver. 2.1
Sequence 4, Application US/10043418
Publication No. US20020184662A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                      TYPE: PRT;
CRGANISM: Arabidopsis
US-10-043-418-4
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                                                                       LVVMSDHVASTGELFLDNGIEMDIGGPGGKWTLVRFFAESGINN--LTISSEVVNRGYAM 837
                                                                                                                                                                        YYTLMYDANIRGSPIARPLSFTFPDDVATYGISSQFLIGRGIMVSPVLQPGSSIVNAYSP 719
                                                                                                                                                                                                                                                                                                                                                  SQRWVMDKITILGLKRRVKIKEYTVQKDAGAIKVKGLGRRTSSHNQGGF-FVSVISDLRQ 896
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480 APTPGSTLDNPPYKINNSGGRVPINSKTIPATAMHYGNVTEYNAHNLYGFLESQATREAL 539
                                                                                                                                                                                                                                                                                                                    LVALAEDGTASGYLFLDDGDSPEY-GRRSDWSMVRFNYKIPNNKGAIKVKSEVVHNSYAQ 804
               447 - PEPMYALDDPPYRINNDGTGRPINNKTYRPLAVHYGGVTEYEEHNLFGLLEARATGRGV
                                                                                                               GFAESTTEELCCRWIQLGAFYPFSRDHSARDTTHQELYLWESVAASARTVLGLRYELLPY
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APPLICANT: MacDougall, John R
APPLICANT: Smithson, Glennda
TITLE OF INVENTION: Proteins and Nucleic Acids Encoding Same
FILE REFERENCE: 21402-228
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CURRENT FILING DATE: 2001-12-21
PRIOR APPLICATION NUMBER: 60/257,495
PRIOR FILING DATE: 2000-12-21
PRIOR APPLICATION NUMBER: 60/258,171
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 125, Application US/10032189 Publication No. US20030170630A1 GENERAL INFORMATION:
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Grosse, William M
Lepley, Denise M
Burgess, Catherine E
Shimkets, Richard A
Grosse, William M
Szekeres, Edward S
Vernet, Corine A.M.
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Gangolli, Esha A
Fernandes, Elma R
Rieger, Daniel K
Edinger, Shlomit R
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APPLICANT: TChernev, Velizar T
APPLICANT: Liu, Xiaohong
APPLICANT: Spytek, Kimberly A
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Millet, Isabelle
Sciore, Paul
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Boldog, Ferenc L
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864 VVGEEFELKV 873
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APPLICANT:
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VRSSPMVGSTHGVFLLMSNGMDVEY-TGDRITYKVIGGIIDLYIFAGRTPEMVLDQYTKL 310
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                      PRIOR APPLICATION NUMBER: 60/269,940
PRIOR APPLICATION NUMBER: 60/269,940
PRIOR APPLICATION NUMBER: 60/274,192
PRIOR FILING DATE: 2001-03-08
PRIOR FILING DATE: 2001-03-29
PRIOR FILING DATE: 2001-03-29
PRIOR FILING DATE: 2001-03-29
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PRIOR PAPLICATION NUMBER: 60/283,656
PRIOR PAPLICATION NUMBER: 60/309,247
PRIOR PAPLICATION NUMBER: 60/309,247
PRIOR FILING DATE: 2001-07-31
PRIOR FILING DATE: 2001-07-31
PRIOR FILING DATE: 2001-08-17
PRIOR APPLICATION NUMBER: 60/311,754
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Matches 386; Conserva
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                                                       AGSGKYTAHWTGDNAARWDDLQYSIPTMLNFGLFGMPMIGADICGFAESTTEELCCRWIQ 615
                                                                                                                                                                                                                            733 VSVS-AGTYVSLSAPPDHINVHIHEGNIVAMQGEAMTTQAARSTPFHLLVVMSDHVASTG 791
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APPLICANT: MacDougall, John R
APPLICANT: Smithson, Glennda
TITLE OF INVENTION: Proteins and Nucleic Acids Encoding Same
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CURRENT FILING DATE: 2001-12-21
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PRIOR FILING DATE: 2000-12-20
PRIOR APPLICATION NUMBER: 60/269,940
PRIOR FILING DATE: 2001-02-20
PRIOR APPLICATION NUMBER: 60/274,192
PRIOR FILING DATE: 2001-03-08
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Publication No. US20030170630A1
GENERAL INFORMATION:
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Grosse, William M
Lepley, Denise M
Burgess, Catherine E
Shimkets, Richard A
Grosse, William M
Szekeres, Edward S
Vernet, Corine A.M.
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APPLICANT: Tchernev, Velizar T
APPLICANT: Liu, Xiaohong
APPLICANT: Spytek, Kimberly A
APPLICANT: Zerhusen, Bryan D
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Gangolli, Esha A
Fernandes, Elma R
Rieger, Daniel K
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Millet, Isabelle
Sciore, Paul
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APPLICANT: Waldman, Scott A.
APPLICANT: Bark, Jason
APPLICANT: Schulz, Stephanie
TITLE OF INVENTION: Compositions And Methods For Identifying And Targeting Carcer Cel
TITLE OF INVENTION: Alimentary Canal Origin
FILE REPERENCE: TJU12413
CURRENT APPLICATION NUMBER: US/09/819,247
PRIOR APPLICATION NUMBER: 60/192,229
PRIOR FILING DATE: 2000-03-27
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                                    SLSNYTSSVSVSAGTYVSLSAPPDHINVHIHEGNIVAMQGEAMTTQAARSTPFHLLVVMS 784
                                                                                                169 RYEVPHOYVKEFTGPTVSDTLYDVK-----VAQN-------PFSI 201
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SOFTWARE: PatentIn version 3.0
SEQ ID NO 2
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ORGANISM: Homo sapiens
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Best Local Simi
Matches 311;
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206 HLYGLGEHTKPTFQLAH-NQILTLMNADIASFN--RDLNLYGSHPFYMDVRSSPMVGSTH 262
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APPLICANT: SCIOLE, Factor
APPLICANT: MacDougall, John R
APPLICANT: Smithson, Glennda
TITLE OP INVENTION: Proteins and Nucleic Acids Encoding Same
FILE REFERENCE: 21402-226
CURRENT FILING DATE: 2001-12-21
PRIOR APPLICATION NUMBER: 60/257,495
PRIOR APPLICATION NUMBER: 60/258,171
PRIOR APPLICATION NUMBER: 60/258,171
PRIOR FILING DATE: 2000-12-20
PRIOR FILING DATE: 2000-12-20
PRIOR PELING DATE: 2000-12-20
PRIOR PILING DATE: 2001-03-20
PRIOR PLING DATE: 2001-03-20
PRIOR PELING DATE: 2001-03-29
PRIOR PELING DATE: 2001-03-29
PRIOR PELING DATE: 2001-03-29
PRIOR PELING DATE: 2001-04-11
PRIOR PELING DATE: 2001-04-11
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PRIOR PELING DATE: 2001-03-30
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PRIOR PELING DATE: 2001-08-17
PRIOR PELING DATE: 2001-08-17
PRIOR PELING DATE: 2001-08-17
PRIOR PELING DATE: 2001-08-17
PRIOR PELING DATE: 2001-08-17
                                                                                                                                                         Sequence 44, Application US/10032189
Publication No. US20030170630A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                    APPLICANT: Alsobrook II, John P
APPLICANT: Tchernev, Velizar T
APPLICANT: Liu, Xiaohong
APPLICANT: Spytek, Kimberly A
APPLICANT: Zerhusen, Bryan D
APPLICANT: Patturajan, Meera
APPLICANT: Grosse, William M
APPLICANT: Lepley, Denise M
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Burgess, Catherine I
Shimkets, Richard A
Grosse, William M
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Szekeres, Edward S
Vernet, Corine A.M
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gangolli, Esha A
Fernandes, Elma R
Rieger, Daniel K
Edinger, Shlomit R
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Casman, Stacie J
Boldog, Ferenc L
Gorman, Linda
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gunther, Brik
Millet, Isabelle
Sciore, Paul
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SEQ ID NO 44
LENGTH: 912
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ORGANISM: Homo sapiens
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APPLICANT:
APPLICANT:
APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           513 NEPSVF------RGP--EQTMOKNAIHHGNWEHRELHNIYGFY 547
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 261 THGVFLLNSNGM------DVEYT------GDR--ITYKVIGGIIDLYIFAG 297
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RIPEMVLDOYTKLIGRPAPMPYWAFGFHQCRWGYRDVNBIETVVDKYABARIPLEVMWTD 357
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  IDYMDAFKDFTLDPVHFPLDKMQQFVTKLHRNGQRYVPILDPGINTNKSYGTFIRGMQSN 417
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   399 IEHTEGKRYFTWDKNRFPNPKRMQEL--LRSKKRKLVVISDPHIKIDPDYSVYVKAKDQG 456
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LFGMPMIGADICGFAESTTEELCCRWIQLGAFYPFSRDHSARDTTHQELYLW-ESVAASA 646
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 914;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        17.6%; Score 853.5; DB 12; 31.7%; Pred. No. 2.1e-65;
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PRIOR APPLICATION NUMBER: 60/277,826
PRIOR FILING DATE: 2001-03-22
PRIOR SPELICATION NUMBER: 60/279,840
PRIOR PELLING DATE: 2001-03-29
PRIOR PELLING DATE: 2001-03-29
PRIOR PELLING DATE: 2001-04-11
PRIOR FILING DATE: 2001-04-13
PRIOR FILING DATE: 2001-04-13
PRIOR FILING DATE: 2001-07-31
PRIOR PILING DATE: 2001-07-31
PRIOR APPLICATION NUMBER: 60/311,754
PRIOR PILING DATE: 2001-08-17
PRIOR PELING DATE: 2001-08-17
NUMBER OF SEQ ID NOS: 260
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ; TYPE: PRT; ORGANISM: Homo sapiens
US-10-032-189-42
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Similarity
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LENGTH: 914
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     298
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23; Gaps 95; Length 912; Query Match
17.5%; Score 850.5; DB 12; Length
Best Local Similarity 31.5%; Pred. No. 3.8e-65;
Matches 218; Conservative 116; Mismatches 264; Indels

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TYPE: PRT
ORGANISM: Homo sapiens
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                                                                                                                                                                              457 VYNQEGEDFEGVCWPGLSSYLDFTNPKVRE-WYSSLFAFPVYQGSTDIL----FLWNDMNE
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                                          GVFLLNSNGM-----DVEYT-----
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Publication No. US20030170630A1
GENERAL INFORMATION:
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APPLICANT: Tchernev, Velizar T
APPLICANT: Liu, Xiaohong
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Boldog, Ferenc L
Gorman, Linda
Gangolli, Esha A
Pernandes, Elma R
Rieger, Daniel K
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Vernet, Corine A.M
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206 HLYGLGEHTKPTFQLAH---NQILTLWNADIASFN--RDLNLYGSHPFYMDVRSSPWVGS 260 261 THGVFLLNSNGM-----DVEYT-----GDRITYKVIGGIIDLYIFAG 297 279 TIGIFWLNASETLVEINTEPAVEYTLTQMGPVAAKQKVRSRTHVHWMSESGIIDVFLLTG 338 471 NEASNFITSAPTPGSTLDNPPYKINNSGRVPINSKTIPATAMHYGNVTEYNAHNLYGFL 530 548 HQMATAEGLIK-RSKGKERPPVLTRSPPAGSQKYGAVWTGDNTAEWSNLKISIPMLLTLS 606 298 RTPEMVLDQYTKLIGRPAPMPYWAFGFHQCRWGYRDVNEIBTVVDKYAEARIPLEVMWTD 357 358 IDYMDAFKDFILLDPVHFPLDXMQQFVIKLHRNGQRYVPILDPGINTNKSYGTFIRGMQSN 417 399 IEHTEGKRYFTWDKNRFPNPKRMQEL--LRSKKRKLVVISDPHIKIDPDYSVYKAKDQG 456 VFIK-RNGNPYLGSVWPGPVYYPDFLDPAARSFWVDEIKRF-----RDILPIDGIWIDM 470 457 FFVRNQEGEDFEGVCMPGLSSYLDFTNPRVRE-NYSSLFAFPVYQGSTDIL---FLWNDM 512 513 NEPSVF------RGP-EQTMQKNAIHHGNWEHRELHNIYGFY 547 531 ESQATREALVRPATRG---PPLLSRSTFAGSGKYTAHWTGDNAARWDDLQYSIPTMLNFG 587 Gaps APPLICANT: Millet, Estan
APPLICANT: Sciore, Paul
APPLICANT: Sciore, Paul
APPLICANT: Sciore, Paul
APPLICANT: SLierman, Karen
APPLICANT: Smithson, Glennda
TITLE OF INVENTION: Proteins and Nucleic Acids Encoding Same
FILE REFERENCE: 21402-228
CURRENT APPLICATION NUMBER: US/10/032,189
CURRENT APPLICATION NUMBER: 60/257,495
PRIOR APPLICATION NUMBER: 60/258,171
PRIOR APPLICATION NUMBER: 60/258,171
PRIOR APPLICATION NUMBER: 60/269,940
PRIOR PELING DATE: 2001-02-20
PRIOR PELING DATE: 2001-03-28
PRIOR FILING DATE: 2001-03-28
PRIOR PELING DATE: 2001-03-29
PRIOR PELING DATE: 2001-04-13
PRIOR APPLICATION NUMBER: 60/279,840
PRIOR PELING DATE: 2001-04-13
PRIOR PELING DATE: 2001-04-13
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PRIOR PELING DATE: 2001-04-13
PRIOR PELING DATE: 2001-07-31
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PRIOR FILING DATE: 2001-08-17
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PRIOR FILING DATE: 2001-08-17
PRIOR FILING DATE: 2001-08-17
PRIOR FILING DATE: 2001-08-17 Length 914; Query Match 17.5%; Score 849.5; DB 12; Length Best Local Similarity 31.4%; Pred. No. 4.6e-65; Matches 218; Conservative 117; Mismatches 263; Indels

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156 FRLDLLEDRSL-----LLSVNARGLMAFEHQRAPRVPFSDKVSLALGSVWDKIKNLFSR 209
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PRIOR APPLICATION NUMBER: bu/sus, etc. PRIOR FILING DATE: 2001-07-31
PRIOR APPLICATION NUMBER: 60/311,754
PRIOR PILING DATE: 2001-08-17
PRIOR APPLICATION NUMBER: 60/313,331
PRIOR PILING DATE: 2001-08-17
NUMBER OF SEQ ID NOS: 260
SOFTWARE: Patentin Ver: 2:1
SEQ ID NO 121
                                                                                                                                                                                                                                                              ) ORGANISM: Mus musculus
US-10-032-189-121
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                                       RTVLGLRYELLPYYYTLMYDANLRGSPIARPLSFTFPDDVATYGISSQFLIGRGIMVSPV 706
                                                                                                                                             REAIRERYGLLPYWYSLFYHAHVASQPVMRPLWVEFPDELKTFDMEDEYYLGSALLVHPV 726
                                                                                                                                                                                            LOPGSSIVNAYSPRGN--WVSLSNYTSSVSVSAGTYVSLSAPPDHINVHIHEGNIVAMQG 764
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APPLICANT: MacDougall, John R
APPLICANT: Smithson, Glennda
TITLE OF INVENTION: Proteins and Nucleic Acids Encoding Same
FILE REFERENCE: 21402-228
                                                                                                                                                                                                                                                                                                                                                                                                      SGINNLTISSEVVNRGYAMSORWVMDKITILGLKR 853
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PRIOR PAPLICATION NUMBER: 60/257,495
PRIOR PAPLICATION NUMBER: 60/257,495
PRIOR PAPLICATION NUMBER: 60/259,171
PRIOR PAPLICATION NUMBER: 60/259,171
PRIOR PAPLICATION NUMBER: 60/269,940
PRIOR FILING DATE: 2001-02-20
PRIOR FILING DATE: 2001-03-08
PRIOR FILING DATE: 2001-03-08
PRIOR PAPLICATION NUMBER: 60/277,826
PRIOR FILING DATE: 2001-03-22
PRIOR APPLICATION NUMBER: 60/279,840
PRIOR FILING DATE: 2001-03-29
PRIOR PILING DATE: 2001-03-29
PRIOR FILING DATE: 2001-03-29
PRIOR FILING DATE: 2001-03-29
PRIOR FILING DATE: 2001-04-11
PRIOR FILING DATE: 2001-04-11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ; Sequence 121, Application US/10032189; Publication No. US20030170630A1; GENERAL INFORMATION:
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Shimkets, Richard A
Grosse, William M
Szekeres, Edward S
Vernet, Corine A.M.
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APPLICANT: Tchernev, Velizar T
APPLICANT: Tchernev, Velizar T
APPLICANT: Spytek, Kimberly A
APPLICANT: Zerhusen, Bryan D
APPLICANT: Grosse, William M
APPLICANT: Lepley, Denisse M
APPLICANT: Lepley, Denisse M
APPLICANT: Shimkets, Richard A
APPLICANT: Shimkets, Richard A
APPLICANT: Grosse, William M
APPLICANT: Grosse, William M
APPLICANT: Scheres, Edward S
APPLICANT: Scheres, Edward S
APPLICANT: Vernet, Corine A.M.
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Boldog, Ferenc L
Gorman, Linda
Gangolli, Esha A
Fernandes, Elma R
Rieger, Brima R
Edinger, Shlomit R
Gunther, Erik
Millet, Isabelle
Sciore, Paul
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Szekeres, Edward S
ORGANISM: Homo sapiens
        US-10-032-189-123
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                      770 QAARSTPFHILLVVMSDHVASTGELFLDNGIEMDIGGPGGKWTLVRFFAESGINNLTISSE 829
                                                 843 DCMKDDPITLFVALSPQGTAQGELFLDDGHTFWY--QTRHEFLLRRFSFSG--STLVSSS 898
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APPLICANT: MacDougall, John R
APPLICANT: Smithson, Glennda
TITLE OF INVENTION: Proteins and Nucleic Acids Encoding Same
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TITLE OF INVENTION: Proceins and Nucleic Actic FILE REFERENCE: 21402-224)
CURRENT APPLICATION NUMBER: US/10/032,189
CURRENT FILING DATE: 2001-12-21
PRIOR APPLICATION NUMBER: 60/258,171
PRIOR PILING DATE: 2000-12-20
PRIOR PRILING DATE: 2000-12-20
PRIOR PRILING DATE: 2001-02-20
PRIOR PILING DATE: 2001-02-20
PRIOR PILING DATE: 2001-03-08
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PRIOR PILING DATE: 2001-04-13
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PRIOR PILING DATE: 2001-08-17
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Publication No. US20030170630A1
GENERAL INFORMATION:
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Shimkers, Richard A
Grosse, William M
Szekeres, Edward S
Vernet, Corine A.M.
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APPLICANT: Tchernev, Velizar T
APPLICANT: Liu, Xiaohongram
APPLICANT: Spytek, Kimberly A
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Boldog, Ferenc L
Gorman, Linda
Gangolli, Esha A
Fernandes, Elma R
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Edinger, Shlomit R
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Grosse, William M
Lepley, Denise M
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Millet, Isabelle
Sciore, Paul
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189 YKDQYLQLSSSLPAQQAHLYGLGEHTKPTFQLAHNQIL------TLWNADIASFN-- 237
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                                                                       Gaps
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Query Match 16.9%; Score 823; DB 12; Length 943; Best Local Similarity 31.1%; Pred. No. 1e-62; Matches 221; Conservative 109; Mismatches 279; Indels 102;
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Publication No. US20030170630A1
GENERAL INFORMATION:
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APPLICANT: Tchernev, Velizar T
APPLICANT: Liu, Xiaohong
APPLICANT: Spytek, Kimberly A
APPLICANT: Zerhusen, Bryan D
APPLICANT: Zerhusen, Meera
APPLICANT: Grosse, William M
APPLICANT: Lepley, Denise M
APPLICANT: Burgases, Carberine E
APPLICANT: Burgases, Carberine E
APPLICANT: Shimkets, Richard
APPLICANT: Grosse, William M
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DVATYGISSOFLIGRGIMVSPVLQPGSSIVNAYSP-RGN-WVSLSNYTSSVSVSAGTY-- 740
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451 VD--EIKRFRDILPIDGIWIDMNEASNFITSAPTPGSTLDNPPYKINNSGGRVPINSKTI 508
                                                                                                                                                                              TGDNAARWDDLQYSIPTMLNFGLFGMPMIGADICGFAESTTEELCCRWIQLGAFYPFSRD 625
                                                                                                                                                                                                                                                                    HSARDTTHQELYLWESVAAS-ARTVLGLRYELLPYYYTLMYDANLRGSPIARPLSFTFPD 684
                                                                                        PATAMHYGNVTEYNAHNLYGFLESOATREALVRPATRG---PFLLSRSTFAGSGKYTAHW
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APPLICANT: Sciore, Paul
APPLICANT: Ellerman, Karen
APPLICANT: MacDougall, John R
APPLICANT: Smithson, Glennda
TITLE OF INVENTION: Proteins and Nucleic Acids Encoding Same
                                          522 ANMFSYDNYEGSAPNLFVWNDMNEPSVP------NGP---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FILE REFERENCE: 21402-228
CURRENT APPLICATION NUMBER: US/10/032,189
CURRENT FILING DATE: 2001-12-21
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PRIOR FILING DATE: 2000-12-21
PRIOR PELING DATE: 2000-12-20
PRIOR PELING DATE: 2000-12-20
PRIOR APPLICATION NUMBER: 60/269, 940
PRIOR APPLICATION NUMBER: 60/269, 940
PRIOR APPLICATION NUMBER: 60/274, 192
PRIOR FILING DATE: 2001-02-00
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Shimkers, Richard A
Grosse, William M
Szekeres, Edward S
Vernet, Corine A.M.
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APPLICANT: Tchenrev, Velizar T
APPLICANT: Liu, Xiaohong
APPLICANT: Spytek, Kimberly A
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Fernandes, Elma R
Rieger, Daniel K
Edinger, Shlomit R
Gunther, Erik
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Grosse, William M
Lepley, Denise M
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Ferenc L
Linda
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US-10-032-189-120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      291 NPMALYGSVPVL-----LAHNPHRDLGIFWLNAAETWVDISSNTAGKTLFGKMMDYLQ 343
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                                                                                                                                                                                                                                                                    PPLICANT: Ellerman, Karen
PPLICANT: MacDougall, John R
PPLICANT: Smithson, Glennda
ITLE OF INVENTION: Proteins and Nucleic Acids Encoding Same
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CURRENT APPLICATION NUMBER: US/10/032,189
                                                                                                                                                                                                                                                                                                                                                                                                                     CURRENT FILING DATE: 2001-12-21
PRIOR PULICATION NUMBER: 60/257,495
PRIOR FILING DATE: 2000-12-21
PRIOR FILING DATE: 2000-12-20
PRIOR FILING DATE: 2000-12-20
PRIOR FILING DATE: 2001-02-20
PRIOR PILING DATE: 2001-02-20
PRIOR PELLING DATE: 2001-03-08
PRIOR PELLING DATE: 2001-03-08
PRIOR FILING DATE: 2001-03-08
PRIOR FILING DATE: 2001-03-29
PRIOR FILING DATE: 2001-03-29
PRIOR PELLING DATE: 2001-04-11
PRIOR APPLICATION NUMBER: 60/279,840
PRIOR PILING DATE: 2001-04-11
PRIOR PELING DATE: 2001-04-11
PRIOR PELING DATE: 2001-04-11
PRIOR PELING DATE: 2001-04-13
PRIOR PILING DATE: 2001-04-13
PRIOR PILING DATE: 2001-07-31
PRIOR PELING DATE: 2001-08-17
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Rieger, Daniel K
Edinger, Shlomit R
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Gangolli, Esha A
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Sciore, Paul
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ORGANISM: Homo sapiens
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Best Local S
Matches 221
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APPLICANT:
APPLICANT:
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180 PSNPTTFLIYKDQYLQLSSSLPAQQAHLYGLGEHT-----KPTFQLAHNQILTLWNADIA 234
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           261 YGPMSVGLDFSLPGME-HVYGIPEH-----ADNLRLKVTEGGEFYRLYNLDVFQYELY 312
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    313 NPMALYGSVPVL-----LAHNPHRDLGIFWLNAAETWVDISSNTAGKTLFGKMDYLQ 365
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           332 RDVNEIETVVOKYAEARIPLEVM#TDIDYMDAFKDFTLDPVHFPLDKMQQFVTKLHRNGQ 391
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      392 RYVPILDPGINTNKSYGTFIRGMQSNVFIK-RNGNPYLGSVWPGPVYYPDFLDPAARSFW 450
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              451 VD--EIKRFRDILFIDGIWIDMNEASNFITSAPTPGSTLDNPPYKINNSGGRVPINSKTI 508
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             544 ANMFSYDNYEGSAPNLFVWNDMNEPSVF-----NGP-----EVTM 578
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           509 PATAMHYGNVTEYNAHNLYGFLESQATREALVRPATRG---PFLLSRSTFAGSGKYTAHW 565
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Matches 221; Conservative 109; Mismatches 279; Indels 102;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 966;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   16.9%; Score 821; DB 12; 31.1%; Pred. No. 1.6e-62;
PRIOR APPLICATION NUMBER: 60/277,826
PRIOR FILING DATE: 2001-03-22
PRIOR PAPPLICATION NUMBER: 60/279,840
PRIOR FILING DATE: 2001-03-29
PRIOR FILING DATE: 2001-03-29
PRIOR FILING DATE: 2001-04-11
PRIOR PELLING DATE: 2001-04-13
PRIOR FILING DATE: 2001-04-13
PRIOR FILING DATE: 2001-04-13
PRIOR FILING DATE: 2001-07-31
PRIOR PLING DATE: 2001-07-31
PRIOR APPLICATION NUMBER: 60/311,754
PRIOR FILING DATE: 2001-08-17
PRIOR APPLICATION NUMBER: 60/313,331
PRIOR FILING DATE: 2001-08-17
PRIOR SEQ ID NOS: 260
NUMBER OF SEQ ID NOS: 260
                                                                                                                                                                                                                                                                                                                                                                                                             LENGTH: 966
TYPE: PRT
ORGANISM: Homo sapiens
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16.8%; Score 818; DB 12; Length 944;
Best Local Similarity 31.0%; Pred. No. 2.8e-62;
Matches 225; Conservative 107; Mismatches 272; Indels 122;
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TILE OF INVENTION, DATE BARDHAGA

CURRENT APPLICATION NUMBER: US/10/032,189

CURRENT FILING DATE: 2001-12-21

PRIOR APPLICATION NUMBER: 60/257,495

PRIOR FILING DATE: 2000-12-21

PRIOR PELLING DATE: 2000-12-20

PRIOR FILING DATE: 2001-02-20

PRIOR FILING DATE: 2001-02-20

PRIOR FILING DATE: 2001-03-08

PRIOR FILING DATE: 2001-03-08

PRIOR PELLING DATE: 2001-03-08

PRIOR APPLICATION NUMBER: 60/277,826

PRIOR APPLICATION NUMBER: 60/279,840

PRIOR PELLING DATE: 2001-03-29

PRIOR PELLING DATE: 2001-04-11

PRIOR FILING DATE: 2001-08-17

 Sequence 124, Application US/10032189; Publication No. US20030170630A1; GENERAL INFORMATION:
                                                                                                           APPLICANT: Alsobrook II, John P
APPLICANT: Tchernev, Velizar T
APPLICANT: Liu, Xiaohong
APPLICANT: Spytek, Kimberly A
APPLICANT: Zerhusen, Bryan D
APPLICANT: Patturajan, Meera
APPLICANT: Grosse, William M
APPLICANT: Lepley, Denise M
APPLICANT: Burgess, Catherine E
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Casman, Stacie J
Boldog, Ferenc L
Gorman, Linda
Gangolli, Esha A
Fernandes, Elma R
Rieger, Daniel K
Edinger, Shlomit R
Miller, Erik
Miller, Fasbelle
Sciore, Paul
Elerman, Karen
MacDougall, John R
Smithson, Glennda
                                                                                                                                                                                                                                                                                                                                                                                                                                               Richard A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Grosse, William M
Szekeres, Edward S
Vernet, Corine A.M.
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US-10-032-189-124
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Gangolli, Esha A Fernandes, Elma R Rieger, Daniel K Edinger, Shlomit R Gunther, Erik Millet, Isabelle

2001-12

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APPLICANT: Ellerman, Karen
APPLICANT: MacDougall, John R
APPLICANT: Smithson, Glennda
TITLE OF INVENTION: Proteins and Nucleic Acids Encoding Same
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CURRENT FILING DATE: 2001-12-21
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PRIOR APPLICATION NUMBER: 60/257,495
PRIOR FILING DATE: 2000-12-21
PRIOR FILING DATE: 2000-12-20
PRIOR FILING DATE: 2001-02-20
PRIOR FILING DATE: 2001-02-20
PRIOR FILING DATE: 2001-02-20
PRIOR FILING DATE: 2001-03-08
PRIOR FILING DATE: 2001-03-08
PRIOR FILING DATE: 2001-03-08
PRIOR FILING DATE: 2001-03-08
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PRIOR PRILING DATE: 2001-03-17
PRIOR PRILING DATE: 2001-03-17
PRIOR PRILING DATE: 2001-03-17
PRIOR APPLICATION NUMBER: 60/313,331
PRIOR PRILING DATE: 2001-03-17
PRIOR APPLICATION NUMBER: 60/313,331
PRIOR PRICE PRICE 2001-08-17
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PRIOR APPLICATION NUMBER: 60/313,331
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PRIOR APPLICATION NUMBER: 60/313,331
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PRIOR APPLICATION NUMBER: 60/309,247
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; ORGANISM: Homo sapiens
US-10-032-189-38
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APPLICANT:
APPLICANT:
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------GIIDLYIFAGRTPEMVLDQYTKLIGRPAPMPYWAFGFHQ 326
                                                                                                                                                                                                                                                                                                  339 LDYLQGSGETPQTDVRWMSESGIIDVFLLLGPSVFDVFRQYASLTGTQALPPLFSLGYHQ 398
                                                                                                                                                                                                                                                                                                                                                                                               327 CRWGYRDVNEIETVVDKYABARIPLEVMWTDIDYMDAFKDFTLDFVHFPLDKMÇQFVTKL 386
                                                                                                                                                                                                                                                                                                                                                                                                                                           399 SRWNYRDEADVLEVNQGFDDHNLPCDFIWLDIEHADGKRYFTWDPSRFP--QPRTMLEHL 456
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     387 HRNGQRYVPILDPGINTNKSYGTFIRGMQSNVFIK-RNGNPYLGSVWPGPVYYPDFLDPA 445
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 500 RVPINSKTIPATAMHYGNVTEYNAHNLYGFLESQATREALV--RPATRGPFLLSRSTFAG 557
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                                                                                                           SFN--RDLNLYGSHPFYMDVRSSPMVGSTH---GVFLLNSNGMDVEYTGDRITYKVIG-- 287
                                                                                                                                                                           286 QYELYNPMALYGSVPVL-----LAHSPHRDLGIFWLNAAETWVDISSNTAGKTLFGKM 338
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  446 ARSFWYDEIKRFRDILPIDG-----IWIDMNEASNFITSAPTPGSTLDNPPYKINNSGG 499
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      785 ----YHGPQTLYLPVTLSSIP----VFQRGGTIVPRWMRVRRSSDCMKDDPITLFVALS
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                                                                                                                                                 261 THGVFLLNSNGMDVEYTGDRITYKVIG--------GIIDLYIFA 296
                                                                                                                                                                          297 GRIPEMVLDQYIKLIGRPAPMPYWAFGFHQCRWGYRDVNBIETVVDKYAEARIPLEVMWT 356
                                                                                                                                                                                                                                                  394 GPTPSDVFKQYSHLTGTQAMPPLFSLGYHQCRWNYEDEQDVKAVDAGFDEHDIPYDAMML 453
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                                                                                                                                                                                                                                                                                                                           417 NVFIK-RNGNPYLGSVMPGPVYYPDFLDPAAR----SFWVDEIKRFRDILPIDGIWIDMN
                                                                                                     DIDYMDAPKDFTLDPVHFPLDKMQQFVTKLHRNGQRYVPILDPGINTNKSYGTFIRGMQS
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                                     Gaps
                                     93;
   Length 967;
Query Match 16.5%; Score 802.5; DB 12; Length Best Local Similarity 31.1%; Pred. No. 6.7e-61; Matches 199; Conservative 109; Mismatches 239; Indels
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Sequence 38, Application US/10032189 Publication No. US20030170630A1 GENERAL INFORMATION:

APPLICANT: Alsobrook II, John P
APPLICANT: Tchernev, Velizar T
APPLICANT: Liu, Xiaohong
APPLICANT: Spytek, Kimberly A
APPLICANT: Serbusen, Bryan D
APPLICANT: Grosse, William M
APPLICANT: Grosse, William M
APPLICANT: Lepley, Denise M
APPLICANT: Lepley, Denise M
APPLICANT: Shimkets, Richard A
APPLICANT: Scheres, William Y
APPLICANT: Scheres, William Y
APPLICANT: Szekeres, Edward S
APPLICANT: Vernet, Corine A.M.

Lepley, Denise M Burgess, Catherine E Shimkets, Richard A Grosse, William X Szekeres, Edward S Vernet, Corine A.M.

Stacie J Ferenc L

Li, Li Casman, Boldog,

APPLICANT: APPLICANT: APPLICANT:

Search completed: October 27, 2003, 10:38:11 Job time : 113.802 secs

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TELEFAX: 608-251-9166
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LENGTH: 877 amino acids
TYPE: amino acid
TOPOLOGY: linear
                   1137
2628
3144
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3144
3144
10182
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1289
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MOLECULE TYPE: protein
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US-08-430-925A-4
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                                                        ; Search time 16.5211 Seconds (without alignments) 2340.767 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                  Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                 US-10-043-418-2
4862
1 MERSKLPRYICPTLAVVLPL.....RQLVGQAFKLELEFEGATRV 914
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2: /cgn2 6/ptodata/2/iaa/5B COMB.pep:*
3: /cgn2 6/ptodata/2/iaa/6A COMB.pep:*
4: /cgn2 6/ptodata/2/iaa/6B COMB.pep:*
5: /cgn2 6/ptodata/2/iaa/PCTUS COMB.pep:*
6: /cgn2 6/ptodata/2/iaa/PCTUS COMB.pep:*
GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
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US-09-376-34-2

US-08-633-770A-2

US-08-633-770A-2

US-08-633-770A-1

US-09-275-608-3

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US-09-275-608-3

US-09-275-608-3

US-09-375-608-3

US-09-634-28-331

US-09-634-28-331

US-09-634-28-331

US-09-107-532A-2

US-09-107-532A-4996

US-08-107-532A-4996

US-08-107-532A-4996

US-08-21-645-12

US-09-221-645-12

US-09-221-645-12

US-09-221-645-12

US-09-221-645-12

US-09-221-645-12

US-09-221-645-12
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US-09-107-532A-6126
US-09-041-886-28
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-09-437-054A-17
                                                                                                                                                                                           Total number of hits satisfying chosen parameters:
                                                                                                                                                                         328717 seqs, 42310858 residues
                                                                                                                                                                                                                                                                                                                                                                                                         SUMMARIES
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Maximum Match 100%
Listing first 45 summaries
                                        OM protein - protein search, using sw model
                                                           2003, 10:19:13
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Gapop 10.0 , Gapext 0.5
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Maximum DB seq length: 2000000000
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Match Length DB
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No.
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14, Appl
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12, Appl
115, Appl
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GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Tibbot, Brian K
ITILE OF INVENTION: Cloned Alpha-Glucosidase from Barley
NUMBER OF SEQUENCES: 7
CORRESPONDENCE ADDRESS:
ADDRESSE: Quarles & Brady
STREET: 1 South Pinckney Street
CITY: Madison
STREET: 1 South Pinckney Street
CITY: Madison
STREE: 1 South Pinckney Street
CITY: Madison
STREET: 1 South Pinckney Street
CITY: Madison
STREET: 1 South Pinckney Street
CITY: Madison
STREET: 1 South Pinckney Street
COUNTRY: US
SOUNTRY: US
SOUNTRY: US
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Patentin Release #1:0, Version #1:30
CURRENT APPLICATION DATA:
CHRENT APPLICATION NUMBER: US/08/430,925A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 48.7%; Score 2370; DB 1; Length 877; Best Local Similarity 51.2%; Pred. No. 4.5e-204; Matches 466; Conservative 147; Mismatches 235; Indels 6;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      US-09-041-886-29
US-09-041-886-30
US-09-041-886-30
US-09-252-991A-24829
US-08-570-311-14
US-08-45-3245-6
US-08-457-2738-42
US-08-457-2738-42
US-09-134-001C-3159
US-09-134-001C-3159
US-09-134-001C-3159
US-09-136-002-18
US-09-186-02-2
US-09-186-02-2
US-09-186-02-2
US-09-186-002-2
US-09-186-002-2
US-09-186-002-2
US-09-186-002-2
US-07-876-280-4
US-08-063-170-4
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59: 960296.93171
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FILING DATE:
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Seay, Nicholas J
REGISTRATION NUMBER: 27,386
REFRENCE/DOCKET NUMBER: 9602
TELECHMUNICATION INFORMATION:
TELEPHONE: 608-251-900
TELEFAX: 608-251-9166
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721 GNWVSLSNYTSSVSVSAGTYVSLSAPPDHINVHIHEGNIVAMQG--EAMTTQAARSTPFH 778
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                                                                                                                                                                                                                                                                                                                                                    PPPPSPPLSSLOHLPK--PIPQNOPTITVLSHPHSDL----AFTLF-HTTPFGFTIYRK 167
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GRPAPMPYWAFGFHOCRWGYRDVNEIETVVDKYAEARIPLEVMWTDIDYMDAFKDFTLDP 371
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   430 SVWPGPVYYPDFLDPAARSFWVDEI--KRFRDILPIDGIWIDMNEASNFITSAPTPGSTL 487
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                                                                                                                                                                                                                                                                                                                                                                                       120 P-----STKLWLPKISSVENGLSSSVYLSDGHSAVLRHDPFELFIRDDSSGDRVISL 171
                                                                                                                                                                                                                                                                                                  230 SLALKPTRGPNVDESEPYRLFNLDVFEYIHDSPFGLYGSIPFMV---SHGKARGSSGFFW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              372 VHFP-LDKMQQFVTKLHRNGQRYVPILDPGINTNKSYGTFIRGMQSNVFIK-RNGNPYLG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 676 TLFREANTTGVPVVRPLWMEPPSDBATFSNDETFWVGSSILVQGIYTERAKHASVYLPGK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              736 QSWYDLR--TGAV-YKGGVTHKLEVTEESIPAFORAGTIIARKDRFRRSSTQMA-NDPYT
                                                                                                                                                                                                                                          TLRLILLLLCSHLHSVLSWKKEEFRTCHQTPFCKRARSRAPGSSSLIA-TDVTISHG-D
                                                                                                                                                                                                                                                                              LTALLQLIRNSPVYGPDIHFLSFTASFEEDDTLRIRFTD----ANNRRWEIPNEVLPRP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ----KPTF--QLAHNQILTLWNADIASFNRD--LNLYGSHPFYMDVRSSPMVGSTHGVFL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LNSNGMDVE-----YTGDRIT--YKVIGGIIDLYIFAGRTPEMVLDQYTKLI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       347 GTPAMPQLFSIAYHOCRWNYRDEEDVEHVDSKFDELDIPYDVLWLDIEHTDGKRYFTWDR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              513 -NGP----EVTMPRDVTHYGGVEHRELHNAYGYYFHMATANGLLK---RGE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    547 ----PFLLSRSTFAGSGKYTAHWTGDNAARWDDLQYSIPTMLNFGLFGMPMIGADICGFA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ESTTEELCCRWIQLGAFYPFSRDHSARDTTHQELYLW-ESVAASARTVLGLRYELLPYYY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   13 TLAVVLPLVLCMVVEGATTSKNDN-------QGEAIGYGYQVKNAKVDNSTGKS
                                                                                                                                                                                                                                                                                                                                                                                                                            ----SNPTTFLIYKDQYLQLSSSLPAQQAHLYGLGEHT-
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                                                                                                                                                                    Gaps
                                                                                                                             Query Match 18.2%; Score 884.5; DB 4; Length 914; Best Local Similarity 29.7%; Pred. No. 2e-70; Matches 272; Conservative 138; Mismatches 370; Indels 135.
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 97
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SOFTWARE: Microsoft Office SEQ ID NO 8
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                                                      TYPE: PRT
CRGANISM: Glycine
US-09-437-054A-8
                                      LENGTH: 914
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                                                                                                                                                                                                                                                                              363 AFKDFTLDPVHFPLDKXQQFVTKLHRNGQRYVPILDPGINT---NKSYGTFIRGAQSNVF 419
 ----DVQRLAVYASLETDSRLRVRITDADHPRWEVPQDIIPRPAPGDVLHDAPPASSAP 113
                                                                                                                               LSSLQHLPKPIPQNQPTTTVLSHPHSDLAFTLFHTTPFGFTIYRKSTHDVLFDATPIPSN
                                                                                                              183 PTTFLIYKDQYLQLSSSLPAQQAHLYGLGEHTKPTFQLAHNQILTLWNADIASFNRDLNL
                                                                                                                                                                                     YGSHPFYMDVRSSPMVGSTHGVFLLNSNGMDVEYTGDRITYKVIGGIIDLYIFAGRTPEM
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Patent No. 6316698
GENERAL INFORMATION:
APPLICANT: Allen, Stephen M.
APPLICANT: Kinney, Anthony J.
TITLE OF INVENTION: Plant Alpha-Glucosidase II
FILE REFERENCE: BB1273 US NA
CURRENT APPLICATION NUMBER: US/09/437,054A
CURRENT FILING DATE: 1998-No. 6316698ember-10
PRIOR FILING DATE: 1998-No. 6316698ember-10
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vvGEEFELKV 873
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TILE OF INVENTION: Hyperthermophilic Alpha-Glucosidase Gene and Its Use FILE REFERENCE: N1231-200
CURRENT APPLICATION NUMBER: US/09/376,343
CURRENT FILING DATE: 1999-08-18
EARLIER APPLICATION NUMBER: 60/096,860
EARLIER APPLICATION NUMBER: 60/096,860
EARLIER FILING DATE: 1998-08-18
NUMBER OF SEQ ID NOS: 4
SEQ ID NOS: 4
LENGTH: 693
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ORGANISM: Sulfolobus solfataricus US-09-376-343-2
                                                                                                                                                                                                                                                                         ; Sequence 2, Application US/09376343; Patent No. 6506592; GENERAL INFORMATION:
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                                                                               KG 873
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16.8%; Score 816; DB 4; Length 919;
Best Local Similarity 29.8%; Pred. No. 3e-64;
Matches 215; Conservative 116; Mismatches 283; Indels 108;
                                                                                                   US-09-437-054A-17

Sequence 17, Application US/09437054A

Fatent No. 6316699

GENERAL NIFORMATION:
APPLICANT: Allen, Stephen M.
APPLICANT: Allen, Stephen M.
TITLE OF INVENTION: Plant Alpha-Glucosidase II Homologs
FILE REFERENCE: BB1273 US NA.
CURRENT FILING DATE: 2001-05-14

PRIOR FILING DATE: 2001-05-14

PRIOR FILING DATE: 1998-No. 6316698ember-10

NUMBER OF SEQ ID NOS: 19

SOFTWARE: Microsoft Office 97

SEQUENCE OF THE OFFICE OFFI
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YPSDAFI-ERIILLG
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499 GRVPINSKTIPATAMHYGNVTEYNAHNLYGFLESQATREALVRPA--TRGPFLLSRSTFA 556
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: Patentin Release #1.0, Version #1.25 (EPO)
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SSEE: Knobbe, Martens, Olson & Bear
: 620 Newport Center Drive 16th Floor
Newport Beach
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NAME: Altman, Daniel E
REGISTRATION NUMBER: 34,115
REFERENCE/DOCKET NUMBER: DYOUG.001APC
TELECOMUNICATION INFORMATION:
TELEPHONE: 714-760-0404
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/EP94/03398
FILING DATE: OCT-15-1994
ATTORNEY/AGENT INPORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER: US/08/633,770A
FILING DATE: July 8, 1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                | : | : : : | : | 869 SSADPKGHLETPIWI-ERVVIMG 890
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 2, Application US/08633770A
Patent No. 5908760
GENERAL INFORMATION:
APPLICANT: Bojsen, Kirsten
APPLICANT: Yu, Shukun
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      IBM Compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 1070 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER READABLE FORM:
MEDIUM TYPE: Diskett
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       U.S.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           180 PSNPTTFLIYKDQYLQLSSSLPAQQAHLYGLGEHT-----KPTFQLAHNQILTLWNADIA 234
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         281 QYELNNPMALYGSVPVLLAHSFHRDL-----GIFWLNAARTWVDISSNTAGKTLF 330
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GMDVEY----TGDR----ITYKVIGGIIDLYIFAGRTPEMVLDQYTKLIGRPAPMPYWAFG 323
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FHOCRWGYRDVNEIETVVDKYAEARIPLEVMWTDIDYMDAFKDFTLDPVHF--PLDKMQQ 381
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                                                                                                                  Sequence 1, Application US/08897843A
Sequence 1, Application US/08897843A
Patent No. 6514493
GENERAL INFORMATION:
APPLICANT: Deleo, Albert B.; Loftus, Douglas; Appella, Ettore
TITLE OF INVENTION: CDNA CLONE FOR MUR.NE TUMOR
TITLE OF INVENTION: REJECTION ANTIGEN GP110 AND TUMOR PEPTIDE VACCINE
NUMBER OF SEQUENCES:
CORRESPONDENCE ADDRESS:
ADDRESSEE: Diane R. Meyers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                235 SF--NRDLNLYGS-----SN-THPFYMDVRSSPMVGSTHGVFLLN-----SN----SN----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 14.0%; Score 681.5; DB 4; Length 938; Best Local Similarity 27.9%; Pred. No. 3.9e-52; Matches 207; Conservative 115; Mismatches 264; Indels 157; Gaps
COUNTAIN.

ZIP: 15219

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: TEM PC compatible
COMPUTER: TEM PC compatible
COMPUTER: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/897,843A
FILING DATE:
CLASSIFICATION: 424
INFORMATION FOR SEQ ID No: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 938 amino acids
TYPE: amino acid
TYPE: amino acid
                                                                                                                                                                                                                                                                                                     3: Diane R. Meyers
600 Grant Street, 42nd Floor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ORGANISM: Mus musculus
DEVELOPMENTAL STAGE: Embryo
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                                                                                                                                                                                                                                                                                                                     STREET: 600 Grant
CITY: Pittsburgh
STATE: PA
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HYPOTHETICAL: NO
ANTI-SENSE: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FRAGMENT TYPE: NORIGINAL SOURCE:
                                                                                     RESULT 5
US-08-897-843A-1
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APPLICANT: Krāgh, Karsten
APPLICANT: Christensen, Tove
APPLICANT: Christensen, Tove
APPLICANT: Marcussen, Jan
TITLE OF INVENTION: ALPHA-1,4-GLUCAN LYASE FROM A FUNGUS, ITS
TITLE OF INVENTION: PURIFICATION GENE CLONING AND EXPRESSION IN MICROORGANISMS
OWRESPONDENCE 12
CORRESPONDENCE ADDRESS: |: |:||| : ||:||| | |-----EVIMLKDAVHYGGWEHRDIHNIYGLYVHMATADGLIQRSGGIERPFVLSRAFFS 601 557 GSGKYTAHWIGDNAARWDDLQYSIPTMLNFGLFGMPMIGADICGFAESTIEELCCRWIQL 616 : | | | :|:|:|:| | | :::| | | :::| | | :::| | | :::| | | :::| | | :::| | | :::| | | :::| | | :::| | ::| | :::| | :::| | :::| | :::| | :::| | :::| | :::| | :::| | :::| | :::| | :::| | :::| | :::| | :::| | :::| | :::| | :::| | :::| | :::| | :::| | :::| | :::| | :::| | :::| | :::| | :::| | :::| | :::| | :::| | :::| | :::| | :::| | :::| | :::| | :::| | :::| | :::| | :::| | :::| | :::| | :::| | :::| | :::| | :::| | :::| | :::| | :::| | :::| | :::| | :::| | :::| | :::| | :::| | :::| | :::| | :::| | :::| | :::| | :::| | :::| | :::| | :::| | :::| | :::| | :::| | :::| | :::| | :::| | :::| | :::| | :::| | :::| | :::| | :::| | :::| | :::| | :::| | :::| | :::| | :::| | :::| | :::| | :::| | :::| | :::| | :::| | :::| | :::| | :::| | :::| | :::| | :::| | :::| | :::| | :::| | :::| | :::| | :::| | :::| | :::| | :::| | :::| | :::| | :::| | :::| | :::| | :::| | :::| | :::| | :::| | :::| | :::| | :::| | :::| | :::| | :::| | :::| | :::| | :::| | :::| | :::| | :::| | :::| | :::| | :::| | :::| | :::| | :::| | :::| | :::| | :::| | :::| | :::| | :::| | :::| | :::| | :::| | :::| | :::| | :::| | :::| | :::| | :::| | :::| | :::| | :::| | :::| | :::| | :::| | :::| | :::| | :::| | :::| | :::| | :::| | :::| | :::| | :::| | :::| | :::| | :::| | :::| | :::| | :::| | :::| | :::| | :::| | :::| | :::| | :::| | :::| | :::| | :::| | :::| | :::| | :::| | :::| | :::| | :::| | :::| | :::| | :::| | :::| | :::| | :::| | :::| :::| | :::| | :::| | :::| | :::| | :::| | :::| | :::| | :::| | :::| | :::| | :::| | :::| | :::| | :::| | :::| | :::| | :::| | :::| | :::| | :::| | :::| | :::| | :::| | :::| | :::| | :::| | :::| | :::| | :::| | :::| | :::| | :::| | :::| | :::| | :::| | :::| | :::| | :::| | :::| | :::| | :::| | :::| | :::| | :::| | :::| :::| | :::| | :::| | :::| | :::| | :::| | :::| | :::| | :::| | :::| | :::| | :::| | :::| | :::| | :::| | :::| | :::| | :::| | :::| | :::| | :::| | :::| | :::| | :::| | :::| | :::| | :::| | :::| | :::| | :::| | :::| | :::| | :::| | :::| | :::| | :::| | :::| | :::| | :::| | :::| | :::| | :::| | :::| | :::| | :::| | :::| SECONDITIEVALSPOGTAQGELFLDDGHTPNY--QTRHEFLLRRFSFSG--STLVS 868 602 GSORFGAVWIGDNIAEWDHLKISIPMCLSLALVGLSFCGADVGGFFKNPEPELLVRWYQM 661 GAFYPFSRDHSARDTTHQELYLW----ESVAASA-----RIVLGLRYELLPYYYTLMY 665 662 GAYGPFFRAHAT------WTLGGESMAVSVSIPRCNPRCLVPAIFFAALLVYPLLS 711 712 ----SIVNAYSPRGNWVSLSNYTSSVSVSAGTYVSLSAPPDHINVHIHEGNIVAMQGBAM 767 768 TTQAARSTPFHLLVVMSDHVASTGELFLDNGIBMDIGGPGGKWTLVRFFAESGINNLTIS 827 771 MTFRAIRSIMGPRPCICPVTLSSIPVFQGGGTIV----PRWMRVR------R

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APPLICANT: Marcussen, Jan.
TITLE OF INVENTION: ALPHA-1,4-GLUCAN LYASE FROM A FUNGUS, ITS
TITLE OF INVENTION: PURIFICATION GENE CLONING AND EXPRESSION IN MICROORGANISMS
NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:
ADDRESSEE: Knobbe, Martens, Olson & Bear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ----SNPTTF-----LIYKDQY 193
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   210 LDI----VKPGHGEYVĞWGEMGGIQFMKEPTFMNYFNFDNMQYQQVY----AQGALDSRE- 261
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        241 NLYGSHPFYMDVRSSPMVGSTHGVFLLNSNGMDVEYTGDRITYKVIG---GIIDLY-IFA 296
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          262 PLYHSDPFYLDVNSNPEHKNITATFIDNYSQIAIDFGKTNSGYIKLGTRYGGIDCYGISA 321
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         297 GRIPEMVLDQYIKLIGRPAPMPYWAFGFHQCRWGYRDVNEIETVVDKYAEARIPLEVMWT 356
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      357 DIDYMDAFKDFTLDPVHFPLDKMQQFVTKLHRNGQRYVPILDPGINTNK---SYGTFIRG 413
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         439 VDKKYYFIMDDRYTEGTSGNAKDVRYMYYGGGNKVEVDPNDVNGRPDFKDNYDFPANFNSK 498
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Cuery Match 10.3%; Score 498.5; DB 2; Length 1066; Best Local Similarity 24.2%; Pred. No. 1.4e-35; Matches 200; Conservative 118; Mismatches 272; Indels 237;
                                                                                                                                                                                                                                                                                                                                                                                                         SOFTWARE: Patentin Release #1.0, Version #1.25 (EPO) CURRENT APPLICATION BATA:
APPLICATION NUMBER: US/08/633,770A
FILING DATE: July 8, 1996
                                                                                   STATE: CA Beach COUNTRY: U.S. B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NAME: Altman, Daniel E
REGISTRATION NUMBER: 34,115
REFERENCE/DOCKET NUMBER: DYOUG.001APC
TELECOMMUNICATION:
TELEPHONE: 714-766-0404
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/EP94/03398
FILING DATE: CTT-15-1994
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           158 TPFGFTIYRKSTHDVLFDATPIP---
     Christensen, Tove
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                414 MQSNVFIK-----RNGN-
                                                                                                                                                                                                                                                                                                                                  : Diskette
IBM Compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1066 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE CHARACTERISTICS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                     COMPUTER READABLE FORM:
MEDIUM TYPE: Diskett
                                                                                                                                                                                                                                                                                                                                                                                 OPERATING SYSTEM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              amino acid
                                                                                                                                                                                                                                                                              ZIP: 92660
                                                                                                                                                                                                                                                                                                                                                            COMPUTER:
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                                                                                                                                                                                                                                                                                                                                                       211 DI---IKPGHGEYVĞMĞEMGGIEFMXEPTFMNYFNFDNYQYQQVY----AQGALDSRE-P 262
                                                                                                                                                                                                                                                                                                                                                                                                         242 LYGSHPFYMDVRSSPMVGSTHGVFLLNSNGMDVEYTGDRITYKVIG---GIIDLY-IFAG 297
                                                                                                                                                                                                                                                                                                                                                                                                                                           RIPEMVLDQYTKLIGRPAPMPYWAFGFHQCRWGYRDVNEIETVVDKYAZARIPLEVMWTD 357
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         358 IDYMDAFKDFTLDPVHFPLDKMQQFVTKLHRNGQRYVPILDPGINTN---KSYGTFIRGM 414
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     382 VDFQDNFRTFTTMPITFPNPK--EMFTNLRNNGIKCSTNITPVISIRDRPNGYSTLNEGY 439
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               480 APTPGSTLDNPPYKINNSGGRVPINSKTIP----ATAMHYGNVTE------YNA 523
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                524 HNL----YGFLESQATREALVRPATRGPFLLSRSTFAGSGKYTAHWTGDNAARWDDLQYS 579
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    580 IPTMLNFGLFGMPMIGADICGFAESTTE-----ELCCRWIQLGAFYPFSRDHSARD 630
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     647 VSQVLSLGLNGVCIAGSDTGGFEPARTEIGEEKYCSPELLIRWYTGSFLLPWLRNHYVKK 706
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       -----TTHQEL---YLWESVAASARTVLGLRYELLPYYYTLMYDANLRG 671
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      716 AYSPR-----GNWV---SLSNYTSSVSVSAGTYVSLSAPPDH-----INVHI 754
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        827 TWYPSNLRPWDDQGVALGNPVEGGSVINYTARI------VAPEDYNLFHNVVPVYI 876
                                                                                                                                                                                                       ----SNPTTF-----LIYKDQYL
                                                                                                                                                                                                                                                      153 PFRIOVVRLLT - PLVDPFPIPNVANATARVADKVVWOTSPKTFRKNLHPGHKMLKDTVL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               415 QSNVFIKRN--------GN------GN------
                                                                                                                                                        Gaps
                                                                                                   Query Match
10.5%; Score 509; DB 2; Length 1070;
Best Local Similarity 24.7%; Pred. No. 1.6e-36;
Matches 194; Conservative 108; Mismatches 244; Indels 240;
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Patent No. 5908760
GENERAL INFORMATION:
APPLICANT: Bojsen, Kirsten
APPLICANT: Yu, Shukun
APPLICANT: Kragh, Karsten
                                                                                                                                                                                                       159 PFGFTIYRKSTHDVLFDATPIP-
                            MOLECULE TYPE: protein
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            HEGNIV 760
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                                                 US-08-633-770A-2
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1092 amino acids
              TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-275-608-3
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                                                                                                                                                                                                                                                                              831 PSNLRPWDDQGVALGNPVEGGSVINYTARI------VAPEDYNLFHSVVPVYREG 880
                                                                                             LNFGLFGMPMIGADICGF----AESTTEELC----CRWIQLGAFYPFSRDHSARD--- 630
                                                                                                                                                                                                     ARPLSFTFPDDVATYG----ISSQFLIGRGIMVSPVLQ-----PGSS----IVNAYS 718
                                        YGFLESQATREALVRPATR----GPFLLSRSTFAGSGKYTAHWTGDNAARWDDLQYSIPTM 583
PR-----GNWV---SLSNYTSSVSAGTYVSLSAPPDH----INVHIHEG
                                                                                                                                                  -----TIHQEL----YLWESVAASARTVLGLRYELLPYYYTLMYDANLRGSPI
                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: YU, Shukun
APPLICANT: YU, Shukun
APPLICANT: JSEN, Kirsten
APPLICANT: MACCUSSEN, Jan
APPLICANT: MACCUSSEN, Jan
TITLE OF INVENTION: ITS USE IN THE PRODUCTION OF 1,5-ANHYDROFRUC
TITLE OF INVENTION: TOSE
NUMBER OF SEQUENCES: 21
CORRESPONDENCE ADDRESS:
ADDRESSEE: Knobbe, Martens, Olson & Bear
                                                                                                                                                                                                                                                                                                             NIV-AMQGEAMITO-AARSTPFHLLVVMSDHVASTGELFLDNGIEMD 802
                                                                                                                                                                                                                                                                                                                                       881 AIIPQIEVROWIGOGGANRIKFNIYPGKDKEYCT----YLDDGVSRD 923
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         E: Knobbe, Martens, Olson & Bear
620 Newport Center Drive 16th Floor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER: IBM Compatible
OPERATING SYSTEM: Windows
SOFTWARE: FastSEQ for Windows Version 2.0b
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/275,608
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APPLICATION NUMBER: PCT/EP95/02172
FILING DATE: 06-JUN-1995
APPLICATION NUMBER: 08/836,156
FILING DATE: 15-APR-1997
APPLICATION NUMBER: ECT/EP94/03397
FILING DATE: 15-CCT-1994
ATTORNEY/AGENT INFORMATION:
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Patent No. 6541237
GENERAL INFORMATION:
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REGISTRATION NUMBER: 34,115
REFERENCE/DOCKET NUMBER: DYC
TELECOMMUNICATION INFORMATION:
TELEPHONE: 714-760-0404
TELEPRAX: 714-760-9502
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STATE: CA
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TELEFAX: 71
TELEX:
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979 GGVTTNAEDFGKYSVISVKAAQEGSQMSVKFDNBVYEHOWGAŚ---FYVRVRNMGAPSNI 1035
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                                                                                                                               179 IPSNPTTFLIYKDQYLQLSSSLPAQQAHLYGLGE------HTKPTFQLAHNQI-LTLW 229
                                                                                                                                                                                                                                                                                                                 PDFLDPAARSFWVDEIKRFRDILPIDGIWIDM------NEASNFITSAPTPGSTLD 488
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                                                                                                                                                                                                                                                                                                                                                                                                                                                    GADICGF-----AESTTEELCCRWIQLGAFYPFSROHSAR------DTTHQELYLWES
                                                                                                                                                                                                                                                                      230 NADIASFNRDLNL---YGSHPFYMDVRSSPMVGSTHGVFLLNSNGMDVEY-----
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                                                               Gaps
                                                               Indels 209;
DB 4; Length 1092;
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Ouery Match 7.1%; Score 347.5; DB 4; Best Local Similarity 20.8%; Pred. No. 5.6e-22; Matches 182; Conservative 138; Mismatches 344;
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436 ---VYYPDFLDPAARSFWVDEIKRFRDILPIDGIWIDMNEASNFITSAPTP-----GSTL 487
                                                                                    281 ECDALFPDWGRPDVAQWWGDNYKKLFSI-GLDFVWQDMTVPAMMPHRLGDPVGTNSGETA 339
                                                                                                                                                                                                                                                             595 GADICGFAE----STTEELCCRWIQLGAFYPFSRDHSAR-----DTTHQELYLWESV 642
221 CQTNVTCFLKNEKNPYEVNQSLREKQLYTKSDSLDNIDFGTTPDGPSDAYIGHLDYGGGV 280
                                                                                                                                       DNPPYKINNSGGRVPINS--KTIPATAMHYGN-----VTEYNAHNLYGFLESQATREAL 539
                                                                                                                                                                                340 PGWPNDKDPSNGRYNWKSYHPQVLVTDMRYDDYGRDPIVTQRNLH-AYTLCES-TRREGI 397
                                                                                                                                                                                                                                                                                                                                                                     458 GSDIGGFTEHDKRNPCTPDLMMRFVQAGCLLPWFRNHYDRWIESKKHGKNYQELYMYRDH 517
                                                                                                                                                                                                                                540 VRPAT-----RGPFLLSRSTFAGSGKYTAHWTGDNAARWDDLQYSIPTMLNFGLFGMPMI 594
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APPLICANT: MARCUSSEN, JOHN
TITLE OF INVENTION: ALPHA-1,4-GLUCAN LYASE FROM
TITLE OF INVENTION: A FUNGUS INFECTED ALGAE, ITS PURIFICATION
NUMBER OF SEQUENCES: 25
                                                                                                                                                                                                                                                                                                                                                                                                                     643 AASARTVLGLRYELLPYYYTLMYDANLRGSPIARPLS 679
                                                                                                                                                                                                                                                                                                                                                                                                                                                  SSEE: Knobbe, Martens, Olson & Bear
T: 620 Newport Center Drive 16th Floor
Newport Beach
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRIOR APPLICATION DATA:
APPLICATION NUMBER: 9321301.5
FILING DATE: 15-OCT-1993
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ Version 1.5
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     REFERENCE/DOCKET NUMBER: DY
TELECOMMUNICATION INFORMATION
TELEPHONE: 714-760-0404
TELEFAX: 714-760-9502
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            YU, SHUKUN
BOJSEN, KIRSTEN
KRAGH, KARSTEN
BOJKO, MAJA
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COMPUTER: IBM Compatible
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SEQUENCE CHARACTERISTICS:
LENGTH: 1091 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME: Altman, Daniel E
REGISTRATION NUMBER: 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CORRESPONDENCE ADDRESS: ADDRESSEE: Knobbe, M
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ZIP: 92660
COMPUTER RBADABLE FORM:
MEDIUM TYPE: Diskett
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STATE: CA
COUNTRY: U.S.A.
7IP: 92660
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US-08-633-768A-2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       58 NVSQSYTNTGDDAWAGQKDLAYMGAQCGPFDQHFVYEAGDGLEDVVTAFSYLQGKEYENQ 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   313 ----RPAPMPYWAFGFHQCRWGYRDV-----NEIETWVDXYAEARIPLEVMWTD 357
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   118 GLNIRSAMPPKYVFGFFQGVFGATSLLRDNLPAGENNVSLEEIVEGYQNQNVPFEGLAVD 177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 358 IDYMDAFKDFTLDPVHFPLDKMQQFVTKLHRNGQRYVPILDPGINTNKSYGTFI--RGM- 414
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               -- 435
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 6.9%; Score 336; DB 4; Length 570; Best Local Similarity 24.3%; Pred. No. 2.1e-21; Matches 140; Conservative 81; Mismatches 210; Indels 146; Gaps
                                                                                                                                                     TITLE OF INVENTION: ALPHA-1,4-GLUCAN LYASE AND
TITLE OF INVENTION: ITS USE IN THE PRODUCTION OF 1,5-ANHYDROFRUC
TITLE OF INVENTION: TOSE
NUMBER OF SEQUENCES: 21
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               -------EGSVWPGP-
                                                                                                                                                                                                                                                                      SSEE: Knobbe, Martens, Olson & Bear
[: 620 Newport Center Drive 16th Floor
Newport Beach
                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: Windows
SOFTWARE: FastSEQ for Windows Version 2.0b
CURRENY APPLICATION DATA:
APPLICATION NUMBER: US/09/275,608
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CLASSIFICATION:
PRIOR APPLICATION DATA:
PRIOR APPLICATION NUMBER:
FILING DATE: 06-JUN-1995
APPLICATION NUMBER: 08/836,156
FILING DATE: 15-APR-1997
APPLICATION NUMBER: PCT/EP94/03397
FILING DATE: 15-CCT-1994
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DYOU9.001C1
                Sequence 4, Application US/09275608
Patent No. 6541237
GENERAL INFORMATION:
APPLICANT: YU, Shukun
APPLICANT: MARCUSSEN, Jan
APPLICANT: MARCUSSEN, Jan
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NAME: Altman, Daniel E
REGISTRATION NUMBER: 34,115
REFERENCE/DOCKET NUMBER: DY
TELECOMMUNICATION INFORMATION:
TELEPHONE: 714-760-0404
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          415 -QSNV--FIKRNGNPY----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LENGTH: 570 amino acids
TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELEFAX: 714-760-9502
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TOPOLOGY: linear
MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER READABLE FORM:
MEDIUM TYPE: Diskett
                                                                                                                                                                                                                                                                                                                                                                       U.S.A.
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                                                                                                                                                                                                                                                                                                                                                                     COUNTRY: U
ZIP: 92660
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                                                                                                                                                                                                                  ZIP: 92660
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskett
                                                                                                                                                                                                   U.S.A.
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                                                                                                                                                                           STATE: CACOUNTRY: U.S
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                                                                                                                                                                  886 YLPVITKWYKFGPDYDTKRLDSALDGGQMIKNYSVPQSDSPIFVREGAILPTRYTLDGSN 945
                                                                         152 FTLFHTTPFGFTIY-----RKSTHDVLFDATPIPS----NPTTFLIYKDQ-YLQLSS 198
                                                                                                         186 FLKFETKDLNVIIYGNFKTRVTRKRDGKGIMENNEVPAGSLGNKCRGLMFVDRLYGTAIA 245
                                                                                                                                            SL-----PAQQAHLYGLGEHTKPTFQLAHNQ-----ILTLWNADIASFNR-DL 240
                                                                                                                                                                                                                  241 NL--YGSHP-FYMDVR-SSPMV-----GS-----THGVFL------LNSNGMDVEYTG 278
                                                                                                                                                                                                                                                 306 IAPGYPSDPNFYIPMYFAAPWVVKGCSGNSDEQYSYGWFMDNVSQTYMNTGGTSWNCGE 365
                                                                                                                                                                                                                                                                                      DRITY--KVIGGIIDLYIFA-GRIPEMVLDQYTKLIG------RPAPMPYWAFGFH 325
                                                                                                                                                                                                                                                                                                          ENLAYMGAQCGPFDQHFVYGDGDGLEDVVQAFSLLQGKEFENQVLNKRAVMPPKYVFGYF 425
                                                                                                                                                                                                                                                                                                                                                        QCRWGYRDV------NBIETVVDKYABARIPLBVMWTDIDYMDAFKDFTLDPVHF 374
                                                                                                                                                                                                                                                                                                                                                                               ---QQFVTKLHRN---GQRY---VPILDPGIN---- 402
                                                                                                                                                                                                                                                                                                                                                                                                                                                              486 TANKVGTGGDSNNKSVFEWAHDKGLVCQTNVTCFLRNDNGGADYEVNQTLREKGLYTKND 545
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 --INKSYGTFIRGMOSNVFIKRNGNP---YLGSVWPG----PVYYPJFLDPAARSFWVD 452
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EI-KRFRDILPIDGIWIDMNEASNFITSAPTP---GSTLD-NPPYKINN----SGGRVPI 503
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           552
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            646 KSYHPOVLVTDMRYENHGREPMFTQRNMHAYTLCESTRKEGIVANADTLTKFRRSYIISR 705
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 553 STFAGSGKYTAHWTGDNAARWDDLQYSIPTMLNFGLFGMPMIGADICGFAESTTEELC-- 610
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ---CRWIQLGAFYPFSRDHSAR-----DTTHQELYLWESVAASARTVLGLRYELLPYY 660
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          YTLMYDANLRGSPIARPLSFTFPDDVATYGISSQFLI----GRGIMVSPVLQPGSSIVNA 716
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  YSP-RGNWVSLS-NYTS---SVSVSAGTYV-SLSAPPDHINVHIHEGNIVAMQ-----G 764
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EAMTTQAARSTPFHLLVVMSDHVASTGELFLDN-GIEMDIGGPG-------GKWT 811
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   766 DLMVRFVQAGCLLPWFRNHYGRLVEGKQEGKYYQELYMYKDEMATLRKFIEFRYRWQEVL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         504 NS--KTIPATAMHY---GNVTEYNAHNLYGFLESQATR-EALVRPAT-----RGPFLLSR
                                        Gaps
Query Match 6.4%; Score 310; DB 3; Length 1091; Best Local Similarity 21.5%; Pred. No. 1.3e-18; Matches 187; Conservative 131; Mismatches 340; Indels 212;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1005 TIKFAYDTYQYVFDGPFYVRIRNLTTASKI 1034
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Sequence 1, Application US/08633768A Patent No. 6013504 GENERAL INFORMATION: APPLICANT: YU, SHUKUN APPLICANT: BOJSEN, KIRSTEN APPLICANT: KRAGH, KARSTEN

US-08-633-768A-1

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152 FILFHTTPFGFTIY------RKSTHDVLFD----ATPIPSNPTTFLIYKDQ-YLQLSS 198
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               363 AYMGAQ-----YGPFDQHFVYGAGGGMECVVTAFSLLQGKEFENQVLNKRSVMPPKYVFG 417
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          324 FHQCRWGYRDV------NBIETVVDKYAEARIPLEVMWTDIDYMDAFKDFTL--- 369
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            370 ------DP----VHFPLDK---MQQFVTKLHRN---GQRYVPILDPGINTNKSY 407
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 478 FWTANRVGTGGDPNNRSVFEWAHDKGLVCQTNITCFLRNDNEGQDYE--VNQTLRERQLY 535
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           408 --GTFIRGMQSNVFIKRNGNPYLGSVWPG-----PVYYPDFLDPAARSFWVDEIKRFRDI 460
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         536 TKNDSLTGTDFGMTDDGPSDAYIGHLDYGGGVECDALFPDWGRPDVAEWWGNNYKKLFSI 595
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  -----FYMDVRSSPMVGSTHGVFLLNSNGMDV 274
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    275 EYTGDRITYKVIGGIIDLYIF-AGRTPEMVLDQYTKLIG------RPAPMPYWAFG 323
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 6.3%; Score 30%; Dength 1088; Best Local Similarity 21.8%; Pred. No. 2e-18; Matches 184; Conservative 120; Mismatches 355; Indels 184; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             199 SL-----PAQQAHLYGLGE---HTKPTFQLAHNQI-LTLWNADIASFNR-DLN----
APPLICANT: BOJKO, MAJA
APPLICANT: NIELSEN, JOHN
APPLICANT: MARCUSSEN, JAN
TITLE OF INVENTION: ALPHA-1,4-GLUCAN LYASE FROM
TITLE OF INVENTION: A FUNGUS INFECTED ALGAE, ITS PURIFICATION
NUMBER OF SEQUENCES: 25
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                           ADDRESSEE: Knobbe, Martens, Olson & Bear
STREET: 620 Newport Center Drive 16th Floor
CITY: Newport Beach
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      OPERATING SYSTEM: DOS
SOFTWARE: FASESEQ Version 1.5
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/633,768A
FILING DATE: 02-JUL-1996
CLASSIFICATION N: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 9321301.5
FILING DATE: 15-OCT-1993
ATTORNEY/AGENT INFORMATION:
NAME: Altenan, Daniel E
REGISTRATION NUMBER: 34,115
REPERRINCE/DOCKET NUMBER: BYOUT.001APC
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECHANS: 714-760-9502
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELEX:
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
IRNGTH: 1088 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER: IBM Compatible OPERATING SYSTEM: DOS
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ORGANISM: Triticum aestivum
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UNSURB
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US-09-437-054A-10
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US-09-437-054A-10
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US-08-306-546C-2
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                                                                                                                     648 VTOMRYENHGREPMVTQRNIH-AYTLCES-TRKEGIVENAOTLTKFRRSYIISRGGYIGN 705
                                                                                                                                                                                                      706 OHFGGMWVGDNSTTSNYIGMMIANNINMNMSCLPLVGSDIGGFTSYDNENORTPCTGDLM 765
                                                                                                                                                                                                                                                  663
                                                                                                                                                                                                                                                                          766 VRYVQAGCLLPWFRNHYDRWIESKDHGKDYQELYMYPNEMDTLRKFVEFRYRWGEVLYTA 825
                                                                                                                                                                                                                                                                                                                                  MYDANLRGSPIARPLSFTFPDDVATYGISSQFLI----GRGIMVSPVLQPGSSIVNAYSP 719
                                                                                                                                                                                                                                                                                                                                                                            885
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      770 QA-ARSTPFHLLVVMSDHVASTGELFLDNGIEMDIGGPGGKWTLVRFFAE--SGINNLTI 826
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 106 LONLKSFADYADQHGVATGLWTQQN-----LSPVDPA----NPKPDDRDFAKEVAIGVK 155
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          507 TIPATAMHYGNVTEYNAHNLYGF-LESQATREAL---VRPATRGPFLLSRSTFAGSGKYT 562
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               156 ALKTDVAWVGSG-----YSFGLDGLAKADAMMTQVKGDSLRPFAITLDGWAGTQRYA 207
                                  596 -GLDFVWQDMTVPAMMPHKIGDDINVKPD----GNWPNADDPSNGQ--YNWKTYHPQVL 647
LPIDGIWIDM-----NEASNFITSAPTPGSTLDNPPYKINNSGGRVPINSKT----IP
                                                                                ATAMHYGN-----VTEYNAHNLYGFLESQATREALVRPAT-----RGPFLLSRSTFAGS
                                                                                                                                                                 559 GKYTAHWTGDNAARWDDLQYSIPTMLNFGLFGMPMIGADICGFAESTTE-----ELC
                                                                                                                                                                                                                                                  CRWIQLGAFYPFSRDHSAR-----DTTHQELYLWESVAASARTVLGLRYELLPYYYTL
                                                                                                                                                                                                                                                                                                                                                                          826 MYONAAFGKPIIKAASMYNNDSNVRRAQNDHFLLGGHDGYRILCAPVVWENSTERELYLP
                                                                                                                                                                                                                                                                                                                                                                                                                                                          886 VLTQWYKFGPDFDTKPLEGAMNGGDRIYNYPVPQSESPIFVREGAILPTRYTLNGENKSL
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3.8%; Score 182.5; DB 4; Length 3
Best Local Similarity 23.4%; Pred. No. 7.2e-08;
Matches 70; Conservative 46; Mismatches 146; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: O'TOOLE, Paul W.
APPLICANT: Reid, Julian R.
APPLICANT: COOLDEAN, Timotheorides, material TITLE OF INVENTION: Polymucleorides, material TITLE OF INVENTION: them and methods for us FILE REFERENCE: 11000:104301
CURRENT APPLICATION NUMBER: US/09/634,238
CURRENT FILING DATE: 2000-08-08
NUMBER OF SEQ ID NOS: 422
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Patent No. 6544772
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Havukkala, Ilkka J.
Bloksberg, Leonard, N.
Lubbers, Mark W.
Dekker, James
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: PRT ORGANISM: Lactobacillus rhamnosus
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O'Toole, Paul W.
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APPLICANT:
APPLICANT:
461
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                                       208 GVWTGDQTGGQWEYIRPHIPTYIGTGLSGQPYVGSDMDGIFGGGNPIVNTRDFQWKAFTP 267
                                                                                                                                622 FSRDHSARDTTHQELYLW-ESVAASARTVLGLRYELLPYYYTLMYDANLRGSPIARPLSF 680
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563 AHWTGD-NAARWDDLQYSIPTMLNFGLFGMPMIGADICGFAESTTEELCCRWIQLGAFYP 621
                                                                                                                                                                                                 268 IQLNMDGWGANPKTPFSFDQQTTAINRAYNKQKTMLMPYNYTASAQSVFDGKPMVRGLFL 327
                                                                                                                                                                                                                                                                        681 TFPDDVATYG--ISSQFLIGRGIMVSPVLQ-----PGSSIVNA-YSPRGNWVSLSNYT 730
                                                                                                                                                                                                                                                                                                            4 MRYSLLPYYYSLFQEASVTGVPVMRPLWLEFPDDKETYNNGEAFMVGPSILAQGIYEEGQ 63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
3.6%; Score 175.5; DB 4; Length 150;
Best Local Similarity 30.1%; Pred. No. 6.5e-08;
Matches 46; Conservative 24; Mismatches 70; Indels 13;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 2, Application US/08306546C
Patent No. 5605797
GENERAL INFORMATION:
APPLICANT: Friderici, Karen
APPLICANT: Jones, Margaret
APPLICANT: Chen, Hong
APPLICANT: Cavanagh, Kevin
TITLE OF INVENTION: Bovine Beta-Mannosidase Gene and Methods
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Allen, Stephen M.
APPLICANT: Allen, Stephen M.
APPLICANT: Kinney, Anthony J.
TITLE OF INVENTION: Plant Alpha-Glucosidase II Homologs
FILE REPERENCE: BB1273 US NO9/437,054A
CURRENT APPLICATION NUMBER: US/09/437,054A
CURRENT FILING DATE: 2001-05-14
PRIOR FILING DATE: 1998-NO. 6316698ember-10
NUMBER OF SEQ ID NOS: 19
SOFTWARE: Microsoft Office 97
SOFTWARE: Microsoft Office 97
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742 KAGESVLLYTKPVPELLKGCPGCTRQSCVVSFYLSTDGELLSPINYHFLSSLKNAKG--- 798
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                                                                                                                                                                                                                                                                                                                                                                                                          636 -----FYRRSRSEIVNGKGHTMGALYWQLNDIWQAPSWSS-LEYGGKWKMLHYFARHFF 688
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        504 NSKTIPATAMHYGNVTEYNAHNLYGF--LESQATREALVRPATRGPFLLSRSTFAGSGKY 561
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           689 -----APLL-PVGFEDKDMLFIYGASHLHSDQQMMLTVRVHTWSSLELVCSESTNPFVI 741
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     --LHKANITATISQQGDTFVFDLKTSAVAPFVWL-----DVGSIPGRFSD 841
                                                                                542 NWRTFPKARF----VSEYGYQSWPSFSTLEKVSSEEDW---SYRSSFALHRQHLINGNNE 594
                                                                                                                                                                     562 TAHW-----TGDNAARWDDLQYSIPTMLNFGLFGMPMIGADICGFAESTTEELCCR
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                                                                                                                                                                                                                                                                                                                              613 WIQLGAFYPFSRDH--SARDTTHQELY----LWESVAASARTVLGLRYELLPYYYTLMY
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APPLICANT: Chen, Hongaret
APPLICANT: Chen, Hong
APPLICANT: Cavanagh, Kevin
TITLE OF INVENTION: Bovire Beta-Mannosidase Gene and Methods
TITLE OF INVENTION: of Use
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MEDIDA TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Harness, Dickey & Pierce, P.L.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           666 DANLRGSPIARPLSFTFPDDVATYGIS-----
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APPLICATION NUMBER: US/08/530,524A
FILING DATE: September 19, 1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 2, Application US/08530524A Patent No. 5837836 GENERAL INFORMATION:
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REGISTRATION NUMBER: 36,683
REFERENCE/DOCKET NUMBER: 6550
TELECOMMUNICATION INFORMATION:
TELEPHONE: (810)641-1600
TELEFACK: (810)641-0270
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      narness, Dic.
LIRET: P.O. Box 828
CITY: Bloomfield Hills
STATE: Michigan
COUNTRY: USP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FILING DATE: September 19
CLASSIFICATION: 536
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 : 879 amino acide
amino acid
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CORRESPONDENCE ADDRESS:
ADDRESSEE: Harness, 1
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MOLECULE TYPE: protein
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MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       842 NGFLM 846
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            105 TVAVVILNSVPIGKTDNMFRRY--SFDITHTVKAVNIIEVRFOSPVVYANORSERHTAYW 162
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     105 EIPNEVLPRPPPPPPPPPSPPPLSSLQHLPKPIPQNQ------PTTTVLSHPHSDLAFT 153
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             163 ------VPPNCPPPVQDGECHVNFİRKMQCSFGWDWGPSFPTQGIWKDVRIE-AYN 211
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             154 LPHTTPFGFT-IYR-----KSTHDVLFDATPIPSNPTTFLIYKDQYLQLSSSLPA 202
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            244 ------GSHP---FYMDVRSSPMVGSTHGVFLLNSNGMDVEYTGDRITYKVIGGI 289
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   323 FRTVELVEEPIQNSPGLSFYFKINGLP-----IFLKGSNWIPADSFQDRVTSAMLRLL 375
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    290 IDLYIFAGRTPEMVLDQYTKLIGRPAPMPYWAFGFHQCRWGYRDVNEIETVVDKYAEARI 349
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 376 LOSVVDANMALRV------WGGGVYB-------QDEFYELCD 405
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2.5%; Score 119.5; DB 1; Length 879;
Best Local Similarity 19.3%; Pred. No. 0.13;
Matches 175; Conservative 111; Mismatches 292; Indels 327;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SOFTWARE PATENTIA Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/306,546C
FILING DATE: September 15, 1994
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Smith, DeAnn F.
REGISTRATION NUMBER: 36,683
REFERENCE/DOCKET UNDERER: 6550-00003
TELECOMMUNICATION:
TELECHONE: (810)641-1600
                                                               CORRESPONDENCE ADDRESS:
ADDRESSEE: Harness, Dickey & Pierce, P.L.C.
STREET: P.O. Box 828
CITY: Bloomfield Hills
STATE: Michigan
                                                                                                                                                                                                                                                                                                                     ZIP: 48303
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
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amino acid
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TITLE OF INVENTION:
                                          NUMBER OF SEQUENCES:
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2.5%; Score 119.5; DB 2; Length 879;

Query Match

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Best Local Similarity 19.3%; Pred. No. 0.13; Matches 175; Conservative 111; Mismatches 292; Indels 327; Gaps 51;	61 TALLOLIRNSPUYGPDIHFLSFTASFEEDDTLRIRFTDANNRRW 104	105 TVAVVLLNSVPIGKTDNMFRRYSFDITHTVKAVNIIEVRFQSPVVYANQRSERHTAYW 162	EIPNEVLPRPPPPPSPPPLSSLQHLPRPIPQNQPTTTVLSHPHSDLAFT	163VPPNCPPPVQDGECHVNFIRKMQCSFGWDWGPSFPTQGIWKDVRIE-AYN 211	LPHTTPFGFT-1YRKSTHDVLFDATP1PSNPTTFL1YKDQYLQLSSSLPA : : : : : : : : : : :	212 VCHLNYFMFTPIYDNYMKTWNLKIESSFDVVSSKLVSGEAIVAI-PELNIQQTNNIEL 268	QOAHLYGLGEHTKPTFQLAHNQILTLWNADIASFNRDLNLY	269 QHGERTVELFVKIDKAIIVETWWPHGHGNQTGYNMSVIFELDGGLRFEKSAKVY 322	244GSHPFYMDVRSSPMVGSTHGVFLLNSNGMDVEYTGDRITYKVIGGI 289 :	IDLYIFAGRIPEMVLDQYTKLIGRPAPM	: : : : 376 LQSVVDANMNALRV	350 PLEVM-WTDIDYMDAFKDFTLDPVHFPLDKMQQFVTKLHRNGQRYVPILD-PGINT 403	406 ELGIMIWQDFWFACALYPTDKDFMDSVREEVTHQVRLKSHPSIITWSGNNE 457	404 NKSYGTFIRGMQSNVFIKRNGNPYLGSVWPGPVYYPDFLDPAARSFWVDEIKRF 457	458 NEAALMMGWYDTKPGYLQTYIKDYVTLYVKNI 489	458 RDILPIDGIMIDMREASNFITSAPTPGSTLDNPPXINNSGGRVPI 503	490 RTIVLEGDOTRPFITSSPINGAKTIAEGWLSPNPYDLNYGDVHFYDYVSDCW 541	504 NSKIIPATAMHYGNVTEXNAHNLYGFLESQATREALVRPATRGPFLLSRSTFAGSGKY 561	542 NWRÍFPKARFVSEYGYQSWPSFSTLEKVSSEEDWSYRSSFALHRQHLINGNNE 594	562 TAHWTGDNAARWDDLQYSIPTMLNFGLFGMPMIGADICGFABSTTEELCCR 612	595 MLÄQIELHFKLPNSTÖQLRÄFKÖTLÄLTQVÄQAQCVKTETE 635	613 WIQLGAFYPFSRDHSARDTTHQELYLWESVAASARTVLGLRYELLPYYYTLMY 665	636FYRRSRSEIVNGKGHTMGALYMQLNDIWQAPSWSS-LEYGGKWKMLHYFARHFF 688	666 DANLRGSPIARPLSFTFPDDVATYGISSOFFLI 697	689APLL-PVGFEDKDMLFIYGASHLHSDQQMMLTVRVHTWSSLELVCSESTNPFVI 741	698 GRGIMVSPVLOPGSSIVNAY-SPRGNWVSLSNYTSSVSVSAGTYV 741	742 KAGESVLLYTKPVPELLKGCPGCTRQSCVVSFYLSTDGELLSPINYHFLSSLKNAKG 798	742 SLSAPPDHINVHIHEGNIVAMQGEAMTTQAARSTPFHLLVVMSDHVASTGELFLD 796	799DYGSIPGRESD 841	797 NGIEM 801	842 NGFLM 846	
ocal S		105	105	163	154	212	203	269	323	290	376	350	406	404	458			504	542	562	595	613	636	999	689	698	742	742	799	797	842	
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Search completed: October 27, 2003, 10:26:41 Job time : 22:5211 secs

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Buckwheat alpha-gl
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Buckwheat alpha-gl
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Potato alpha-gluco
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2942.169 Million cell updates/sec
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2: /SIDSI/gcgdata/geneseqp-embl/AA191.DAT:*
4: /SIDSI/gcgdata/geneseqp-embl/AA191.DAT:*
4: /SIDSI/gcgdata/geneseqp-embl/AA1991.DAT:*
5: /SIDSI/gcgdata/geneseqp-embl/AA1981.DAT:*
6: /SIDSI/gcgdata/geneseqp-embl/AA1982.DAT:*
7: /SIDSI/gcgdata/geneseqp-embl/AA1986.DAT:*
8: /SIDSI/gcgdata/geneseqp-embl/AA1980.DAT:*
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10: /SIDSI/gcgdata/geneseqp-embl/AA1991.DAT:*
11: /SIDSI/gcgdata/geneseqp-embl/AA1991.DAT:*
12: /SIDSI/gcgdata/geneseqp-embl/AA1992.DAT:*
13: /SIDSI/gcgdata/geneseqp-embl/AA1993.DAT:*
14: /SIDSI/gcgdata/geneseqfgeneseqp-embl/AA1992.DAT:*
15: /SIDSI/gcgdata/geneseqfgeneseqp-embl/AA1993.DAT:*
16: /SIDSI/gcgdata/geneseqfgeneseqp-embl/AA1993.DAT:*
17: /SIDSI/gcgdata/geneseqfgeneseqp-embl/AA1993.DAT:*
18: /SIDSI/gcgdata/geneseqfgeneseqp-embl/AA1999.DAT:*
18: /SIDSI/gcgdata/geneseqfgeneseqp-embl/AA2001.DAT:*
22: /SIDSI/gcgdata/geneseqfgeneseqp-embl/AA2001.DAT:*
23: /SIDSI/gcgdata/geneseqfgeneseqp-embl/AA2001.DAT:*
24: /SIDSI/gcgdata/geneseqg-embl/AA2001.DAT:*
24: /SIDSI/gcgdata/geneseqfgeneseqp-embl/AA2001.DAT:*
25: /SIDSI/gcgdata/geneseqfgeneseqp-embl/AA2001.DAT:*
26: /SIDSI/gcgdata/geneseqfgeneseqp-embl/AA2001.DAT:*
                                                                                                                               Search time 49.3092 Seconds
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1 MERSKLPRYICPTLAVVLPL.....RQLVGQAFKLELEFEGATRV
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GenCore version 5.1.6
(c) 1993 - 2003 Compugen Ltd.
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                                                                                                                               October 27, 2003, 10:19:13;
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Maximum Match 100%
Listing first 45 summaries
                                                                                      OM protein - protein search, using sw model
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ABB09152
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ABB57174
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Gapop 10.0 , Gapext 0.5
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seq length: 200000000
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Match Length
                    Copyright
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2848
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2370
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Perfect score:
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Maximum DB
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Glycosyltransferas Aspergillus niger Sequence of glucoa Glucoamylase encod Aspergillus oryzae Human hSI protein	human dia galactosi an alpha-g ria monocy NOVIIC pro	NOV11d NOV11b lydrate protein protein	S. TUDENCRUM ALPHA Human NOVILA prote Breast and ovarian Drosophila melanog Drosophila melanog S. solfataricus ma Plasmid pNOV4839 m Plasmid Ausovasıl m MalA fusion protei	
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ALIGNMENTS

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A recombinant vector containing alpha-glucosidase gene, and a transformant useful for preparation of alpha-glucosidase -
                                                                              Common buckwheat alpha-glucosidase polypeptide #1.
                                                                                             Common buckwheat; alpha-glucosidase; enzyme;
Fagopyrum esculentum Moeench.
                    AAU97731 standard; Protein; 901 AA
                                                                                                                                                                                                                                  (NISO ) NIPPON SHOKUHIN KAKO KK,
                                                                                                                                                                                          31-AUG-2000; 2000JP-0262104.
                                                                                                                                                                                                             31-AUG-2000; 2000JP-0262104
                                                           (first entry)
                                                                                                                                Fagopyrum esculentum
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                                                                                                                                                  JP2002065273-A
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RESULT 1
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Claim 2; Page 7-8; 18pp; Japanese

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                       The invention relates to a recombinant vector containing alpha-glucosidase gene derived from buckwheat. A transformant containing the recombinant vector can be used for preparing alpha-glucosidase by culturing the transformant and isolating alpha-glucosidase from the culture. This sequence represents a buckwheat alpha-glucosidase protein.
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                                                                                                                                                                                                                                                                            542; Conservative 131; Mismatches 187; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  38 GEAIGYGYQVKNAKVDNSTGKSLTALLQLIRNSPVYGPDIHFLSFTASFEEDDTLRIRFT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                             The present sequence represents an alpha-glucosidase isolated from buckwheat (Fagopyrum esculentum Moeench). The alpha-glucosidase gene can be used for the preparation of alpha-glucosidase derived from
                                                                                                                       Buckwheat; alpha-glucosidase; enzyme; Fagopyrum esculentum Moeench;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          16;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 901;
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61.9%; Pred. No. 1.3e-221;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          187;
                                                                                               Buckwheat alpha-glucosidase protein SEQ ID NO:1
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/label= alpha_glucosidase
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label= signal
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                        ABB09151 standard; Protein;
                                                                                                                                                                                                                                                                                                       31-AUG-2000; 2000JP-0262102
                                                                                                                                                                                                                                                                                                                              31-AUG-2000; 2000JP-0262102
                                                                        (first entry)
                                                                                                                                                           Fagopyrum esculentum
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                         N-PSDB; ABL51446
                                                                                                                                                                                                                                                        JP2002065272-A
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     buckwheat
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     LDPGINTN-KSYGTFIRGMQSNVFIKRNGNPYLGSVWPGPVYYPDFLDPAARSFWVDEIK
              GNVTEYNAHNLYGFLESQATREALVRPATRGPFLLSRSTFAGSGKYTAHMTGJNAARWDD
                                                                            LVGKGVMVSPVLTQGATSVTAYFPSGNWFNLFDYTKTVSSPTNGSFVTLDAPLEEINVHV
                                                                                                                                                                                                HEGNIVAMOGEAMTIQAARSTPFHLLVVMSD--HVASTGELFLDNGIEMDIGGPGGKWTL
                                                                                                                                                                                                        VRFFAE-SGINNLTISSEVVNRGYAMSQRWVMDKITILGLKRRVKIKEYTVQKDAGAIKV
                                                                                                                                                                                                                                       LOYSIPTMLNFGLFGMPMIGADICGFAESTTEELCCRWIQLGAFYPFSRDHSARDTTHQE
                                                                                                                                 LYLWESVAASARTVLGLRYELLPYYYTLMYDANLRGSPIARPLSFTFPDDVATYGISSQF
                                                                                                                                                                 LIGRGIMVSPVLQPGSSIVNAYSPRGNWVSLSNYTSSV-SVSAGTYVSLSAPPDHINVHI
                                    RFRDILPIDGIWIDMNEASNFITSAPTPGSTLDNPPYKINNSGGRVPINSKTIPATAMHY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A recombinant vector containing alpha-glucosidase gene, a transformant useful for preparation of alpha-glucosidase
                                                                                                                                                                                                                                                                                                                                                                   Common buckwheat alpha-glucosidase polypeptide #2.
                                                                                                                                                                                                                                                              KGLGRRTSSHNQGGFFVSVISDLRQLVGQAFKLELE 907
                                                                                                                                                                                                                                                                        SVKGARKCSRGTGKFDVVEIPNLSLLVGRNFKLDIQ
                                                                                                                                                                                                                                                                                                                                                                                  Common buckwheat; alpha-glucosidase; enzyme;
Fagopyrum esculentum Moeench.
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                                                                                                                                                                                                                                                                                                                                                                                                          Fagopyrum esculentum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WPI; 2002-474198/51
N-PSDB; ABK86270.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SVSVSA-GTYVSLSAPPDHINVHIHEGNIVAMQGEAMTTQAARSTPFHLLVVMSD--HVA 788
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  847
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SPIARPLSFTFPDDVATYGISSQFLIGRGIMVSPVLQPGSSIVNAYSPRGNWVSLSNYTS 731
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the recombinant vector can be used for preparing alpha-glucosidase by culturing the transformant and isolating alpha-glucosidase from the culture. This sequence represents a buckwheat alpha-glucosidase protein.
                                                                                                                                                                                                                                                      PQNQPTTTVLSHPHSDLAFTLFHTTPFGFTIYRKSTHDVLFDA-TPIPSNPTTFLIYKDQ
                                                                                                                                                                                                                                                                                                                                                                      YLQLSSSLPAQQAHLYGLGEHTKPTFQLAHNQILTLWNADIASFNRDLNLYGSHPFYMDV
                                                                                                                                                                                                                                                                                                                                                                                                                                        RSSPMVGSTHGVFLLNSNGMDVEYTGDR1TYKVIGGI1DLYIFAGRTPEMVLDQYTKLIG
                                                                                                                                                                                                                                                                                                                                                                                                                                                          RPAPMPYWSFGFHQCRYEYRNISVVENVVKAYSTWRIPLEAMWTDIDYMEANKDFTVDPV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          HPPLDKMQQFVTKLHRNGQRXVPILDPGINTN-KSYGTFIRGMQSNVFIKRNGNPYLGSV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RSTFAGSGKYTAHWTGDNAARWDDLQYSIPTMLNFGLFGMPMIGADICGFAESTTEELCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RWIQLGAFYPFSRDHSARDTTHQELYLWESVAASARTVLGLRYELLPYYYTLMYDANLRG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STGELFLDNGIEMDIGGPCGKWTLVRFFAE-SGINNLTISSEVVARGYAMSORWVMDKIT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SIGSVFLDNGVDIEMGDDGGRWSLVTFSAGLVGNNKVTITSSVVNGRFALSQGWKISKVT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      14 LAVVLPLVLCMVVEGATTSKNDNQGEAIGYGYQVKNAKVDNSTGKSLTALLQLIRNSPVY
                                                                                                                                                                                                   14 LLLAATLLFCSLF---VVSESD---EVVGYGYRVVRAKVDSSS-NTLTAFLKLINASSLY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             YKINNSGGRUPINSKTIPATAMHYGNVTBYNAHNLYGFLESQATREALVRPATRGPFLLS
                                                                                                                                        Gaps
                                                                                                                                    22;
                                                                                                     Length 901,
                                                                                                                                    Indels
                                                                                                Ouery Match 58.1%; Score 2824; DB 23; Best Local Similarity 60.2%; Pred. No. 1.2e-219; Matches 542; Conservative 136; Mismatches 200;
                                                                    901 AA;
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358 NFPLDKMQRFVNKLHKNGQKYVAILDPGININTTTYGTFQRAMKADIFIKRQGEPYQGEV 417
                         WPGPVYYPDFLDPAARSFWVDEIKRFRDILPIDGIWIDMNEASNFITSAPTPGSTLDNPP 491
                                             WPGPVYFPDFLNPKTTIFWISEIQTFFNALPVDGLWIDMNEVSNFISSPPIPDSPLDNPP 477
                                                                                                                                                             671
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                                                                                                                                                                                                                                                                          TVSSPANGSFVTLDAPLKEINVHVREGSILALQGEAMTTREARNTPFELVVVISDSGNGS 777
                                                                                                                                                                                                                                                                                                                                              ILGLKRRVKIKEYTVQKDAGAIKVKGLGRRTSSHNQGGFFVSVISDLRQLVGQAFKLELE 907
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      This sequence represents a novel barley alpha-glucosidase protein.
Recombinant alpha-glucosidase can be used to increase the rate of starch
                                                                    YKINNSGGRVPINSKTI PATAMHYGNVTEYNAHNLYGFLESQATREALVRPATRGPFLLS
                                                                                 RSTFAGSGKYTAHWTGDNAARWDDLQYSIPTMLNFGLFGMPMIGADICGFAESTTEELCC
                                                                                                                            RWIQLGAFYPFSRDHSARDTTHQELYLWESVAASARTVLGLRYELLPYYYTLMYDANLRG
                                                                                                                                                                                                          SPIARPLSFTFPDDVATYGISSQFLIGRGIMVSPVLQPGSSIVNAYSPRGNWVSLSNYTS
                                                                                                                                                                                                                                                     SVSVSA-GTYVSLSAPPDHINVHIHEGNIVAMQGEAMTTQAARSTPFHLLVVMSD--HVA
                                                                                                                                                                                                                                                                                                  STGELFLDNGIEMDIGGPGGKWTLVRFFAB-SGINNLTISSEVVNRGYAMSQRWVMDKIT
                                                                                                                                                                                                                                                                                                                                                           DNA encoding barley alpha-glucosidase protein - useful for producing recombinant protein to increase rate of starch grain hydrolysis when
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Alpha-glucosidase; barley; starch grain hydrolysis; alpha-amylase;
glucoamylase; industry; germplasm; hydrolytic enzyme.
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N-PSDB; AAV11736.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RSSPMVGSTHGVFLLNSNGMDVEYTGDRITYKVIGGIIDLYIFAGRTPEMVLDQYTKLIG 312
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RPAPMPYWAFGFHQCRWGYRDVNEIETVVDKYAEARIPLEVMWTDIDYMDAFKDFTLDPV 372
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      73
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     74 GPDIHFLSFTASFEEDDTLRIRFTDANNRRWEIPNEVLPRPPPPPSPPLSSLQHLPKPI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  YLQLSSSLPAQQAHLYGLGEHTKPTFQLAHNQILTLWNADIASFNRDLNLYGSHPFYMDV
                                                                                                                                                                                                                                                                                                                                                                                                              The present sequence represents an alpha-glucosidase isolated from buckwheat (Fagopyrum esculentum Moeench). The alpha-glucosidase gene can be used for the preparation of alpha-glucosidase derived from
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                          Suckwheat; alpha-glucosidase; enzyme; Fagopyrum esculentum Moeench;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      22;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 901;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             58.1%; Score 2824; DB 23; 60.2%; Pred. No. 1.2e-219;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    542; Conservative 136; Mismatches 200;
                                                                    Buckwheat alpha-glucosidase protein SEQ ID NO:2.
                                                                                                                                                                                                                                                                                                                                                                   A buckwheat-derived alpha-glucosidase gene
                                                                                                                                                                                  32..901
/label= alpha_glucosidase
                                                                                                                                                   Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                         Claim 1; Page 9-10; 21pp; Japanese.
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                                                                                                                                                                l..31
/label= signal
                                                                                                                                                                                                                                                                                                            (NISO ) NIPPON SHOKUHIN KAKO
ABB09152 standard; Protein;
                                                                                                                                                                                                                                                               31-AUG-2000; 2000JP-0262102
                                                                                                                                                                                                                                                                                      31-AUG-2000; 2000JP-0262102
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                                                                                                                                                                                                                    JP2002065272-A
                                             01-JUL-2002
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                                                                                                                             Fagopyrum
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(AGRE ) HOECHST-SCHERING AGREVO GMBH.
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                                                                    AAY51670 standard; Protein; 682
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           glucoamylase in industrial starch hydrolysis systems. Useful DNA sequence characteristics from this enzyme can be identified which can be used as hybridisation probes for identifying germplasm with high levels of
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grain hydrolysis when used together with alpha-amylase or can supplement
                                                                                                                                               71 PVYGPDIHFLSFTASFEEDDTLRIRFTDANNRRWEIPNEVLPRP------PPPPSPPP
                                                                                                                                                                                           |----DVQRLAVYASLETDSRLRVRITDADHPRWEVPQDIIPRPAPGDVLHDAFPASSAP
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                                                                                                                                                                                                                                       VLDQYTKLIGRPAPMPYWAFGFHQCRWGYRDVNEIETVVDKYAEARIPLEVMWTDIDYMD
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                                                                                                                                  16 VVLPLVLCMVVEGATTSKNDNQGEA---IGYGYQVKNA-KVDNST-GKSLTALLQLIRNS
                                                                                                                                                                                                                                                                     183 PTTFLIYKDQYLQLSSSLPAQQAHLYGLGEHTKPTFQLAHNQILTLWNADIASFNRDLNL
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                                                                                                               Gaps
                                                                                                             62;
                                                                                         Length 877;
                                                                                                             Indels
                                                                                     ery Match 48.7%; Score 2370; DB 19; st Local Similarity 51.2%; Pred. No. 7.4e-183; tches 466; Conservative 147; Mismatches 235;
                                              efficient hydrolytic enzymes.
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This invention describes a novel potato alpha-glucosidase (I). (I) is used to produce transgenic plants (or plant or bacterial cells) that produce starch with modified degrees of branching, amplose/amylopectin ratio, phosphate content, starch granule size and/or sidechain structure, and thus altered physical and chemical properties. This starch is used for all usual applications, particularly in preparation of foods, packaging materials and disposable articles, but also for hydrolysis to glucose (for manufacture; in adhesives; for treating textiles; for soil stabilization; as wetting agent in plant protection and fertilizer compositions; as binding agent in pharmaceuticals and cosmetics; as additive for rubber, building materials, leather and in casting; as flockulant for soil or coal slurries; and in polymers, as simple filler or reactive component, e.g. in polywrethane feams. Modified starch produced using plants that contain (I) are easily hydrolyzed, reducing the requirement for expensive enzymes. This sequence represents the
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                                                                                                  Alpha-glucosidase; potato; transgenic plant; starch; branching; amylose; amylopectin; granule size; sidechain; food; packaging; hydrolysis; paper; pulp; adhesive; soil stabilization; wetting agent; plant protection; fertilizer
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Potato alpha-glucosidase protein fragment.
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2; Page 1154-1158; 2690pp; English
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                                                                                                                    TYVSLSAPPDHINVHIHEGNIVAMQGEAMTTQAARSTPFHLLVVMSDHVASTGELFLDNG
                                                 I EMDIGGPGGKWTLVR FFAESGINNLTISSEVVNRGYAMSQRWVMDKITILGLKRRVKIK
                                                                                                                                                                                                                                                                                  EYTVQKDAGAIKVKGLGRRTSSHNQG------GFFVSV-ISDLRQLVGQAFKLEL
               FYPFSRDHSARDTTHQELYLWESVAASARTVLGLRYELLPXYYTLMYDANLRGSPIARPL
                                                                                                                                                                                            PFSFPQDAKTFDISTQFLLGKGVMISPILKQGATSVDAYFPAGNWFDLFNYSRSVSLNQG
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                                       PDFLDPAARSFWVDE1KRFRD1LP1DG1W1DMNEASNF1TSAPTPGSTLDNPPYK1NNSG
                                                                        GRVPINSKTIPATAMHYGNVTEYNAHNLYGFLESQATREALVRPATRGPFLLSRSTFAGS
                                                                                                           GKYTAHWIGDNAARWDDLOYSIPIMLNFGLFGMPMIGADICGFAESTIEELCCRWIQLGA
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The present invention describes a method for examining ischaemic conditions, comprising measuring the expression levels of particular genes (1) in a test sample condetermining the expression profile of a gene group in the sample comprising genes selected from (1). The method is useful for examining the ischaemic condition (e.g. compression levels of particular genes (ABI99202 to ABI99912, encoding expression levels of particular genes (ABI99202 to ABI99912, encoding the protein sequences in ABB57020 to ABB59912, encoding the protein profile of a gene group comprising these genes are expression levels or expression profiles produced by these genes are used as an indicator when screening for ischaemic condition-improving drugs or therapeutics for ischaemic condition improving represent PCR primers for a mouse ischaemic condition related sequence, which are used in the exemplification of the present invention.
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   145 HPHSDLAFTLFHTTPFGFTIYRKSTHDVLFDATPIPSNPTTFLIYKDQYLQLSSSLPAQQ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              58 IVNKTATDANE-----AAKGYELVNV---TTTAKGLTGILKLNEATNIYGYDFDYLNLSV 109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                144
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        110 EYQSDDRLNVHIEPVDTDNVFILPESLVAKPSADDGDKIESFHF-------153
Q-SKGQWLTLEAPLDTINVHLREGYIIPLQGPSLTTTESRKQPMALAVALTASGEADGEL 858
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The present sequence represents Endomyces fibuliger (also called Saccharomycopsis fibuligera) glucoamylase GLA2. The invention describes the recombinant GLA2 enzyme, which is useful for hydrolysing carbohydrate-containing materials, especially materials containing rice carbohydrates. The glucoamylase is used to produce glucose and alcohol from starch containing raw materials. GLA2 is useful for hydrolysing carbohydrate containing materials e.g. mixtures of a source of proteins and a source of carbohydrates, especially a mixture of leguminous plant or of a cooked oleaginous plant and of a cooked or roasted cereal source e.g. a mixture of soya or cooked beans and of cooked or roasted wheat or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          84
                                                                                                      SFEEDDTLRIRFTDAMNRRWEIPNEVLPRPPPPPPPPLSSLQHLPKPIPQNQPTTTVLS
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                                                            FLDNGIEMDIGGPGGKWTLVRFFAESGINNLTISS -- EVVNRGYAMSQRWVMDKITILG-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              glucose, alcohol; starch; leguminous plant; cooked; oleaginous plant; roasted; cereal; soya; wheat; rice.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Endomyces fibuliger; glucoamylase; GLA2; hydrolysis; carbohydrate;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       for
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    New recombinant glucoamylase from Endomyces fibuliger, useful hydrolyzing carbohydrate-containing materials
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 963;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        *Match 28.2%; Score 1372; DB 20; Local Similarity 33.2%; Pred. No. 7.3e-102; les 317; Conservative 156; Mismatches 332;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Endomyces fibuliger glucoamylase GLA2 protein.
                                                                                                                                                                                                                         ATAPTQVLSNGIPVSNFTYSPDNKSLAI 938
                                                                                                                                                                            -----LKRRVKIKEYTVQKDAGAIKV 871
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                                                                                                                                                                                                                                                                                                                                                                                   AAY49895 standard; Protein; 963
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Saccharomycopsis fibuligera
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Kochhar S;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (NEST ) SOC PROD NESTLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WPI; 1999-622099/54.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Pridmore RD,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      06-MAY-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                28-JAN-2000
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Matches 317
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TELREKEKELLVALDNDGKAKGELYIDDGBSLE---QESYTAVKFEYAHGV--VTLDG 879
                                                                                                                            TQAARSTPFHLLVVMSDHVASTGELFLDNGIEMDIGGPGGKWTLVRFFAESGINNLTISS 828
592 AMEARRPGLR-PFIITRSTFPHAGSKVGLWLGDNLSNWNQYRESIRTMLAYTSIFQFGMV 650
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GADICGFAESTTEELCCRWIQLGAFYPFSRDHSARDTTHQELYLWESVAASARTVLGLRY
                                                                                                       655 ELLPYYYTLMYDANLRGSPIARPLSFTFPDDVATYGISSQFLIGRGIMVSPVLQPGSSIV
                                                                                                                                                                            NAYSPRGN-----WVSLSNYTSSVSVSAGTYVSLSAPPDHINVHIHEGNIVAM-QGEAMT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 7 PRYICPTLAVVLPLVLCMVVEGATTSKN-----DNQGEAIGYGYQVKNAKVDNSTGKS
                                                                    GSDVCGFGGDTNEELCARWASLGAFQTFFRNHAQYEAVPQEFYQWESVAESARRAIGARY
                                                                                                                                                                                                            DVYLPEGKVFYDWWTH-----EAIQGEGGSYSVTGVNTTMIPLFIRGGVILPLRENSAMT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Glycosyltransferase was prepared from a culture of A. niger containing recombinant DNA encoding GTase (AAQ50468). GTase can be obtained effectively using this method and in larger quantities. The probes (AAQ50466-67) were used to detect transformants containing the GTase gene.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Prepn. of glucosyl:transferase - using glucosyl:transferase gene from recombinant DNA of Aspergillus niger
                                                                                                                                                                                                                                                                                                                                            DB 14; Length 985;
                                                                                                                                                                                                                                                                                                                     EVVNRGYAMSQRWVMDKITILGLKRRVKIKEYTVQ-----KDAGAIKVKG 873
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              324; Conservative 156; Mismatches 306; Indels 209;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GTase; Aspergillus niger; plasmid;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             27.6%; Score 1339.5; DB 32.6%; Pred. No. 3.3e-99;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (AMAN) AMANO PHARM KK. (UOZU/) UOZUMI T.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Glycosyltransferase;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         N-PSDB; AAQ50468.
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                                                                                                                                                                                                                                                                                                                    The present sequence represents a sugar transferase protein of Acremonium sp. 34G13. The protein preferably catalyses the glucose transfer of an alpha-1 right arrow 3 bond or the glucose transfer of an alpha-1 right arrow 4 bond to a sugar receptor by reacting with a substrate selected from starch and its decomposition
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    102
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    YPEYAIHNKAAFRDDWNADKGG---ISNKTVNTNVIHQNGLAEYDVHNLYGAMASSASRD 591
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       .03 RWEIPNEVLPRPPPPPPPPPSSLQHLPKPIPQNQPTTTVLSHPHSDLAFTLFHTTPFGF 162
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GDRITYKVIGGIIDLYIFAGRTPEMVLDQYTKLIGRPAPMPYWAFGFHQCRWGYRJVNEI 337
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ETVVDKYAEARIPLEVMWTDIDYMJAFKDFTLDPVHFPLDKMQQFVTKLHRNGQRYVPIL 397
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           OPEGTECEDGETAGSSKRDGSFGQPGLVTRQPGFSRPRHPFHRRQEYEGDQKGLPGRDLL 534
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              189 NPPYKINN------SGGRVPINSKTIPATAMHYGNVTEYNAHNLYGFLESQATRE 537
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ALV -- RPATRGPFLLSRSTFAGSGKYTAHWTGDNAARWDDLQYSIPTMLNF-GLFGMPMI 594
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    85
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TIYRKSTHDVLFDATPIPSNPTTFLIYKDQYLQLSSSLPAQQAHLYGLGEHTKPTFQLAH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                180 GYIRTEWNQDSYGVPNGANLYGSHPVYIDHRET----GTHGVLFLNSNGMDVJIDEDEEG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                223 NQILTLWNADIASFNRDLNLYGSHPFYMDVRSSPMVGSTHGVFJLNSNGMDV----EYT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GYQVKNAKVDNSTGKSLTALLQLI-RNSPVYGPDIHFLSFTASFEEDDTLRIRFTDANNR
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                                                                                                                                                                                                            New sugar transferase gene and enzyme - useful for catalysing transfer of an alpha-1 right arrow 3 bond to a sugar receptor
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                                                                                                                                                                                                                                                                                    Claim 1; Pages 13-17; 20pp; Japanese
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                                                                                                                        (KIRI ) KIRIN BREWERY KK
                                                                                                                                                                                                                                                 saccharide preparation
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                                                                                                                                                                            N-PSDB; AAX04639
                                                  :9-JUN-1997;
                                                                                       19-JUN-1997;
                19-JAN-1999
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407 YVPIVDAALYIPNPENASDAYATYDRGAADDVFLKNPDGSLYIGAVWPGYTVFPDWHHPK 466
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PPPPSPPDLSSLQHLPKPIPQNQPTTTVLSHPHSDLAFTLFHTTPFGFTIYRKSTHDVLF 174
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DATPIPSNPTTFLIYKDQYLQLSSSLPAQQAHLYGLGEHTKPTFQLAHNQILTLWNADIA 234
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ----STEGTVLVYENQFIEFVTALP-EEYNLYGLGBHI-TQFRLQRNANLTIYPSDDG 227
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ---SSPMVGSTHGVFLLNSNGMD 273
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      228 T-PIDONLYGOHPFYLDTRYYKGDRONGSYIPVKSSEADASODYISLSHGVFLRNSHGLE 286
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DNA encoding truncated variants of Aspergillus glucosyltransferase is claimed. Deletion from the N- or C-terminal reduces Grase estivity of the protein. Specifically, glucoamylass with reduced Grase activity can be prepared. The full-length Grase structural gene was isolated as a 4.3kb Sphl fragment from chromosomal DNA of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 Similarity 32.6%; Score 1339.5; DB 14; Length 985; Similarity 32.6%; Pred. No. 3.3e-99; Conservative 156; Mismatches 306; Indels 209;
                                                                                                                                                                                                                                                                                                                                                       Glucoamylase prepn. with reduced glucosyl-transferase activity using microorganism transformed using plasmids including DNA fragments having deletion of N-end or C-end of Aspergillus
                                   GTase; glucoamylase; GAase; recombinant production; truncated;
N-terminal deletion; C-terminal deletion.
 Aspergillus niger glucosyltransferase.
                                                                                                                                                                                                                                                                                                                                                                                                                                            Disclosure; Page 6-9; 11pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SFNRDLNLYGSHPFYMDVR-
                                                                                                                                                                                                                     92JP-0101761
                                                                                                                                                                                     92JP-0101761
                                                                                  Aspergillus niger #499
                                                                                                                                                                                                                                                        (AMAN ) AMANO PHARM KK
                                                                                                                                                                                                                                                                                                                                                                                                           glucosyl-transferase
                                                                                                                                                                                                                                                                                                          WPI; 1993-364284/46.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                985 AA;
                                                                                                                                                                                                                                                                                                                         N-PSDB; AAQ50982.
                                                                                                                                                                                                                                                                      UOZUMI T.
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60 LTALLQLI-RNSPVYGPDIHFLSFTASFEEDDTLRIRF----TDANNRRWEIPNEVLPRP
                   78 FTASLQLAGRPCNVYGTDVESLTLSVEYQDSDRLNIQILPTHVDSTNASWYFLSSNL---
                                                                                                  ----VPRPKASLN-------ASVSQSDLFVSWSNEPSFNFKVIRKATGDALF
                                                                                                                                                              ----STEGTVLVYENQFIEFVTALP-EEYNLYGLGEHI-TQFRLQRNANLTIYPSDDG
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                                                                   115 PPPPSPPPLSSLQHLPKPIPQNQPTTTVLSHPHSDLAFTLFHTTPFGFTIYRKSTHDVLF
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                                                                                                                                                                                                                                                                                                                                                                                                                                                            HGVFLLNSNGMDVEYTGDRITYKVIGGIIDLYIFAGRTPEMVLDQYTKLIGRPAPMPYWA 321
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FGFHQCRWGYRDVNEIETVVDKYAEARIPLEVMWTDIDYMDAFKDFTLDPVHFPLDKMQQ 381
              A cosmid library is constructed from genomic DNA of ATCC26076 and this screened for inserts contg. the AA gene by ability to transform S.cerevisiae GRP 18 to histidine prototrophy. One positive cosmid (32kb; pYc1) was digested with EcoRI, religated and used to transform E.coli JA221. A GA-contg. cosmid (about 40 kb) was isolated. This was cut with BamHI and religated to give the plasmid pcJD5-AMGI contg. a 12kb fragment (in AAN81526).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    HSDLAFTLFHTTPFGFTIYRKSTHDVLFDATPIPSNPTTFLIYKDQYLQLSSSLPAQQAH
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   495 PFTVGSKATSYPVGFDVSNASEWKSIQSSISATAKTSSTSSVSSSSSTIDYMNTLAPGKG
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                                                                                                                                                                                                                                 34 NDN--QGEAIGYGYQVKNAKVDNSTGKSLTALLQLIRNSPVYGPDIHFLSFTASFEEDDT
                                                                                                                                                                                                                                                   LYGLGEH-----TKPTFQLAHNQILTLWNADIASFNRDLNLYGSHPFYMDVRSSPMVGST
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                                                                                                                                                                                                    Matches 318; Conservative 152; Mismatches 315; Indels 173;
                                                                                                                                                                         Length 958;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  434 GPVYYPDFLDPAARSFWVDEIKRFRDILPIDGIWIDMNEASNF
                                                                                                                                                                         DB 9;
                                                                                                                                                                       27.2%; Score 1324.5; DB 33.2%; Pred. No. 5.2e-98;
                                                                                                                                                                                        Similarity
                                                                                                                                              958 AA;
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                                                                                                                                                                                                                              QLGAFYPFSRDHSARDTTHQELYLWESVAASARTVLGLRYELLPYYYTLMYDANLRGSPI
                                                                                                                                                                                                                                                                                                                  767 MRALSWEFPNDPTLAAVETQFWVGPAIMVVPVLBPLVNTVKGVFPGVGHGEVWYDW----
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                                                                                                                                                                                                                                                                                                                                                                         -YTQAAVDAKPGVNTTISAPLGHIPVYVRGGNILPMQEPALTTREARQTPWALLAALGSN
                                                                                                                                                                                                                                                                                                                                                                                                     VASTGELFLDNG1EMD1GGPGGKWTLVRFFAESGINNLT1SSE-VVNRGYAMSQ---RW-
                                                                                                                                                                                                                                                                                       ARPLSFTFPDDVATYGISSQFLIGRGIMVSPVLQPGSSIVNAYSP---RG----NWVSLS
                            AVDFWANELVIWSKKVAFDGVWYDMSEVSSFCVGSCGTGNLTLNPAHPSFLLPGEPGDII
                                                           - PTPG-STLDNPPYKINN
                                                                                                                                                                       FAGSGKYTAHWIGDNAARWDDLQYSIPIMLNFGLFGMPMIGADICGFAESTIEELCCRWI
                                                                                                                SGGRVPINSKTIPATAMHYGNVTEYNAHNLYGFLESQATREAL - - VRPATRGPFLLSRST
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               genomic DNA of Schwarniomyces
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Polypeptide prodn. from cells transformed with yeast DNA -
esp. coding alpha amylase or glucoamylase, able to convert
starch to ethanol
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                                                                                                                                                                                                                                                                                                                                                                                                                                                            ---VMDKITILGLKRRVKIKEYTVQKDAGAIKVKG 873
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       -----VNKEPSAVTLNG 946
ARSFWYDEIKRFRDILPIDGIWIDMNEASNF
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence of glucoamylase encoded by
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Brewing; beer; breadmaking; biomass
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(first entry)
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N-PSDB; AAN81526.
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118 LNVHI
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                                                                                         HSDLAFTLFHTTPFGFTIYRKSTHDVLFDATPIPSNPTTFLIYKDQYLQLSSSLPAQQAH 206
                                                                                                                    154 NSDLVFE-YSNTDFSFEVIRSSTKEVLFST---KGNP---LVFSNQFIQFNSSLPKNHV- 205
                                                                                                                                                                       HGVFLLNSNGMDVEYTGDRITYKVIGGIIDLYIFAGRTPEMVLDQYTKLIGRPAPMPYWA 321
                                                                                                                                                                                                                              FGFHQCRWGYRDVNEIETVVDKYAEARIPLEVMWTDIDYMDAFKDFTLDPVHFPLDKMQQ 381
                                                                                                                                                                                                                                                                                                                              FVTKLHRNGQRYVPILD-----PGINTNKSYGTFIRGMQSNVFIKR-NGNPYLGSVWP 433
                                                                                                                                                                                                                                                                                                                                                 489 ---NPPYKINNSGGRVPINSKTIPATAMHYGNVTEYNAHNLYGFLESQATREAL--VRPA 543
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             544 TRGPFLLSRSTFAGSGKYTAHWTGDNAARWDDLQYSIPTMLNFGLFGMPMIGADICGFAE 603
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STTEELCCRWIQLGAFYPFSRDHSARDTTHQELYLWESVAASARTVLGLRYELLPYYYTL 663
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SSSELCSRWMOLGSFFFYRNHNYLGAIDQEPYVWESVAEATRISMAIRYLLLPYYYTL 733
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ----NWVSLSNYTS-SVSVSAGTYVSLSAPPDHINVHIHEGNIVAMQGEAMTTQAARST 775
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PFHLLVVMSDHVASTGELFLDNGIEMDIGGPGGKWTLVRFFAESGINNLTISSEVVNRGY 835
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        849 PFGLIVALDNDGKAQGSLYLDDGESLVVDSS----LLVSF----SVSDNTLSAS-PSGDY 899
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             495 PFTVGSKATSYPVGFDVSNASEWKSIQSSISATAKTSSTSŠVSSSSŠTIDYMNTLAPGKG 554
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                                LRIRFTDANNRRWEIPNEVLPRPPPPPSPPLSSLQHLP----KPIPQNQPTTTVLSHP
                                                                                                                                                   LYGLGEH-----TKPTFQLAHNQILTLWNADIASFNRDLNLYGSHPFYMDVRSSPMVGST
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                                              836 AMSQRWVMDKITILGLKRRVK-IK-----EYTVQKDAGAIKVKGLGRRTSSHNQGGF 886
                                                               900 KADQ--PLANVTILGVGHKPKSVKFBNANVDFTYKK--STVFVTGLDKYT---KDGAF 950
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 R, S, F and T may be modified by insertions, deletions or substitutions such that biological activity is retained or improved.
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F is e.g. a cellulase, interleukin, insulin-like-growth factor, interferon etc.
T is pref. all or part of the terminator of this sequence (bp 2875-3320).
GAM1 acts as selective marker for the vector carrying the expression
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The expression cassette may contain a regulon (R), a signal peptide sequence (S), a foreign protein sequence (F) and a terminator (T) of which R and/or S and/or T are derived from the glucoamylase gene of S. occidentalis.

R is pref. a 1.3 kb BamHI-PvuII fragment (bases -1 to -320 of this sequence).

S contains all or part of one of the sequences represented
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 27.2%; Score 1321.5; DB 11; Length 958; Best Local Similarity 33.2%; Pred. No. 9e-98; Matches 318; Conservative 151; Mismatches 316; Indels 173;
                                                                                                                                                                                                                                                                                   Schwanniomyces yeast cells, expression cassette; glucoamylase; marker gene; regulon; signal peptide; terminator; autonomously replicating sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Transformed Schwanniomyces yeast cells - contg. an expression cassette contg. regulon, DNA coding for foreign protein and terminator
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              See also AAQ063B8.
(Updated on 25-MAR-2003 to correct PA field.)
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                                                                                                                                                 AAR07575 standard; protein; 958 AA
                                                                                                                                                                                                                                                    Glucoamylase encoded by GAM1 gene.
                                                                                                                                                                                                                                                                                                                                              Schwanniomyces occidentalis
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(first entry)
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SIPTMLNFGLFGMPMIGADICGFAESTTEBLCCRWIQLGAFYPFSRDHSARDTTHQELYL 638
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                                                                                                                                                                                                                                                                                                          791 PSVMVIPVLEPQVDTVQGVFPGVGHGEVWYDWYS----QTAVDAKPGVNTTISAPLGHIP 846
                                                                                                                                                                                                                                                                                                                                                                                                                                     VHIHEGNIVAMOGEAMTTOAARSTPFHLLVVMSDHVASTGELFLDNGIEMDIGGPGGKWT 811
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              812 LVRFFAESGINNLTISSEVVNRGYAMSQRW----VMDKITILGLKRR---VKIKEYTVQK 864
                                                                                                                                                                                                                                                                                                                                                             RGIMVSPVLQPGSSIVNAYSP---RG----NWVSLSNYTSSVSVSAGTYVSLSAPPDHIN 751
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ----YPEDTLSVDFLASRSTLRASARG-TWKEANPLANVTVLGVTEKPSSVTLNGETLSS 951
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                   491 YDMAEVSSFCVGSCGTGNLSMNPAHPPFALPGEPGNVVYDYPEGFNITNATEAASASAGA
                                                          ------PTPG-STLDNPPYKINNSGGRVPINSKTIPATAMHYGNVT
                                                                                              551 ASQSAAASSTTTSAPYLRTTPTPGVRNVDHPPYVINHVQPGHDLSVHAISPNSTHSDGVQ
                                                                                                                                   EYNAHNLYGFLESQATREALVRP-ATRGPFLLSRSTFAGSGKYTAHWTGDNAARWDDLQY
                                                                                                                                                          WESVAASARTVLGLRYELLPYYYTLMYDANLRGSPIARPLSFTFPDDVATYGISSQFLIG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                         Carter JM, Lambkin IJ;
J;
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Patterson CA,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GANLVANIDDPQAVNAQSVCPGYKASDVK---HSSQGFTASLELAGDPCNVYGTDVDSLT 102
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  82 FTASFEEDJTLRIR----FTDANNRRWEI-PNEVLPRPPPPPPPPPSSLQHLPKPIPQN 136
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        -----ASVPQSDFVVSWSNEPSFNFKVIRKATGDVLF-----NTKGSTLVYENÇFIEF 193
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WIDIDYMDAFKDFTLDPVHFPLDKMQQFVTKLHRNGQRYVPILDPGI-----NTNKSYG 408
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            490
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        QPTTTVLSHPHSDLAFTLFHTTPFGFTIYRKSTHDVLFDATPIPSNPTTFLIYKDQYLQL 196
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ----SSPMVGSTHGVFLLNSNGMDVEYTGDRITYKVIGGIIDLYIF 295
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AGRIPEMVLDQY-TKLIGRPAPMPYWAFGFHQCRWGYRDVNBIETVVDKYAEARIPLEVM 354
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    VGGQNKSHTIVKSSEAEPSQEYVSYSHGVFLRNAHGQEILLRDQKLIWRTLGGSVDLTFY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TEIRGMOSNVFIKR-NGNPYLGSVWPGPVYYPDFLDPAARSFWVDEIKRFRDILPIDGIW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         28 GATTSKNDNQGEAIGY-----GYQVKNAKVDNSTGKSLTALLQLIRN-SPVYGPDIHFLS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SSSIPAQQAHLYGLGEHTKPTFQLAHNQILTLWNADIASFNRDLNLYGSHPFYMDVR---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Aspergillus orrzae contains two novel enhancer elements: ore designated "enhancer-B") corresponds to the consensus sequence CGGNATTA and the other (designated "enhancer-C") is of sequence CCAATCAGCGT. By inserting at least one of the enhancer elements into a promoter region which is functional in fungi, the activity of the promoter is enhanced Using such improved promoters, a gene of interest can be expressed efficiently in transformed fungi. The present sequence is encoded by the agdA gene.
                                                                                                                                                                                                                                                                                                                                       Fungal DNA enhancer element - used to transform other host fungus e.g Aspergillus oryzae, to produce large quantities of a gene
Fungus; fungal; enhancer element; promoter; recombinant protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    184;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               26.9%; Score 1307; DB 18; Length 985; 31.8%; Pred. No. 1.4e-96;
                                                                                                                                                                                                                                                                                                                                                                                                                                                       The promoter region of the alpha-glucosidase (agdA) gene of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    312; Conservative 165; Mismatches 321; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     103 LTVEYQAKDRLNIQIVPTYFDASNASWYILSEELVPRP
                                                                                                                                                                                                                                                                                                                                                                                                                  Disclosure; Page 14-19; 25pp; Japanese
                                                                                                                                                     95JP-0163579
                                                                                                                                                                                        95JP-0163579
                                                                                                                                                                                                                             KOKUZEI CHO CHOHAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  468 IDMNEASNF --
                                                                                                                                                                                                                                                                                  WPI; 1997-126425/12.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Similarity
                                     Aspergillus oryzae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           985 AA;
                                                                                                                                                                                                                                               OZEKI KK.
                                                                                                                                                                                                                                                                                                      N-PSDB; AAT65017
                                                                                                                                                   29-JJN-1995;
                                                                                                                                                                                        29-JUN-1995;
                                                                            JP09009968-A
                                                                                                               14-JAN-1997
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product
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This sequence is the human hSI protein. The invention relates to purified proteins (I) that bind specifically to at least one of the gastro-intestinal (GI) tract receptors human intestinal peptide-associated transporter (HPTI), hPEPTI, D2H and human percorist shown and animal GI tissue (into the blood) to respect through human and animal GI tissue (into the blood) for in vivo delivery, particularly for treatment or prevention of hypertension, diabetes, osteoporosis, haemophilia, anaemia, cancer, magraine, or angina pectoris. Specifically they are used to deliver insulin or leuprolide, but many other suitable therapeutic agents are disclosed, including genes or inhibitory nucleic acid, imaging agents and cancers. (I) may also provide targeting to the GI tract. Other uses of (I) are: (I) to determine the level of specified receptors in a sample (I) are: (I) to determine the level of specified receptors in a sample (I) are binding assay); and (ii) to screen for molecules that bind (I).

Immunogenic analogues or derivatives of (I) are used to raise antibodies measure (I), e.g. for imaging, monitoring treatment, tissue analysis etc., also for peptide purification and immobilisation. through, the gastrointestinal tract, e.g. insulin or leuprolide Disclosure; Fig 3; 294pp; English

1827 AA; Sequence

Gaps Indels 114; Query Match 26.8%; Score 1304; DB 20; Length 1827; Best Local Similarity 34.6%; Pred. No. 6.5e-96; Matches 311; Conservative 157; Mismatches 316; Indels 114;

RWEIPNEULPRPPPPPSPPPLSSLQHLPKPIPQNQPTTTULSHPHSDLAFTLFHTTPFGF 162 43 YGYQVKNAKVDNSTGKSLTALLQLIRNSPVYGPDIHFLSFTASFEEDDTLRIRFTDANNR 102 ----PPSI 201 163 TIYRKSTHDVLFDATPIPSNPTTFLIYKDQYLQLSSSLPAQQAHLYGLGEHTKPTFQLAH 222 169 RYEVPHQYVKEFTGPTVSDTLYDVK-----VAQN-----103 ò g a ò ઠે g ò

252 DLSWKTW----PIFTRDQLPGDNNNNLYGHQTFFWCIEDTS--GKSFGVFLMNSNAMEIF 305 223 NQILTLWNADIASFNRDL-----NLYGSHPFYMDVRSSPMVGSTHGVFLLNSNGMDVE

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PILDPGINTNK----SYGTFIRGMQSNVFIKRN--GNPYLGSVWPGPVYYPDFLDPAAR 447

395

LDKLMYSKTICMDAVQNWGK--QYDVHSLYGYSWAIATEQAVQKVFPNKRS-FILTRSTF ----INSKTIPATAM-HYGNVTEYNAHNLYGFLESQATREAL--VRPATRGPFLLSRSTF 535 503

555

591

651

ò g LGAFYPFSRDHSARDTTHQELYLW---ESVAASARTVLGLRYELLPYYYTLMYDANLRGS 672 652

673 PIARPLSFTFPDDVATYGISSQFLIGRGIMVSPVLQPGSSIVNAYSPRGNWVSLSNYTSS 732 769 AKRPWRKQRVDMYLPADKIGLHLRGGYIIPIQBPDVTTTASRKNPLGLIVALGENNTAKG 828 ELFLDNGIEMDIGGPGGKWTLVRFFAESGINNLTISSEVVNRGYAMSQRWVMDKITILGL 851 852 KRRVKIKEYTVQKDAGAIKVKGLGRRTSSHNQGGFFVS----VISDLRQLVGQAFKLE 905 884 TDSVI-----EVRVAENNQPMNAHSNFTYDASNQVLLIADLKLNLGRNFSVQ 930 733 VSVS-AGTYVSLSAPPDHINVHIHEGNIVAMQGEAMITQAARSTPFHLLVVMSDHVASTG 829 792 원 ઠે g ò g ò

completed: October 27, 2003, 10:25:28 he : 54.3092 secs time Search (

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Q91yfe arabidopsis
O22444 arabidopsis
O22444 arabidopsis
Q91ly2 hordeum vul
G8vwv9 pinus pinas
O9avc3 physcomitre
O9zp26 arabidopsis
Q91gc6 oryza sativ
Q91gc6 oryza sativ
Q91gc7 arabidopsis
Q91ac7 arabidopsis
O73626 coturnix co
Q8bgi6 mus musculu
Q91247 mus musculu
Q9145 mus musculu
Q9145 mus musculu
Q9147 homo sapien
Q9myn4 bos taurus
                                                             October 27, 2003, 10:19:13 ; Search time 61.7736 Seconds (without alignments) 3772.184 Million cell updates/sec
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4768
1 MKKKIPSLALGILLVFLLQY.....VAEISGLNLJLGREFKLVLH 903
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GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
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Listing first 45 summaries
                                           OM protein - protein search, using sw model
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1: sp_archea:*

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3: sp_fungi:*

4: sp_human:*

5: sp_invertebrate:*

6: sp_mammal:*

7: sp_mhc:*
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Q9uv08 emericella	Q9urx4 schizosacch	073632 coturnix co	Q8te24 homo sapien	Q9c1s7 emericella		Q21750 caenorhabdi	Q9nfy8 penaeus van		ın	Q9rhz2 alicyclobac			O8izm4 homo sapien	σ	Q93y12 arabidopsis	Q8rdl1 thermoanaer	Q8iwz0 homo sapien	Q8bvw0 mus musculu	Q92f84 listeria in	Q8yn00 anabaena sp	024375 solanum tub	Q9lug2 arabidopsis	Q14697 homo sapien	O08794 mus musculu	Q9p0x0 homo sapien		Q8yae7 listeria mo	P79403 sus scrofa	
80AD60	Q9URX4	073632	Q8TE24	Q9C1S7	Q19004	021750	Q9NFY8	020722	Q9FN05	Q9RHZ2	Q81ZMS	Q8TBT4	Q81ZM4	6NIX8O	Q93Y12	Q8RDL1	OBIMZO	QBBVW0	Q92F84	OBYNOO	024375	Q9LUG2	014697	008794	030060	Q8BHN3	Q8YAE7	P79403	
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ALIGNMENTS

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                                                                                                                           834 SIGKVTFVGFENVENVKTYEVRTSERLRSPRISLIKTVSDNDDPRFLSVEVSKLSLLLVGK 893
             SRLENISGELFLDDGENLRMGAGGGNRDWTLVKFRCYVTGKSVVLRSEVVNPEYASRAKW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SVYAPDIKSLNLHVSLETSERLRIRITDSSQQRWEIPETVIPRAGNHSP-----RRFST
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         YRTLLSSPTTNRRKILLSHPNSDLTFSLINTTPFGFTISRKSTHDVLFDATPDPTNPNTF
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                                                                                             838 VIDKVTILGLRKGTKINGYTVRTGAVTRKGDKSKLKSTPDRKG-EFIVAEISGLNLLLGR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LIFIDQYLHLISSLPGTRAHIYGLGEHSKPTFQLAHNQTLTMRAADIPSSNPDVNLYGSH
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
eurosids II; Brassicales; Brassicaceae; Arabidopsis.
NCBI_TaxID=3702;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STRAIN-Landsberg,
MEDLINE-98045620; PubMed-9411456;
Monroe J.D., Hall B.D., Gough C.M., Stephen A.L.;
Monroe J.D., Hall B.D., Gough C.M., Stephen A.L.;
Nucleotide sequence of an alpha-glucosidase gene (Accession No. AF014806) from Arabidopsis thaliana (PGR97-141).";
Plant Physiol. 115:863-863(1997).
EMBL, AF014806, ABASE65.1;
EMBL, AF014806, ABASE65.1;
Plant PPOSSTS, Glyco.hydro.31: 12
PROSITE; PS00129; GLYCOSYL_HYDROL_F31_1; 1.
PROSITE; PS0017; GLYCOSYL_HYDROL_F31_2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         59.3%; Score 2825.5; DB 10; Length 902; 59.5%; Pred. No. 3.8e-205;
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                                                                                                                                                                                                                                                                                                                                                                                                                                   01-JAN-1998 (TrEMBLrel. 05, Created)
01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
Apha-glucosidase 1 (EC 3.2.1.20).
Agiul.
Arabidopsis thaliana (Mouse-ear cress).
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KFEMRL 899
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Ishida J., Jones T., Kamiya A., Karlin-Neumann G., Kawai J., Lam B., Lee J.M., Lin J., Miranda M., Narusaka M., Nguyen W., Palm C.J., Quach H.L., Sakutai T., Satou M., Seki M., Southurk A., Tang C.C., Toriumi M., Wallender E.K., Wu H.C., Yamada K., Yu G., Yuan S., Shinozaki K., Davis R.W., Theologis A., Ecker J.R.; Yana Joppsis ORF clones."; "Arabidopsis ORF clones."; "Arabidopsis ORF clones."; "Submitted (NOV-2002) to the EMBL/GenBank/DDBJ databases.

BMBL, ALI63814; CAB87690.1; "BMBL/GenBank/DDBJ databases.

BMBL, ANOS3414; AAK96644.1; "BMBL/GenBank/DDBJ databases."

REMEL, PRO0222; ANN7233.1; "BMBL, BT002222; ANN7233.1; "BMBL, BT002222; ANN7233.1; "BMBL, BT002222; ANN7233.1; "BMBL, BT00222;  ANN7233.1; "BMBL, BB56817DAA000B3B CRC64; "BMBL, BB56817DAA000B3B CRC64; "BMBL, BB56817DAA000B3B CRC64; "BMBL, BB56817DAA000B3B CRC64; "BMBL, BB56817DAA000B3B CRC64; "BMBL, BB56817DAA000B3B CRC64; "BMBL, BB56817DAA000B3B CRC64; "BMBL, BB56817DAA000B3B CRC64; "BMBL, BB56817DAA000B3B CRC64; "BMBL, BB56817DAA000B3B CRC64; "BMBL, BB56817DAA000B3B CRC64; "BMBL, BB56817DAA000B3B CRC64; "BMBL, BB56817DAA000B3B CRC64; "BMBL, BB56817DAA000B3B CRC64; "BMBL,
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                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
59.4%; Score 2830.5; DB 10
Best Local Similarity 59.6%; Pred. No. 1.6e-205;
Matches 540; Conservative 138; Mismatches 205;
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                              ILLVFLLQYLVAGISTSENDPBGVIGYGYKVKSVKVDSGTRRSLTALPQLVKNSSVYGPD
                                                                                                                                   SSPITNRRKILLSHPNSDLIPSLINTIPFGFTISRKSTHDVLFDATPDPTNPNTFLIFID
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Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Coniferopsida, Coniferales, Pinaceae, Pinus.
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01-MAR-2002 (TrEMBLrel. 20,
01-MAR-2003 (TrEMBLrel. 23,
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MEDLINE=20265959; PubMed=10806244;
MEDLINE=20265959; PubMed=10806244;
Medline=20265959; PubMed=10806244;
Medline=20265959; PubMed=10806244;
The Print Physiol. 121:275-286 (2000).

EMBL; AF118226; AAF76254.1;
Medrine=2026; PRR000322; Glyco hydro_31.

RinterPro; IPR002032; Glyco hydro_31.

RinterPro; Glyco hydro_31.

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Rosolite; PS00105; Glyco hydro_31.

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Bukaryota, Viridiplantee; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooideae;
Triticeae; Hordeum.
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894 KFEMRL 899
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Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Bryophyta;
Bryopsida; Funariidae; Funariales; Funariaceae; Physcomitrella.
NCBI_TaxID=145481;
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Hiwatashi Y., Nishiyama T., Hasebe M.;

Hiwatashi Y., Nishiyama T., Hasebe M.;

"Establishment of gene- and enhancer-trap systems of the moss physicomitrella patens.";

"Dhyscomitrella patens.";

"Submitted (MAR-2001) to the EMBL/GenBank/DDBJ databases.

R EMBL; AB057422; BAB39467.1;

R InterPro; IPR001064; Crystallin.

R InterPro; IPR001022; Grystallin.

R PROSITE; PS00122; Glyco hydro_31. 1.

R PROSITE; PS00129; GLYCOSYL HYDROL F31.1; 1.

R PROSITE; PS00109; GLYCOSYL HYDROL F31.2; 1.

C SEQUENCE 916 AA; 102282 Mw; AĀCEZĀCGE440DB83 CRC64;
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44.9%; Score 2140.5; DB 10; Lengt
Best Local Similarity 47.0%; Pred. No. 3.4e-153;
Matches 441; Conservative 150; Mismatches 252; Indels
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Last sequence update)
Last annotation update)
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                                                    TISSUB-Etiolated hypocotyl;
Sanchez M., Gianzo C., Sampedro J., Revilla G., Zarra I.;
Changes in alpha-xylosidase gene expression during intact and auxin-
induced growth of pine hypocotyls.";
Submitted (NOV-2001) to the EMBL/GenBank/DD3J databases.
EMBL, AF446201, AAL40352.1;
InterPro; IPR001322; Glyco hydro_31.
InterPro; IPR001922; HLM-Dasic.
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PROSITE; PS00129; GLYCOSYL_HYDROL F31_1; 1.

PROSITE; PS00707; GLYCOSYL_HYDROL_F31_2; 1.

PROSITE; PS007038; HLH 1; 1.

SEQUENCE 910 AA; 100609 MW; C4B75C7306CC16F9 CRC64;
                                                                                                                                                                                                                                                                                                            Query Match

46.8%; Score 2233; DB 10;
Best Local Similarity 48.9%; Pred. No. 3.3e-160;
Matches 456; Conservative 136; Mismatches 274;
NCBI_Tax1D=71647;
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333 NDVAYDRAKLLAFLDKIHKIGMKYIVINDPGIGVNASYGTFQRAMAADVFIKYEGKPFLA 392
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                                                                                  VYGPDIQLISITASLESNDRLRVRITDAKHRRWEIPDNILHRHOPPPPPPHSLSSLYRTL 126
                                                                                                           LSSPTTNRRKILLSHPNSDLTFSLINTTPFGFTISRKSTHDVLFDATPDPTNPNTFLIFI 186
                                                                                                                                                                                                           107 RKSPIT-----VQBISGSELIFS-YTTDPFTPAVKRRSNHETLFNTT-----SSLVFK 153
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                          ARKVLGLRYTLLPYFYTLMYEAQLNGIPIARPLFFSFPDDIKTYGISSQFLLGKGVMVSP
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MDLRNVGGKAYAHAVLLLLNSNGMDVFYRGDSLTYKVIGGVFDFYFIAGPSPLNVVDQYTQ
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SLALGILLVFLLQYLVAGISTSENDPEGVIGYGYKVKSVKVDSGTRRSLTALPQLVKNSS
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01-WAY-2000 (TrEMBLrel. 13, Last sequence update)
01-WAX-2003 (TrEMBLrel. 23, Last annotation update)
Alpha-xylosidase precursor (ATIG68560/F24J5_10).
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STRAIN=cv. Columbia; TISSUE=Seedling hypocotyl;
MEDLINB=21295583; PubMed=11402218;
MEDLINB=21295583; PubMed=11402218;
Sampedro J., Sieiro C., Revilla G., Gonzalez-Villa T., Zarra I.;
Cloning and Expression Pattern of a Gene Encoding an alpha-Xylosidase Active against Xyloglucan Oligosaccharides from Arabidopsis.";
Plant Physiol. 126:910-920(12001).
EMBL; AF087483; AAD05539-1; --
InterPro; IPR000322; Glyco-hydro_31.
Fram; PF01055; Glyco-hydro_31; 1.
PROSITE; PS00129; GLYCOSYL_HYDROL_F31_1; 1.
                                                                                                                                                                                             TYQELYRWESVAASARKVLGLRYTLLPYFYTLMYEAQLNGIPIARPLFFSFPDDIKTYGI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STEVQEFAERSCHSGSLVSRVIAGNYALEQGLVLQSIRFLGVSGPVSDVIVNG--ERIVS
                                                                                                                                                                                                                                                                                                                                                                                                                              SSQFLLGKGVMVSPVLKPGVVSVTAYFPRGNWFDLFDYTRSVTASTGRYVTLSAPPDHIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WTFVKFIAASAKOTCIITSDVVSGEFAVSQKWVIDKVTILGLR----KGTKINGYTVRTGA
                                                                                                                                                                                                                                                                             VHIQEGNILAMOGKAMTTQAARKTPFHLLVVMS-DCGAS-FGELFLDDGVEVTMGVNRGK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          : | | | : | : | | | | | CTGSACSPDTLTLGMGKNDSDNDRCLLHCVNGTSRFDDPPYKINHVGTYDNLGVKTIAMT
                                                                                                                                                                                                                                                       TWNDLVYSIPSMLDFGLFGIPMVGADICGFLGNTTEELCRRWIQLGAFYPFSRDHSSLGT
VFLKRN-GKPYLGSVWPGPVYFPDFLKPSALTFWTDEIKRFLNLLPVDGLWIDMNEISNF
                    --- DNPPYKINNSGVMLPIINKTIPPT
                                                                                                                                                                       AMHYGDI PEYNVHNLFGYLEARVTRAALI KLTEKRPFVLSRSTFSGSGKYTAHWTGDNAA
                                                                                                                                                                                                                                                                                                                                                                    Arabidopsis thaliana (Mouse-ear cress).
Eukaryota, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
eurosids II; Brassicales; Brassicaceae; Arabidopsis.
NCBI_TaxID=3702;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
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01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
Alpha-xylosidase precursor (Fragment)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 44.7%; Score 2129; DB 10; Best Local Similarity 44.9%; Pred. No. 2.5e-152; Matches 417; Conservative 167; Mismatches 282;
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-1 19 ALPHA.XYLOSIDASE.
116 907 ALPHA.XYLOSIDASE.
907 AA; 101647 MW; 58ABBD235366CS88
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581 572 632 701 692 761

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115 RKSPIT----VQEISGSELIFS-YTTDPFTFAVKRRSNHETLFNTT-----SSLVFK 161
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                762 AMTTQAARKTPFHLLVVM---SDCGASFGELFLDDGVEVTMGVNRGKWTFVKFIAASAKQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    461 PSGEGPGWVCCLDCKNITKTRWDDPPYKINATGVVAPVGFKTIATSATHYNGVREYDAHS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              246 MDVRSSPVAGSTHGVLLLNSNGMDVEYTGNRITYKVIGGIIDLYFFAGPSPGQVVEQFTR
                                                                                                                                                                        401 QVWPGPVYFPDFLNPKTVSWWGDEIKRPHDLVPIDGLWIDMNEVSNFCSGLCTIPEGKQC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 VLKPGVVSVTAYFPRGNWFDLFDYTRSVTASTGRYVTLSAPPDHINVHIQEGNILAMQGK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 819 TCIITSDVVSGEFAVSQKWVIDKVTILGLRKGTKINGYTVRTGAVTRKGDKSKLKST---
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                                                                                           162 DOYLEISTSLP-KEASLYGLGENSQANGIKLVPNEPYTLYTEDVSAINLNTDLYGSHPMY
                                                                                                                                                                                                                                             306 VIGRPAPMPYWAFGFQQCRYGYHDVYELQSVVAGYAKAKIPLEVMWTDIDYMDAYKDFTL
                                                                                                                                                                                                                                                                                                                                              366 DPVNFPLDKMKKFVNNLHKNGQKYVVILDPGISTNKTYETYIRGMKHDVFLKRNGKPYLG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        -SPPIPG-----STLDNPPYKINNSGVMLPIINKTIPPTAMHYGDIPEYNVHN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         522 LFGYLBARVTRAALIKLTEKRPFVLSRSTFSGSGKYTAHWTGDNAATWNDLVYSIPSMLD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    521 IYGFSETIATHKGLLNVQGKRPFILSRSTFVGSGQYAAHWTGDNQGTWQSLQVSISTMLN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FGLFGIPMYGADICGFLGNTTEBLCRRWIQLGAFYPFSRDHSSLGTTYQELYRWBSVAAS
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                                                                                                                                                                                                                                                                                                                                                                                                                                            426 SVWPGPVYFPDFLKPSALTFWTDEIKRFLNLLPVDGLWIDMNEISNFIS-----
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Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
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01-0CT-2000 (TrEMBLrel. 15, Last sequence update)
01-0CT-2002 (TrEMBLrel. 22, Last annotation update)
EST AU092739(C53221) corresponds to a region of the predicted gene.
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STRAIN=cv. Nipponbare;
Sasaki T., Matsumoto T., Yamamoto K.;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               7 SLALGILLVFLLQYLVAGISTSENDPEGVIGYGYKVKSVKVDSGTRRSLTALPQ1VKNSS 66
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9 AFSLSLLLALILCF-----SPTQSYKTIGKGYRL--VSIEESPDGGFIGYLQVKQKNK
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                                        Bukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, eudicotyledons, core eudicots, Rosidae,
eurosids II, Brassicales, Brassicaceae, Arabidopsis.
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Kim C.J., Chen H., Cheuk R., Shinn P., Bowser L., Carninci P., Chan C.J., Chang C.H., Dale J.M., Hayashizaki Y., Havuan V.W., Lishida J., Jones T., Kanina A., Karlin-Neumann G., Kawai J., Lee J.M., Lin J., Miranda M., Narusaka M., Nguyen M., Onodera C.S., Palm C.J., Quach H.L., Sakurai T., Satou M., Seki M., Southwick A., Tang C.C., Toriumi M., Wong C., Wu H.C., Yamada K., Yu G., Yuan S., Shinozaki K., Davis R.W., Theologis A., Ecker J.R.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
STRANS-CV. Columba.
STRANS-CV. Columba.
STRANS-CV. Columba.
STRANS-CV. Columba.
Lee J.M., Li J., Gonzalez A., Liu A., Liu K., Vaysberg M., Sakano H.,
Lee J.M., Li J., Gonzalez A., Liu A., Liu K., Vaysberg M., Sakano H.,
Chino L., Chiou J., Altafi H., Araujo R., Brooks S.,
Buehler E., Chao Q., Conn L., Conway A.B., Dunn P., Hansen N.,
Howng B., Huizar L., Khan S., Kim C., Palm C., Rowley D., Shinn P.,
Walker M., Davis R.W., Ecker J.R., Federspiel N.A., Theologis A.;
"The sequence of BAC F245 from Arabidopsis thaliana chromosome I.";
Submitted (AUG-1999) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Cheuk R., Chen H., Kim C.J., Koesema E., Meyers M.C., Banh J.,
Bowser L., Carninci P., Dale J.M., Goldsmith A.D., Hayashizaki Y.,
Ishida J., Jiang P.X., Jones T., Kamiya A., Karlin-Neumann G.,
Kawai J., Lam B., Lee J.M., Lin J., Liu S.X., Miranda M., Narusaka I
Nguyen M., Onodera C.S., Palm C.J., Pham P.K., Quach H.L., Sakurai
Satou M., Seki M., Southwick A., Tang C.C., Toriumi M., Yamada K.,
Farmmura Y., Yu G., Yu S., Shinozaki K., Davis R.W., Theologis A.,
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                                                                                                                                                                                       STRAIN=cv. Columbia;
Sampedro J., Sieiro C., Villa T.G., Revilla G., Zarra I.;
"Cloning and expression pattern of an alpha-xylosidase gene !
Arabidopsis thaliana ";
Submitted (APR-1999) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Submitted (DEC-2002) to the EMBL/GenBank/DDBJ databases.
EMBL, AR144078; AAD37363.1; -
EMBL, AC00807, AAD49731.; -
EMBL, AY057482; AAL09716.1; -
EMBL, BY002675; AAO11591.1; -
Interpret IPR000322; GIYCo-hydro_31.
Pfam; PF01055; Glyco-hydro_31; 1.
PROSITE; PS00129; GLYCOSYL_HYDROL_F31_1; 1.
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Submitted (SEP-2001) to the EMBL/GenBank/DDBJ databases.
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102398 MW; 28F9610D8D7EA657 CRC64;
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44.9%; Pred. No. 2.5e-152;
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                                                                                                                                                                                                                                                                                                                                          39 VGSGYKLVSL-VEHPEGGALVGYLQVKQRTSTYGPDIPLLRLYVKHETKDRIRVQITDAD
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                                                                                                                                                                                                                                                          64;
                                                                                                                                                                                                              43.7%; Score 2083; DB 10; Length 929; llarity 46.7%; Pred. No. 8e-149; Conservative 150; Mismatches 269; Indels 64
  PAC
sativa nipponbare(GA3) genomic DNA, chromosome 1,
                 clone:P0504H10.";
Submitted (JUN-2000) to the EMBL/GenBank/DDBJ databases.
EMBL, ADA9356.1;
Gramene; Q9LGG6;
InterPro; IPR000122; Glyco_hydro_31.
Pfam; PF01055; Glyco_hydro_31.
PROSITE; PRO0129; GLYCOSYL HYDROL F31 1; 1.
SEQUENCE 929 AA; 102550 WW; 536EID0B9D7F97BF CRC64;
                                                                                                                                                                                                                               al Similarity
423; Conserv
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Best Local S
Matches 423
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            243 HAVILMNSNGMDVFYRGDSLTYKVIGGVLDFYFFSGPTPLAVVDQYTDFIGRFAPMPYWS
                                                                                                                                                                                                                                                                                                                                                                                                           STRAIN=cv. Record; TISSUE=Tuberising stolon tip; MEDLINE=21362238; PubMed=11465591; Taylor M.A., Ross H.A., McRae D., Wright F., Viola R., Davies H.V.; "Copy-DNA cloning and characterisation of a potato alpha-glucosidase: expression in Escherichia coli and effects of down-regulation in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TRAHIYGLGEHSKP-TFQLAHNQTLTMRAADIPSSNPDVNLYGSHPFYMDVRSSPVAGST
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                                                                                                                                                                                                  Solanum tuberosum subsp. tuberosum.

Wataryota, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Asteridae; lamiids; Solanales; Solanaceae; Solanum.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match 42.9%; Score 2046.5; DB 10; Length 928; Best Local Similarity 44.6%; Pred. No. 4.7e-146; Matches 415; Conservative 151; Mismatches 264; Indels 101;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  928 AA; 104687 MW; CEAC8634F6ED1820 CRC64;
                                              01-OCT-2000 (TrEMBLrel. 15, Created)
01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
Alpha-glucosidase (BC 3.2.1.20).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Fransgenic potato.";
Planta 213:288-264 (2001).

EMBL, AUSTAC44, CAB96077.1; -.

Interpro, IPR000322; Glyco hydro_31.

ProsirE; PS00129; GLYCOSYL HYDROL_F31_1; 1.
PRT;
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816 AKQTCIITSDVVSGEFAVSQKWVIDKVTILGLRK------GTKINGYTVRTGAVTRK 866
                     RTLLSSPTTNRKKILLSHPNSDLTFSLINTTPFGFTISRKSTHDVLFDATPDFTNPNTFL 183
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              QGKAMTTQAARKTPFHLLVVM---SDCGASFGELFLDDGVEVTMGVNRGKWTFVKFIAAS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                           477 KQCPTGEGPGWICCLDCKNITKTRMDEPPYKINATGVQAPIGFKTIATSCTHYNGVLEYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             519 VHNLFGYLEARVTRAALIKLTEKRPFVLSRSTFSGSGKYTAHWTGDNAATWNDLVYSIPS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
eurosids II; Brassicales; Brassicaceae; Arabidopsis.
NCBI_TaxID=3702;
                                                                                                               243 PFYMDVRSSPVAGSTHGVLLLMSNGMDVEYTGNRITYKVIGGIIDLYFFAGPSPGQVVEQ
                                                                                                                                                                               FTRVIGRPAPMPYWAFGFQQCRYGYHDVYELQSVVAGYAKAKI PLEVMWTDI DYMDAYKD
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                                                                                       IFIDQYLHLTSSLPGTRAHIYGLGEHSKP-TFQLAHNQTLTMRAADIPSSNPDVNLYGSH
                                                                                                                                                                                                                                                                                                  FILDPVNFPLDKMKKFVNNLHKNGQKYVVILDPGISTNKTYETYIRGMKHDVFLKRNGKP
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01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
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Q9LZT7
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                                                                                                                                                                                                                                                                                                                                     PFHLLVVM----SDCGASFGELFLDDGVEVTMGVNRGKWTFVKFIAASAKQTCIITSDVVS 828
                                                                                                                                                                                                                                                                                                                                                                                                                            SKYALDKGWYIEKVTVLGL-----NGI---GGAFDILVDGSKVEDT--SKLEFETEEHK 891
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        64 NSSVYGPDIQLLSITASLESNDRLRVRITDAKHRRWEIPDNILHRHQPPPPPPHSLSSLY
                                                                            GEFAVSQKWVIDKVTILGLRKGTKINGYTVRTGAVTRKGDKSKLKSTPDRKGEF-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-MAY-1999 (TrEMBLrel. 10, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-MAY-2000 (TrEMBLrel. 17, Last annotation update)
Alpha-D-xylosidase precursor.
Tropaeolum majus (Common nasturtium).
Tropaeolum majus (Common nasturtium).
Spermatophyta; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; magnoliophyta; eudicotyledons; core eudicots; Rosidae;
eurosids II; Brassicales; Tropaeolaceae; Tropaeolum.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   11 LLLSFLPFILLSSSYGGNSSHSSTPAAPTKIGKGYRLISIEETPDGGFLGHL----QVKQ
CCOVTEXTEMDDEPYXINASGIQAPIGYKTIATSATHYNGVREYDAHSLYGFSETIATHK
                                                    ALIKLTEKRPFVLSRSTFSGSGKYTAHWTGDNAATWNDLVYSIPSMLDFGLFGIPMVGAD
                                                                                                                                                                                             LLPYFYTLMYEAQLNGIPIARPLFFSFPDDIKTYGISSQFLLGKGVMVSPVLKPGVVSVT
                                                                                                                                                                                                                                                                 AYFPRGNWFDLFDYTRSVTASTGRYVTLSAPPDHINVHIQEGNILAMQGKAMTTQAARKT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               L) seeds.";
Submitted (AUG-1999) to the EMBL/GenBank/DDBJ databases.
EMBL, AJ131520; CAA10382.2;
InterPro; IRR000322; Glyco.hydro_31.
Pfam; PF01055; Glyco.hydro_11; 1.
PROSITE; PS00129; GLYCOSYL_HYDROL_F31_1; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        24 POTENTIAL.
935 ALPHA-D-XYLOSIDASE.
104937 MW; 22DE6901E9CE19BD CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
42.6%; Score 2031; DB 10;
Best Local Similarity 44.1%; Pred. No. 7.1e-145;
Matches 411; Conservative 154; Mismatches 311;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FIDKLEEGGHKKSMMLDIKGLELPIGKNFAM 922
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935 A
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                                         838 VIDKVTILGLRKGT-----KINGYTV----RTGAVTRKGDKSKLKSTPDRKGEFIVAEI 887
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              704 AGASEGYASGKLFLDDDELPEMKLGNGKSTYIDFYASVGNESVKIWSQVKEGQFALSQGL
                                                              quail
maltase
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      158 FTISRKSTHDVLFDATPDPTNPNTFLIFIDQYLHLTSSLPGTRAHIYGLGEHSKPTFQLA
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                                                                                                                                                                                                                                                                                                                                                                                Coturnix coturnix japonica (Japanese quail).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Kunita R., Nakabayashi O., Wu J.Y., Hagiwara Y., Mizutani M., Pennybacker M., Chen Y.T., Kikuchi T.; "Molecular cloning of acid alpha-glucosidase cDNA of Japanese (cournix coturnix japonica) and the lack of its mRNA in acid deficient quails.";

Biochim. Biophys. Acta 1362:269-278(1997).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
Nakabayashi O.;
"Genomic sequenses of ggaal and ggaal.";
Submitted (MAR-2002) to the EMBL/GenBank/DDBJ databases.
EMBL; AB000967; BAA225884.1;
EMBL; AB081289; BAC15595.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SMART; SMOGO18; PD; 1, PROSYL HYDROL F31_1; 1. PROSTIE; PSO0129; GLYCOSYL HYDROL F31_2; 1. SEQUENCE 932 AA; 104689 WW; BGZE182F03DE3F61 CRC64;
                                                                                                                                                                                                                                                                                   01-AUG-1998 (TrEMBLrel. 07, Created)
01-AUG-1998 (TrEMBLrel. 07, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
                                                                                                                                                                                                                                                  932 AA
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InterPro; IPR000322; Glyco hydro_31.
InterPro; IPR000319; P_treFoil.
Pfam; PF01055; Glyco hydro_31; 1.
Pfam; PF00088; trefoil; 1.
                                                                                                                                                                                                                                                  PRT;
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                                                                                                                  SGLNLLLGREFKL 900
                                                                                                                                                     823 KGLEMLVGKDFNI 835
                                                                                                                                                                                                                                                  PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                          Acid alpha glucosidase.
GAAI OR GAAI.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TISSUE=Liver;
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                       Mewes H.W
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                   Jordan N., Bangert S., Wiedelmann R., Voss H., Unseld M., Mev
Rudd S., Lemcke K., Mayer K.F.X., Quetier F., Salanoubat M.;
Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases.
                                                                                                            Understand of the Control of the EMBL/GenBank/DDBJ databases. Submitted (APR-2000) to the EMBL/GenBank/DDBJ databases. EMBL, AL162459; CAB82818-1; INTERPYO; IPRO00322, GLYCo. hydro.31. PRO1055; GlYco. hydro.31. PROSITE; PSO0129; GLYCOSYL_HYDROL_F31_1; 1. Hypothetical protein. SEQUENCE 855 AA; 958858 MW; 54CB7A835BBIC50E CRC64;
                                                                                              SEQUENCE FROM N.A.
SEQUENCE FROM N.A.
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                        507 HAQVPFDGMMIDMNEPSNFVRGSQQGCPNNELENPPYV---PGVVGGILQAATICASSHQ
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
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(TrEMBLrel. 19, Last sequence update)
(TrEMBLrel. 23, Last annotation update)
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MEDLINE=22154683; PubMed=12466851;
The FANTOM Consortium,
The RIKEN Genome Exploration Research Group Phase I & II Team;
"Analysis of the mouse transcriptome based on functional annotation 60,770 full-length CDNAs.";
Nature 420:563-573 (2002)
EMBL; AK088481; BAC40382.1;
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01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
Mus musculus (Mouse).

Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Musculus (Mouse).
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TISSUE=Duodenum;
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                                                                                                             Strausberg R.;
Submitted (JUL-2011) to the EMBL/GenBank/DDBJ databases.
EMBL. BC010210; AMH10210.1; -
EMBL. BC010210; AMH10210.1; -
MGD, MGI:95609; Gaa.
InterPro: IPR000322; Glyco.hydro_31.
InterPro: IPR000319; P. trefoil.
Pfam; PF01055; Glyco.hydro_31; 1.
Pfam; PF01055; Glyco.hydro_31; 1.
PROSITE; PS00129; GLYCOSYL_HYDROL_F31_1; 1.
PROSITE; PS00129; GLYCOSYL_HYDROL_F31_2; 1.
PROSITE; PS00129; GLYCOSYL_HYDROL_F31_2; 1.
PROSITE; PS00129; GLYCOSYL_HYDROL_F31_2; 1.
PROSITE; PS00129; GLYCOSYL_HYDROL_F31_2; 1.
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                                                                                  SEQUENCE FROM N.A.
NCBI_TaxID=10090;
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01-MMR-2003 (TrEMBLrel. 23, Created)
01-MMR-2003 (TrEMBLrel. 23, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
Glucosidase, alpha, acid (Pompe disease, glycogen storage disease type
864 ESLAV-LERGAYTLVTF---SAKNNTIVNKLVRVTKEGAELQ---LREVTVLGVA----
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191 YEVPLETPHVHSRAPSPLYSVE------FSEEPFGV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        221 IVRRQLDGRVLLNTTVAP-----LFFADQFLQLSTSLPS--QYITGLAEHLSPLMLSTS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        561 SHQFLSTHYNLHNLYGLTEAIASHRALVKARGTRPFVISRSTFAGHGRYAGHWIGDVWSS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 99 WEIPDNILHRHQPPPPPPPHSLSSLYRTLLSSPTTNRRKILLSHPNSDLTFSLINTTPFGF
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Homo sapiens (Human).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.
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31.5%; Score 1501.5; DB 4; Length 952;
Best Local Similarity 38.0%; Pred. No. 1e-104;
Matches 341; Conservative 138; Mismatches 295; Indels 123;
                                                                                                854 NGYTVRTGAVTRKGDKSKLKSTPDRKGEFIVAEISGLNLLLGREFKL 900
                                                                                                                                         ---TAPTQVLSNGIPVSNFTYSPDNKSLAI----PVSLLMGELFQI 950
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Submitted (NOV-2002) to the EMBL/GenBank/DDBJ databases.
EMBL; BC040431; AH440431.1; -.
SEQUENCE 952 AA; 105323 MW; 6E2717BF7201F469 CRC64;
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Search completed: October 27, 2003, 10:31:02 Job time : 66.7736 secs

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Spinacia oleracea
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GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
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Q9h251 homo sapien											
CADN_HUMAN	CADN RAT	AGA2 PEDPE	AGA1 PEDPE	CD87 DROME	POL HTLV2	VL2_HPV36	SMA9 HUMAN	6PGD_BUCBP	PGMU EMENI	CLUB BACTU	CA1C_HUMAN
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Eukaryota; Magnoliophyta; eudicotyledons; core eudicots;

Caryophyllidae; Caryophyllales; Chenopodiaceae; Beta.
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STRAIN=CV. NK-152;
MEDLINE=97321863; PubMed=9178565;
Matsui H., Iwanami S., Ito H., Mori H., Honma M., Chiba S.;
"Cloning and sequencing of a cDNA encoding alpha-glucosidase
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MEDLINE-95252592; PubMed=7766184;
Iwanami S., Matsui H., Kimura A., Ito H., Mori H., Honma M.,
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15-JUL-1998 (Rel. 36, Created)
30-MAY-2000 (Rel. 36, Last sequence update)
30-MAY-2000 (Rel. 39, Last annotation update)
Alpha-glucosidase precursor (EC 3.2.1.20) (Maltase).
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 putative alpha-glucosidase gene from barley.";
                                                                                                                                                                                                           InterPro; S65057; S65057.
InterPro; IPR000322; Glyco_hydro_31.
Pfam; PF01055; Glyco_hydro_31; 1.
PROSITE; PS00129; GLYCOSYL_HYDROL_P31_1; 1.
PROSITE; PS00707; GLYCOSYL_HYDROL_P31_2; 1.
Hydrolase; Glycosidase; Glycoprotein; Signal.
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                                                           QVVEQFTRVIGRPAPMPYWAFGFQQCRYGYHDVYBLQSVVAGYAKAKIPLEVMWTDIDYM 357
                                                                                               478 IPGSTLDNPPYKINNSGVMLPIINKTIPPTAMHYGDIPEYNVHNLFGYLEARVTRAALIK 537
                                                                                                                                                                         NPNTFLIFIDOYLHLTSSLPGTRAHIYGLGEHSKPTFQLAHNQTLTMRAADIPSSNPDVN
                    LYGSHPFYMDVRSSPVAGSTHGVLLLNSNGMDVEYTGNRITYKVIGGIIDLYFPAGPSPG
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                                                                                                                                                              RNGKPYLGSVWPGPVYFPDFLKPSALTFWTDEIKRFLNLLPVDGLWIDMNEISNFISSPP
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Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooideae;
NCBI_TaxID=4513;
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MEDLINE=96178863; PubMed=8616248;
Tibbot B.K., Skadsen R.W.;
"Molecular cloning and characterization of a gibberellin-inducible,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 15-JUL-1998 (Rel. 36, Created)
15-JUL-1998 (Rel. 36, Last sequence update)
15-JUL-1998 (Rel. 36, Last annotation update)
Alpha-glucosidase precursor (EC 3.2.1.20) (Maltase)
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bloinformatics and the FWBL outstation the Buropean Bloinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@iab-sib.ch).
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Plant Mol. Biol. 30:229-2413[1996].
-!- CATALYTIC ACTIVITY: Hydrolysis of terminal, non-reducing 1,4-
linked D-glucose residues with release of D-glucose.
-!- TISSUE SPECIFICITY: Hydrolysis of terminal, non-reducing 1,4-
-!- TISSUE SPECIFICITY: Hydrolysis of terminal.
AFTER GERMINATION, WHILE LOW IEVELS ARE FOUND IN DEVELOPING SEEDS.
-!- DEVELOPMENTAL STAGE: LEVELS INCREASE STEADILY THROUGHOUT IMBIBITION REACHING MAXIMUM LEVELS AT DAY 7. DURING GERMINATION, LEVELS INCREASE FROM DAY 2, REACH MAXIMUM LEVELS AT DAY 3 AND DECLINE AFTER DAY 5.
-!- INDUCTION: BY GIBBERELLIN A3 (GA).
-!- SIMILARITY: BELONGS TO FAMILY 31 OF GLYCOSYL HYDROLASSES.
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PROSITE; PS00707;
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              Hydrolase;
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388 LKRNGTNFVGNVMPGDVYFPDFMHPAAAEFWAREISLFRRTIPVDGLMIDMNEISNFYN- 446
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                          PPIPGSTLDNPPYKINNSGVMLPIINKTIPPTAMHYGDIPEYNVHNLFGYLEARVTRAAL
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                                                 - PEPANALDDPPYRINNGTGRPINNKTVRPLAVHYGGVTEYEEHNLFGLLEARATGRGV
                                                                           IXLTEKRPFVLSRSTFSGSGKYTAHWTGDNAATWNDLVYSIPSMLDFGLFGIPMVGADIC
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Mucor.
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-!- CATALYTIC ACTIVITY: Hydrolysis of terminal, non-reducing 1,4-linked D-glucose residues with release of D-glucose.
-!- SIMILARITY: BELONGS TO FAMILY 31 OF GLYCOSYL HYDROLASES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         a cDNA encoding
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01-NOV-1997 (Rel. 35, Last sequence update)
15-SEP-2003 (Rel. 42, Last annotation update)
hypa-glucosidase precursor (EC 3.2.1.20) (Maltase)
Mucor javanicus.
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InterPro; IPR000322; Glyco hydro 31.
Pfam; PF01055; Glyco hydro 31; 1.
PROSITE; PS00129; GLYCOSYL HYDROL F31_1; 1.
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"Molecular cloning, sequencing, and exp
alpha-glucosidase from Mucor javanicus.
J. Biochem. 119:500-505 (1996).
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MEDLINE=96271012; PubMed=8830045;
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VGEEFEL 871
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31.4%; Score 1499; DB 1; Length 864;
Best Local Similarity 38.2%; Pred. No. 3.2e-97;
Matches 324; Conservative 147; Mismatches 280; Indels 99
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   64 IDTFGKTIKDITVDVEYETEERLHVKISDKAKKQYLVPDSPLGFERP
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S00707; GLYCOSYL HYDROL F31_2; FALSE_NEG. Glycogidase; Glycoprotein; Signal.
                                                            ALPHA-GLUCOSIDASE
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40 YKVKSVKVDSGTRRSLTALPQLVKNSSVYGP-DIQLLSITASLESNDRLRVRITDAKHRR 98
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STRAIN=BALB/c; TISSUE=Liver;
SIDING J.H., Yang B.Z., Reuser A.J.J., Roe C.R.;
Submitted (SEP-1996) to the EMBL/GenBank/DDBJ databasee.
-!- FUNCTION: ESSENTIAL FOR THE DEGRADATION OF GLYGOGEN TO GLUCOSE
                                                                                                                                                                                                                                                                              01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
30.MAY-2000 (Rel. 39, Last annotation update)
Lysosomal alpha-glucosidase precursor (EC 3.2.1.20) (Acid maltase)
                                                                                                                                                                                                                                                                                                                                                                                                GAA.
Mus musculus (Mouse).
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               -! - CATALYTIC ACTIVITY: Hydrolysis of terminal, non-reducing 1,4-linked D-glucose residues with release of D-glucose.
-! - SUBCELLULAR LOCATION: Lysosomal.
-! - SIMILARITY: Contains 1 P-type (trefoil) domain.
-! - SIMILARITY: DELONGS TO FAMILY 31 OF GLYCOSYL HYDROLASES.
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LYSOSOMAL ALPHA-GLUCOSIDASE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MGD; MGI:95609; Gaa.
InterPro; IRR000322; Glyco hydro_31.
InterPro; IRR000312; Glyco hydro_31.
InterPro; IRR000519; P trefoil.
Pfam; PF01055; Glyco hydro_31; 1.
Pfam; PF01055; Glyco hydro_31; 1.
PROSITE; PS00025; P TREFOIL; 1.
PROSITE; PS000129; GLYCOSYL HYDROL_F31_1; 1.
PROSITE; PS00707; GLYCOSYL HYDROL_F31_2; 1.
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Matches 336; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NCBI_TaxID=10090;
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01-MAR-1989 (Rel. 10, Created)
01-FEB-1991 (Rel. 17, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Lysosomal alpha-glucosidase precursor (EC 3.2.1.20) (Acid maltase)
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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MEDLINE=91379015; PubMed=1898413;
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MEDLINE=90365036; PubMed=2203258;
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                                                               TISSUE=Placenta, Testis, and Urin
MEDLINE=89005058; PubMed=3049072;
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NCBI_TaxID=9606;
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AND 795-803
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Hermans M.M.P., de Graaff E., Kroos M.A., Wisselaar H.A., Oostra B.A.,
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MEDLINE-93186115; PubMed=8094613;
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MEDLINE=21195240; PubMed=11298744;
Okuyama M., Okuno A., Shimizu N., Mori H., Kimura A., Chiba S.;
"Carboxyl group of residue App647 as possible proton donor in catalytic reaction of alpha-glucosidase from Schizosaccharomyces
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Eukaryota, Fungi, Ascomycota, Schizosaccharomycetes;
Schizosaccharomycetales; Schizosaccharomycetaceae;
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16-0CT-2001 (Rel. 40, Last sequence update)
15-SEP-2003 (Rel. 42, Last annotation update)
Alpha-glucosidase precursor (EC 3.2.1.20) (Maltase)
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Huie M.L., Tsujino S., Brooks S.S., Engel A., Elias E., Bonthron D.T.
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missense mutations (D645N, G6488, R672W, R672Q) and two
insertions/deletions in the acid alpha-glucosidase locus of patients
of differing phenotype.";
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MEDLINE=98180719; PubMed=9521422;
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"Identification of a de novo point mutation resulting in infantile
form of Pompe's disease.";
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        VARIANT GSD-11 GLY-VAL-PRO-VAL-SER-ASN-925 INS.
Beeley C. E., Child A.H., Yacoub M.Y.,
"The identification of five novel mutations in the lysosomal acid alpha-(1,4) glucosidase gene from patients with glycogen storage
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31.3%; Score 1492.5; DB 1; Length 952;
Best Local Similarity 37.8%; Pred. No. 1.1e-96;
Matches 339; Conservative 139; Mismatches 296; Indels 123;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               VARIANTS GSD-II ASN-645; TRP-647; SER-648; GLN-672 AND TRP-672
SEQUENCE OF 631-680 FROM N.A., AND VARIANT GSD-II HIS-645
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Raben N., Lee E., Lee L., Hirschhorn R., Plotz P.H.;
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A Rutherford K., Rutter S., Saunders D., Seeger K., Sharp S.,
Skelton J., Simmonds M., Squares R., Squares S., Stevens K.,
Taylor K., Taylor R.G., Tivey A., Walsh S.V., Warren T., Whitehead S.,
A Woodward J., Volckaert G., Aert R., Robben J., Grymonprez B.,
Meltjens I., Vanstreels E., Rieger M., Schaefer M., Mueller-Auer S.,
Gabel C., Fuchs M., Frizc C., Holzer E., Moestl D., Hilbert H.,
A Borzym K., Langer I., Beck A., Lehrach H., Reinhardt R., Pohl T.M.,
Ber P., Zimmermann W., Wedler H., Wambutt R., Purnelle B.,
Goffeau A., Cadieu E., Dreano S., Gloux S., Lelaure V., Mortier S.,
A Galibert F., Aves S.J., Xiang Z., Hunt C., Moore K., Hurst S.M.,
Lucas M., Rochet M., Gaillardin C., Tallada V.A., Garzon A., Thode G.,
Dominguez A., Revuelta J.L., Moreno S., Armetrong J., Forsburg S.L.,
A Shpakovski G.V., Ussery D., Barrell B.G., Nurse P.,
Matte G.V., Ussery D., Barrell B.G., Nurse P.,
Matte G.V., Wissery D., Barrell B.G., Nurse P.,
Matte G.V., Matte G.V., Missery D., Barrell B.G., Nurse P.,
Matte G.V., Matte G.V., Missery D., Barrell B.G., Nurse P.,
Matter G.V., Matter G.V., Missery D., Barrell B.G., Nurse P.,
Matter G.V., Matter G.V., Missery D., Barrell B.G., Nurse P.,
Matter G.V., Missery D., Sarchez D., Missery D., Barrell B.G., Nurse P.,
Matter G.V., Missery D., Missery D., Barrell B.G., Nurse B.,
Matter G.V., Missery D., Barrell B.G., Nurse B.,
Missery D., Missery D., Barrell B.G., Nurse B.,
Missery D., Missery D., Barrell B.G., Nurse B.,
Missery D., Missery D., Missery D., Barrell B.G., Nurse B.,
Missery D., Missery D., Barrell B.G., Nurse B.,
Missery D., Missery D., Barrell B.G., Nurse B.,
Missery D., Missery D., Barrell B.G., Nurse B.,
                                                                                                                                                                                                                                                                  activity toward soluble starch.
-!- CATALYTIC ACTIVITY: Hydrolysis of terminal, non-reducing 1,4-linked D-glucose residues with release of D-glucose.
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                                                                                                                                                                                                                                                    -!- FUNCTION: Hydrolyzes malto-oligosaccharides, but has a low
                                                                                                                                                                                                                                                                                                             SUBCELLULĀR LOCATION: Secreted.
SIMILARITY: BELONGS TO FAMILY 31 OF GLYCOSYL HYDROLASES
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EMBL, AB045751; BAB43946.1; -.
EMBL, AB045751; BAB43946.1; -.
InterProv. IPR000322; Glyco hydro 31.
Pfam; PF01055; Glyco hydro 31; 1.
PROSITE; PS00129; GLYCOSYL HYDROL F31.1; 1.
PROSITE; PS0017; GLYCOSYL HYDROL F31.2; FALSE_NEG.Hydrolase; Glycosidase; Glycoprotein; Signal.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      256 STHGVLLLNSNGMDVEYTGNRITYKVIGGIIDLYFFAG--PSPGQVVEQFTRVIGRPAPM 313
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             426 SVWPGPVYFPDFLKPSALTFWTDEIKRFLNL------LPVDGLWIDMNEISNF----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         493 CGSAMIDLNPAEPLTGISKQYSIPEGFNVSNVTEYSSAYSASLSNYYATATSSVFQIVSP
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                                                                                                                                                                                                                                                                                                                                                                                                                    89 VRITDAKHRRWEIPDNILHRHQPPPPPPPHSLSSLYRTLLSSPTTNRRKILLSHPNSDLTF
                                                                                                                                                                                                                                         159; Gaps
                                                                                                                                                                        Query Match 30.7%; Score 1464.5; DB 1; Length 969; Best Local Similarity 35.8%; Pred. No. 1e-94; Matches 335; Conservative 157; Mismatches 284; Indels 159;
30 30 L -> F (IN REF. 2).

220 220 P -> A (IN REF. 1).

50 507 T -> V (IN REF. 1).

566 566 D -> N (IN REF. 1).

969 AA; 108686 MW; F3122E2CFA551C25
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                                                                                                                                                                                                              0,721-1999 (Rel. 38, Created)
15-JUL-1999 (Rel. 38, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Glucoamvlase 1 precursor (EC 3.2.1.3) (Glucan 1,4-alpha-glucosidase)
                                                                                                                                                                                                                                                                                                                                                                                                    InterPro; IPR000322, Glyco hydro 31.
Pfam: PF01055; Glyco hydro 31; 1.
PROSITE: PS00129; GLYCOSLL HYDROL F31 1; 1.
PROSITE: PS00170; GLYCOSYL HYDROL F31 2; 1.
Hydrolase; Glycosidase; Polysacchāridē degradation; Glycoprotein;
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Saccharomycetales; mitosporic Saccharomycetales; Candida.
                                                                                                                                                                                     STRAIN=SC5314;
MEDLINE=99451422; PubMed=10520161;
Sturtevant J., Dixon F., Madsworth E., Latge J.-P., Zhao X.-J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Best Local Similarity 34.9%; Pred. No. 2e-92;
Matches 335; Conservative 150; Mismatches 310; Indels 165;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            30.0%; Score 1431.5; DB 1; Length 946; 34.9%; Pred. No. 2e-92;
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                                                                            15-JUL-1999 (Rel. 38, Last sequence 28-FEB-2003 (Rel. 41, Last annotation Glucoamylase 1 precursor (EC 3.2.1. (1,4-alpha-D-glucan glucohydrolase) GAM1 OR GCA1. Candida albicans (Yeast).
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                                                STANDARD;
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946 AA;
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                                                                                                                                                                                   SLSSLY----RTLLSSPTTNRRKILLSHPNSDLTFSLINTTPFGFTISRKSTHDVLFDATP 174
                                                                                                                                                                                                                                     116 DLTDVFVLPEELVVKPYLEGDAKTFNFENSDLVFE-YDEEDFGFEVLRSSTREVLFSTKG 174
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15-JUL-1998 (Rel. 36, Last sequence update)
15-SEP-2003 (Rel. 42, Last annotation update)
Alpha-glucosidase precursor (EC 3.2.1.20) (Maltase) (AGL).
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193 FVTLLP-EEYNLYGLGERMN-QLRLLENANLTLYAADI--ADPIDDNIYGHHAFYLDTRY 248
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                                                                                                                                        249 YKVGGQNKSHTIVKSSEAEPSQEYVSYSHGVFLRNAHGQEILLRDQKLIWRTLGGSVDLT
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                                                                                                                                                                                                                                     290 FFAGPSPGQVVEQF-TRVIGRPAPMPYWAFGFQQCRYGYHDVYELQSVVAGYAKAKIPLE
                                                                                                                                                                                                                                                                                349 VMWIDIDYMDAYKDFILDPVNFPLDKMCKFVNNLHKNGOKYVVILDPGI-----STNKT
                                                                                                                                                                                                                                                                                                                                                                                                                                                       369 YLWADIDYMHGYRNFDNDQHRFSYEEGEKFLNKLHAGGRRWVPIVDGALYIPNPENASDA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      489 VWYDWAEVSSFCVGSCGTGNLSMNPAHPPFALPGEPGNVVYDYPEGFNITNATEAASASA
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Bukaryota; Fungi; Ascomycota; Pezizomycotina; Burotiomycetes;
Burotiales; Trichocomaceae; mitosporic Trichocomaceae; Aspergillus.
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15-UUL-1998 (Rel. 36, Lack sequence update)
15-UUL-1998 (Rel. 36, Lack sequence update)
15-SEP-2003 (Rel. 42, Lack annotation update)
Alpha-glucosidase precursor (EC 3.2.1.20) (Maltase)
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MEDLINE=97308536; PubMed=9165762;
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                                                                                     251 SPVAGS ---
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                                      Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes;
Eurotiales; Trichocomaceae; mitosporic Trichocomaceae; Aspergillus.
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MIDELOKE 96012211; PubMed=7549103;
MIDELOKI T., Gomi K., Kitamoto K., Kumagai C., Tamura G.;
Minetoki T., Gomi K., Kitamoto K., Kumagai C., Tamura G.;
Nucleotide sequence and expression of alpha-glucosidase-encoding
gene (agdA) from Aspergillus oryzae.";
Blockici. Biotechnol. Biochem. 59:1516-1521(1995).
Blockici. Biotechnol. Biochem. 59:1516-1521(1995).
CHUCTION: Hydrolyses malto-oligosaccharides, but has a low
activity toward soluble starch.
CATALYTIC ACTIVITY: Hydrolysis of terminal, non-reducing 1,4-
linked D-glucose residues with release of D-glucose.
Induction: By maltose.
SIMILARITY: BELONGS TO FAMILY 31 OF GLYCOSYL HYDROLASES.
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PIR; JC4217; JC4217.
InterPro; IPR000322; Glyco_hydro_31.
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                                                                                                                                                                                          SEQUENCE FROM N.A.
                                                                                                            NCBI_TaxID=5062;
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TINRRKILLSHPNSDLTFSLINTTPFGFTISRKSTHDVLFDATPDPTNPNTFLIFIDQYL 190
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                                                                                                       ----STEGTVLVYENOFI 189
                                                                                                                                                                        190 EFVTALP-BEYNLYGLGEHI-TOFRLORNANLTIYPSD--DGTFIDONLYGOHPFYLDIR 245
                                                                                                                                                                                                                                                          246 YYKGDRQNGSYIPVKSSEADASQDYISLSHGVFLRNSHGLEILLRSQKLIWRTLGGGIDL 305
                                                                                                                                                                                                                                                                                                                     289 YFFAGPSPGQVVEQF-TRVIGRPAPMPYWAFGFQQCRYGYHDVYELQSVVAGYAKAKIPL 347
                                                                                                                                                                                                                                                                                                                                                           306 TPYSGPAPADVTRQYLISTVGLPAMQQYNTLGFHQCRWGYNNWSDLADVVANFEKFEIPL 365
                                                                                                                                                                                                                                                                                                                                                                                                         EVMMTDIDYMDAYKDFTLDPVNFPLDKMKKFVNNLHKNGQKYVVILDPGI-----STNK 401
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GDIPEYNVHNLFGYLEARVTRAALIKL--TEKRPFVLSRSTFSGSGKYTAHWTGDNAATW 569
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              QFMVGPAIMVVPVLEPLVNTVKGVFPGVGHGEVWYDW--YTQAAVDAKPGVNTTISAPLG 843
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                                                                                                                                               191 HLTSSLPGTRAHIYGLGEHSKPTFQLAHNQTLTMRAADIPSSNP-DVNLYGSHPFYMD--
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                                                                                                                                                                                                                                   -----VRSSPVAGS-----THGVLLLNSNGMDVEYTGNRITYKVIGGIIDL
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01-6CT-1996 (Rel. 34, Last sequence update)
01-0CT-19903 (Rel. 41, Last annotation update)
Putative family 31 glucosidase C30D11.01c precursor (EC 3.2.1.-).
SPAC30D11.01C OR SPAC56F8.01.
  -----SVSQSDLFVSWSNEPSFNFKVIRKATGDALF
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            76 SITASLESNDRLRVRI----TDAKHRRWE-IPDNILHRHQPPPPPPPHSLSSLYRTLLSSP 130
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                      from Aspergillus
                                                                                                                       MEDLINE-3105089; PubMed=1368849; Matsui H., Takai N., Takayanagi T., Kimura A., Takata M., Sakai O., Matsui H., Takai N., Takayanagi T., Kimura A., Takata M., Sakai O., Matsui H., Takai N., Takayanagi T., Yomplete amino acid sequence of crystalline alpha-glucosidase from Aspergillus niger., i. Complete amino acid sequence of crystalline alpha-glucosidase from Aspergillus niger.,
-:- FUNCTION: Hydrolyzes malto-oligosaccharides, but has a low activity toward soluble starch.
-:- FUNCTION: Hydrolyzes malto-oligosaccharides, but has a low activity toward soluble starch.
-:- GTALYTIC ACTIVITY: Hydrolysis of terminal, non-reducing 1,4-linked D-glucose residues with release of D-glucose.
-:- SIMILARITY: BELONGS TO FAMILY 31 OF GLYCOSYL HYDROLASES.
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TT -> LL (IN STRAIN GN-8).

D -> A (IN STRAIN GN-8).

N -> M (IN STRAIN GN-8).
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                 "Cloning and sequencing of an alpha-glucosidase niger and its expression in A. nidulans."; J. Biotechnol. 53:75-84(1997).
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Pfam: PF01055; Glyco_hydro_31; 1.
PROSITE; PS00129; GLYCOSYL_HYDROL_F31_1; 1.
PROSITE; PS00707; GLYCOSYL_HYDROL_F31_2; 1.
Hydrolase; Glycosidase; Glycoprotein; Signal.
Masaki H., Kimura A., Chiba S., Uozumi T.;
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GlycoSuiteDB; P56526; -.
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GeneDB SFombe; SPAC30D11.01c; -..
InterPro; IPR000122; Glyco.hydro.31.
Pfam; PF01055; Glyco.hydro.31; 1...
PROSITE; PS00129; GLYCOSYL HYDROL F31_1; FALSE_NBG.
PROSITE; PS00707; GLYCOSYL HYDROL F31_2; 1.
Hypothetical protein; Hydrolase; Glycosidase; Glycoprotein; Signal.
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PUTATIVE FAMILY 31 GLUCOSIDASE
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Schizosaccharomyces pombe (Fission yeast).
Eukaryota, Fungi, Ascomycota; Schizosaccharomycetes;
Schizosaccharomycetales; Schizosaccharomycetaceae;
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MEDLINE=21848401; PubMed=11859360;
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NCBI_TaxID=4896;
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751 QEGNILAMQGKAMTTQAARKTPFHLLVVMSDCGASFGELFLDDGVEVTMGVNRGKWTFVK 810
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linked D-glucose residues with release of D-glucose.
CATALYTIC ACTIVITY: Hydrolysis of terminal 1,4-linked alpha-D-
glucose residues successively from non-reducing ends of the chains
with release of beta-D-glucose.
SUBUNIT: Monomer.
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TISSUE SPECIFICITY: EXPRESSED IN SMALL INTESTINE, GRANULOCYTE, AND
KIDNEY BUT NOT IN SALIVARY GLAND OR PANCREAS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Danielsen E.M.;
"Tyrosine sulfation, a post-translational modification of microvillar enzymes in the small intestinal enterocyte.";
enzymes in the small intestinal enterocyte.";
enso J. 6.2891-2896[1987].
-!- FUNCTION: MAY SERVE AS AN ALTERNATE PATHMAY FOR STARCH DIGESTION WHEN LUMINAL ALPHA-AMYLASE ACTIVITY IS REDUCED BECAUSE OF IMPATURITY ON MAINUTATION. MAY PLAY A UNIQUE ROLE IN THE DIGESTION OF MALLTED DIETARY OLIGOSACCHARIDES USED IN FOOD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TISSUE=Small intestine mucosa;
MEDLINE=89066802; PubMed=3143729;
Naim H.Y., Sterchi E.E., Lentze M.J.;
"Structure, biosynthesis, and glycosylation of human small intestinal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PTM: N- AND O-GLYCOSYLATED.
PTM: DOES NOT UNDERGO INTRACELLULAR OR EXTRACELLULAR PROTEOLYTIC
                                                                                                                                                                                                                                                                                                                                                                          'Human small intestinal maltase-glucoamylase cDNA cloning. Homology
                                                                                                                                                           30-MAY-2000 (Rel. 39, Created)
28-FFB-2003 (Rel. 41, Last sequence update)
28-FFB-2003 (Rel. 41, Last annotation update)
Maltase-glucoamylase, intestinal [Includes: Maltase (EC 3.2.1.20)
(Apha-glucosidase); Glucoamylase (EC 3.2.1.3) (Glucan 1,4-alpha-glucosidase))
                                                                                                                                                                                                                                                             Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                                                                                                              Nichols B.L., Eldering J.A., Avery S.E., Hahn D., Quaroni A., Sterchi E.E.;
                                                                                                                                                                                                                                                                                                                                                                                                                         REVISIONS TO 776; 1049; 1100; 1541; 1612 AND 1811.
Nichols B.L., Eldering J.A., Avery S.E., Hahn D., Quaroni A.,
Sterchi E.E.;
Submitted (DEC-2001) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PTM: SULFATED (BY SIMILARITY), SIMILARITY: BELONGS TO FAMILY 31 OF GLYCOSYL HYDROLASES. SIMILARITY: Contains 2 P-type (trefoil) domains.
                                                811 FIAASAKQTCIITSDVVSGEFAVSQKWVIDKVTILGL 847
                                                                 917 LNSNSNTITCVVSGTMVSSP----SLANITILGL 946
                                                                                                                                      1856 AA
                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.
TISSUE=Small intestine;
MEDLINE=98112863; PubMed=9446624;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   maltase-glucoamylase.";
J. Biol. Chem. 263:19709-19717(1988).
                                                                                                                                                                                                                                                                                                                                                                                                  Biol. Chem. 273:3076-3081(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDLINE=88082658; PubMed=3121301;
                                                                                                                                      STANDARD;
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MGA_HUMAN
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the ENBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           119 NPQGAVSVPMCYYSKNHSYHVEGNLVNTNAGFTARLKNLP----SSPVFGSNVDNVLLTA 174
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 80 SLESNDRLRVRITDAKHRWEIPDNILHRHQPPPPPPPPSSSLYRTLLSSPTTNRRKILL 139
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SIGNAL-ANCHOR (TYPE-II MEMBRANE PROTEIN)
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Best Local Similarity 35.2%; Pred. No. 5.4e-88;
Matches 328; Conservative 146; Mismatches 292; Indels 167; Gaps
                                                                                                                                                                                                                                                            R Genew; HGNC:7043; MGAM.

R Go; GO:005983; Pstarch catabolism; TAS.

R InterPro; IPR000322; Glyco hydro_31.

R InterPro; IPR000519; P_trefoil.

R Fam; PF010155; Glyco hydro_31; 2.

R Pf00018; PD; 2.

R MART; SM0018; PD; 2.

R R ROSITE; PS00129; GLYCOSYL HYDROL F31_1; 2.

R PROSITE; PS00125; Glycosylotein; Hydrolase; Multifunctional enzyme; Transmembrane; Glycoprotein; Hydrolase; T INIT MET

T DOMAIN

12 CYTOPLASMIC (POTENTIAL).
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                                                                  SHPNSDLTFSL-INTTPFGFTISRKSTHDVLFDATPDPTNPNTFLIFIDQYLHLTSSLPG 198
                                                                                                                                                          TRAHIYGLGEHSKPTFQLAHN-QTLTMRAADIPSSNPDVNLYGSHPFYMDVRSSPVAGST 257
                                                                                                                                                                                                   T - - NVYGLGEHVHQQYRHDMNWKTWPIFNRDTTPNGNGTNLYGAQTFFLCLEDA - - SGLS 315
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                                                                                                                                                                                                                                                                        AFGFQQCRYGYHDVYELQSVVAGYAKAKIPLEVMWTDIDYMDAYKDFTLDPVNFPLDKMK 376
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                                                                                                GNAAASLTYQVEISRQPFSIXVTRRSNNRVLFDSSIGP-----LLFADQFLQLSTRLPS
                                                                                                                                                                                                                                                                                                                                                                            ALGEHLSRYEYGTLDNMREVVERNRAAQLPYDVQHADIDYMDERRDFTYDSVDF--KGFP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           QTVFPDYTNPNCAVWTKEFELFHNQVEFDGIWIDMNEVSNFVDGSVSGCSTNNLNNPPF
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Debaryomyces occidentalis (Yeast) (Schwanniomyces occidentalis). Eukaryota; Fungi, Ascomycota; Saccharomycotina; Saccharomycetes; Saccharomycetales; Saccharomycetaceae; Debaryomyces.

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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation -
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ALPHA-1,4 AND ALPHA-1,6 LINKAGES.
-!- CATALYTIC ACTIVITY: Hydrolysis of terminal 1,4-linked alpha-D-glucose residues successively from non-reducing ends of the chains with release of beta-D-glucose.
-!- SIMILARITY: BELONGS TO FAMILY 31 OF GLYCOSYL HYDROLASES.
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                                                                                                 MEDLINE=91071592; PubMed=1979298; Dohmen R.J., Strasser A.W.M., Dahlems U.M., Hollenberg C.P.; "Cloning of the Schwanniomyces occidentalis glucoamylase gene (GAMI)
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BTF; JMOLO2; MOLO2.
INTERPRO; IPRO0322; Glyco hydro_31.
Pfam; PF01055; Glyco hydro_31; 1.
PROSITE; PS00129; GLYCOSYL, HYDROL F31_1; 1.
PROSITE; PS00107; GLYCOSYL, HYDROL F31_2; 1.
Hydrolase; Glycosidase; Polysacchāridē degradation; Glycoprotein;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ancestral gene.";
FEBS Lett. 294:109-112(1991).
-!- FUNCTION: THIS GLUCOAMYLASE HAS A SPECIFICITY TOWARD BOTH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         28.8%; Score 1374; DB 1; Length 958; 33.8%; Pred. No. 2.2e-88;
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                                                                                                                                                                                                                                                                                                                                                                                                                                SIMILARITY TO OTHER FAMILY 31 MEMBERS.
MEDLINE=92077121; PubMed=1743281;
Naim H.Y., Niermann T., Kleinhans U., Hollenberg C.P.,
Strasser A.W. M.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        3 KKIPSLALGILLVFLLQYL-----VAGISTSENDPEGVI--
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                                                                                                                                                                                                                                                                            expression in Saccharomyces cerevisiae.";
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Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
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30-MAY-2000 (Rel. 39, Last sequence update)
38-FEB-2003 (Rel. 41, Last annotation update)
Sucrase-isomaltase, intestinal [Contains: Sucrase Isomaltase (EC 3.2.1.10)}
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                                                                                                                                                                                                                                                                                                                                     SIGNAL-ANCHOR (TYPE-II MEMBRANE PROTEIN).
                                                                                                                                                                                                                                                 Sjoestroem H., Noren O., Christiansen L.A., Wacker H., Spiess M., Aglder-Meler B., Rickli E.B., Semenza G.;
"N-terminal sequences of pig intestinal sucrase-isomaltase and prosucrase-isomaltase. Implications for the biosynthesis and membrane
                                                 Hunziker W., Spiess M., Semenza G., Lodish H.F.;
"The sucrase-isomaltase complex: primary structure, membrane-
orientation, and evolution of a stalked, intrinsic brush border
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Glycoprotein; Hydrolase;
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SIMILARITY: BELONGS TO FAMILY 31 OF GLYCOSYL HYDROLASES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SUCRASE-ISOMALTASE, INTESTINAL
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InterPro; IPR000322; Glyco_hydro_31.
InterPro; IPR000322; Glyco_hydro_31.
Pfam; PF00089; trefoil.
Pfam; PF00089; trefoil.; 2.
Pfam; PF00089; trefoil.; 2.
PROSITE; PS00025; P_TREFOIL; 1.
PROSITE; PS000129; GLYCOSYL_HYDROL_F31_2; 2.
PROSITE; PS00707; GLYCOSYL_HYDROL_F31_2; 2.
Multifunctional enzyme; Transmembrane; Glycoprote; Glycosidase; Repeat; Signal-anchor; Sulfation.
INIT MET 1 1826
SUCRASE.ISOMALTASE,
                                                                                                                                                                                                PRELIMINARY SEQUENCE OF 1-37 AND 1007-1014.
MEDLINE-83105704; PubMed=7152027;
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SEQUENCE FROM N.A.
MEDLINE=86245068; PubMed=3755079;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 272 YIGNRI-TYKVIGGIIDLYFFAGPSPGQVVEQFTRVIGRPAPMPYWAFGFQQCRYGYHDV 330
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                              391 VILDPGISTNK----TYETYIRGMKHDVFLKRNG--KPYLGSVWPGPVYFPDFLKPSAL 443
                                                                                                                                                                                                                                                                                 108 VDNHGYNVEGM---TTTSTGLEARLNRKSTPTLFGNDINNVLLTTESQTANRLRFKLTDP 164
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                                                                          (POTENTIAL).
(POTENTIAL).
(POTENTIAL).
(POTENTIAL).
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RPLFFSFPDDIKTYGISSQFLLGKGVMVSPVLKPGVVSVTAYFPRGNWFDLFDYTRSVTA 731
                                                                                                                                                 STG-----RYVTLSAPPDHINVHIQEGNILAMQGKAMTTQAARKTPFHLLVVMSDCGA 784
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-!- FUNCTION: PLAYS AN IMPORTANT ROLE IN THE FINAL STAGE OF
CARBOHYDRATE DIGESTION.

-!- CATALYTIC ACTIVITY: Hydrolysis of sucrose and maltose by an
alpha-D-glucosidase-type action.

-!- CATALYTIC ACTIVITY: Hydrolysis of 1,6-alpha-D-glucosidic linkages
in some oligosaccharides produced from starch and glycogen by
alpha-amylase, and in isomaltose.
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
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MEDLINE-82167542; PubMed-6802834;
Hauri H.-P., Wacker H., Rickli E.E., Bigler-Meier B., Quaroni A.
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30-MAY-2000 (Rel. 39, Last sequence update)
38-FEB-2003 (Rel. 41, Last annotation update)
Sucrase-isomaltase, intestinal [Contains: Sucrase Isomaltase (EC 3.2.1.10)].
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           villus axis of rat small intestine.";
Biochem. Biophys. Res. Commun. 173:765-773(1990).
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STRAIN=Sprague-Dawley; TISSUE-Duodenum;
MEDLINE=90381315; PubMed=2400788;
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STRAIN-Fischer 344; TISSUE-Intestine;
MEDLINE-91097578; PubMed=2268340;
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P23739;
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376 TVSEVVRRNREAGIPYDAQVTDIDYMEDHKEFTYDRVKF--NGLPEFAQDLHNHG-KYII 432
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               273 TGNR-ITYKVIGGIIDLYFFAGPSPGQVVEQFTRVIGRPAPMPYWAFGFQQCRYGYHDVY 331
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             97 RRWEIPDNILHRHQPPPPPPPPSSLYRTLLSSPTTNRRKILLSHPNSDLTFSLINTTPF
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27.7%; Score 1323; DB 1; 34.9%; Pred. No. 2.2e-84;
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                       ASSOCIATED WITH ONE ANOTHER IN A COMPLEX BY NON-COVALENT LINKAGES. SUBCELLULAR LOCATION: Type II membrane protein. Brush border. PTM: THE PRECURSOR IS PROTEOLYTICALLY CLEAVED WHEN EXPOSED TO PANCREATIC PROTEASES IN THE INTESTINAL LUMEN.

PTM: SULFATED (BY SIMILARITY).

MISCELLANGOUS: THERE IS A HIGH DEGREE OF HOMOLGY BETWEEN THE ISOMALTASE AND SUCRASE PORTIONS (41 % OF AMINO ACID IDENTITY)

INDICATING THAT THIS PROTEIN IS EVOLVED BY PARTIAL GENE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SIGNAL-ANCHOR (TYPE-II MEMBRANE PROTEIN)
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EMBL, X15546; CAA33522.1; -..

EMBL, X15546; CAA3352.1; -..

InterPro; IPR000132; D; Trefoil.

EMBL, EFFORMS; Trefoil.

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    SUBUNIT: THE RESULTING SUCRASE AND ISOMALIASE SUBUNITS STAY
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SIMILARITY: BELONGS TO FAMILY 31 OF GLYCOSYL HYDROLASES.
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Gaps

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596 LTRSTFGGSGRHANHWLGDNTASWEQMEWSITGMLEFGIFGMPLVGATSCGFLADTTEEL 655
          778 VMSDCGASFGELFLDDGVEVTMGVNRGKWTFVKFIAASAKQTCIITSDVVSGEFAVSQKW 837
                                                                             838 VIDKVTILGLRKGTK 852
                                                                                                : :||||: :
879 AFKTIKVLGLREDVR 893
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Search completed: October 27, 2003, 10:20:32 Job time : 17.5556 secs

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GenCore version 5.1.6
(c) 1993 - 2003 Compugen Ltd.
                  Copyright
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using sw model protein search, protein õ October 27, 2003, 10:19:13 :uo

; Search time 23.6046 Seconds (without alignments) 3678.964 Million cell updates/sec

US-10-043-418-3 4768

Title: Perfect score:

1 MKKKIPSLALGILLVFLLQY......VAEISGLNLLLGREFKLVLH 903 Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

283308 seqs, 96168682 residues Searched:

283308 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database

PIR 76:*
1: pir1:*
2: pir2:*
3: pir3:*
1: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	Description	alpha-glucosidase	alpha-glucosidase	alpha-glucosidase	alpha-glucosidase	hypothetical prote	hypothetical prote	alpha-glucosidase	alpha-glucosidase	probable family 31	alpha-glucosidase	probable family 31	glucan 1,4-alpha-g	sucrose alpha-gluc	sucrose alpha-gluc	sucrose alpha-gluc	hypothetical prote	alpha-glucosidase	alpha-glucosidase	hypothetical prote		alpha-glucosidase	alpha-glucosidase	probable alpha-glu	alpha-glucosidase	alpha-glucosidase	glucan 1,4-alpha-g	hypothetical prote		
SUMMARIES	ID		JC5463	T48531	S65057	H96709	T47534	A32609	JC4624	T50267	JC4217	T38598	JN0102	A23945	T10799	UUHU	T15893	S19686	JC1200	T16693	T22575	AG1460	AE2402	T07391	AH1097	AC2472	S46105	T22050	T22044	T32449
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obe	Query	100.0	68.0	59.4	50.8		41.0	31.5	31.4	30.3	29.6	28.9	28.8	28.3	27.7	27.7	4	24.7		θ.	21.8		17.2	17.0	16.8	•	16.5	16.4	16.4	15.8
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alpha-glucosidase	sucrose alpha-gluc	alpha-xylosidase (hypothetical 88.1	glucosidase BH0704	hypothetical prote	hypothetical prote	glycosyl hydrolase	probable glycosyl	alpha-xylosidase -	probable glucosida	alpha-glucosidase	hypothetical prote	hypothetical prote	glycosidase homolo	probable glycosyl
H90486	S11386	D90483	B65167	H83737	D91195	E86042	B87347	AI0968	A72394	AD0104	H97033	A83888	T27893	AG1749	AD0507
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ALIGNMENTS

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alpha-glucosidase (EC 3.2.1.20) - spinach
C;Species: Spinacia oleracea (spinach)
C;Species: Spinacia oleracea (spinach)
C;Species: I-Jun-1999 #sequence_revision 11-Jun-1999 #text_change 21-Jul-2000
C;Accession: 10-9143
C;Accession: T09143
R;Sugimoto, M.; Furui, S.; Suzuki, Y.
Plant Mol. Biol. 33, 765-768, 1997.
P;Attle: Molecular cloning and characterization of a cDNA encoding alpha-glucosidase
A;Reference number: 216585, MUID:97238484; PMID:9132669
A;Reference number: 216585, MUID:97238484; PMID:9132669
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Status: preliminary; translated from GB/EMBL/DDBJ
C;Superimental source: EMBL:DB6624; NID:92081626; PIDN:BAA19924.1; PID:92081627
A;Experimental source: strain Dash
C;Superimental Source: strain Dash
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100.0%; Pred. No. 0;
tive 0; Mismatches
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Best Local Similarity 100.
Matches 903; Conservative
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Nyllernate names: protein T22822.110
C;Species: Arabidopais thaliana (mouse-ear cress)
C;Species: Arabidopais thaliana (mouse-ear cress)
C;Species: 20-Apr.2000 #sequence_revision 20-Apr.2000 #text_change 21-Jul-2000
C;Accession: T48531
R;Bevan, M.; Hilbert, H.; Braun, M.; Holzer, E.; Brandt, A.; Duesterhoeft, A.; Bancro submitted to the Protein Sequence Database, April 2000
A;Reference number: 224490
A;Reference number: 224490
A;Cesssion: T48531
A;Status: preliminary
A;Relatus: preliminary
A;Reatdues: 1-902 ABV
A;Restdues: 1-902 ABV
A;Cross-references: EMBL:AL163814
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C. Comment: This enzyme is a exo-glucohydrolase that catalyzes the hydrolysis of alpha-gl
C. Superfamily: lysosomal alpha-glucosidase; sucrase/isomaltase homology; trefoil homolog
C. Keywords: glycosidase; hydrolase
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A,Residues: 1-913 <MAT1>
A,Cross-references: DDBJ:D89615; NID:g2217947; PIDN:BAA20343.1; PID:g2190276
A,Experimental source: seed; cv. NK-152
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                alpha-glucosidase (EC 3.2.1.20) - sugar beet
NiAlternate rames: alpha-D-glucoside glucohydrolase
Cispecies: Beta vulgaris var. alrissima (sugar beet)
Cispecies: Beta vulgaris var. alrissima (sugar beet)
Cispecies: 17-Jun-1997 #sequence_revision 12-Sep-1997 #text_change 20-Jun-2000
Cispecession: JC5463; PC4330
Cispecession: JC5463; PC4330
Arithe: Cloining and sequencing of a cDNA encoding alpha-glucosidase from su
Aireference number: JC5463; MUID:97321863; PMID:9178565
                KRPFVLSRSTFSGSGKYTAHWTGDNAATWNDLVYSIPSMLDFGLFGIPMVGADICGFLGN
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88.0%; Score 3243.5; DB 2; Length
Best Local Similarity 67.3%; Pred. No. 7.3e-223;
Matches 610; Conservative 122; Mismatches 166; Indels
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C;Keywords: glycosidase; hydrolase
P;149-803/bomain: sucrase/isomaltase homology <SIM>P;149-803/bomain: sucrase/isomaltase homology <SIM>P;149-803/bomain: sucrase/isomaltase
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A,Molecule type: protein
A,Residues: 234-261;310-365,507-541;810-840 <MAT2>
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alpha-glucosidase (BC 3.2.1.20) - barley
C;Species: Hordeum vulgare (barley)
C;Species: Hordeum vulgare (barley)
C;Species: Hordeum vulgare (barley)
C;Species: Hordeum vulgare (barley)
C;Accession: S65057, S66058
R;Tibbot, B.K.; Skadsen, R.W.
A;Reference number: S65057
A;Reference number: S65057
A;Reference number: S65057
A;Residues: 1-877 - T1B>
A;Residues: 1-877 - T1B>
A;Residues: 1-877 - T1B>
A;Coss-references: RMBL: U22450; NID:g944900; PIDN:AAB02985.1; PID:g944901
R;Tibbot, B.K.; Skadsen, R.W.
Plant Mol. Biol. 30, 229-241, 1996
A;Reference number: S65058; MUID:96178863; PMID:8616248
A;Reference number: S65058; MUID:96178863; PMID:8616248
A;Reference number: S65058; MUID:96178863; PMID:8616248
A;Reference number: S65058; MUID:96178863; PMID:8616248
A;Reference number: S65058; MUID:96178863; PMID:8616248
A;Reference number: S65058; MUID:96178863; PMID:8616248
A;Residues: 85-115,'S',117-121,123-170,'D',172-366,'G',368-529,'H',531-685,'G',687-764
A;Coss-references: EMBL:U22450
C;Superfamily: lysosomal alpha-glucosidase; sucrase/isomaltase homology; trefoil homol C;Keywords: glycosidase; hydrolase
F;125-769/Domain: sucrase/isomaltase homology <SIM>
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       KFEMRL 899
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                                  A;Map position: 5
A:Introns: 78/2; 313/1; 390/1; 605/3; 747/1
A;Note: T22222.110
C;Superfamily: lysosomal alpha-glucosidase; sucrase/isomaltase homology; trefoil homolog
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 cultivar Columbia; BAC clone T22P22
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Best Local Similarity
Matches 540; Conserv
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TEELCRRWIOLGAFYPFSRDHSSLGTTYQELYRMESVAASARKULGI 	Db 686 AGRYRLYDYSLAVATRIGKHIYL	RESULT 5 H96709 Hypotherical protein F24J5.20 (imported] - Arabidopsis thaliana C;Species: Arabidopsis thaliana (mouse-ear crees) C;Date: 02-Mar-2001 C;Date: 02-Mar-2001 C;Date: 02-Mar-2001 C;Date: 02-Mar-2001 C;Accession: H96709 C;Date: 02-Mar-2001 C;Accession: H96709 C;Date: 02-Mar-2001 C;Accession: H96709 C;Accession: H96709 C;A: C,A: Conn, L.; Corway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, K.; Chin, C,W.; Chung, M.K.; Conn, L.; Corway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, K.; ansen, N.P.; Hughes, B.; Huizar, L. Nature 408, 816-820, 2000 A;Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C. C,A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maiti, R.; Marziali, Rizzo, M.; Rooney, T.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon, A;Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon, A;Reference and analysis of chromosome 1 of the plant Arabidopsis. A;Accession: H96709 A;Accession: H96709 A;Accession: H96709 A;Accession: H96709 A;Accession: H96709 A;Accession: H96709 A;Accession: H96709 A;Accession: H96709 A;Accession: H96709 A;Accession: H96709 A;Accession: H96709 A;Accession: H96709 A;Accession: H96709 A;Accession: H96709 A;Accession: H96709 A;Accession: H96709 A;Accession: H96709 A;Accession: H96709 A;Accession: H96709 A;Accession: H96709 A;Accession: H96709 A;Accession: H96709 A;Accession: H96709 A;Accession: H96709 A;Accession: H96709 A;Accession: H96709 A;Accession: H96709 A;Accession: H96709 A;Accession: H96709 A;Accession: H96709 A;Accession: H96709 A;Accession: H96709 A;Accession: H96709 A;Accession: H96709 A;Accession: H96709 A;Accession: H96709 A;Accession: H96709 A;Accession: H96709 A;Accession: H96709 A;Accession: H96709 A;Accession: H96709 A;Accession: H96709 A;Accession: H96709 A;Accession: H96709 A;Accession: H96709 A;Accession: H96709 A;Accession: H96709 A;Accession: H96709 A;Accession: H96709 A;Accession: H96709 A;Accession: H96709 A;Accession: H96709 A;Accession: H96709 A;Accession: H96	44.7%; Score 2129; DB 2; Length 915; 11 Similarity 44.9%; Pred. No. 2.2e-143; 13 Similarity 44.9%; Pred. No. 2.2e-143; 14 Conservative 167; Mismatches 282; Indeis 62; Gaps 12; 7 SIALGILLVFLLOYLVAGISTSENDPEGVIGYGYKVKSVKVDSGTRRSLTALPQLVKNSS 66 1 Similarity 1 Similarity 1 Similarity 12; 8 AFSLSLLLALILCFSPTQSYKIIGKVRL-VSIEESPDGGFIGYLQVKQKNK 59 67 VYGPDIQLLSITASLESNDRLRVRITDAKGRRWEIPDNILHRHQPPPPPPHSLSSLYRTL 126 1 Similarity 1 Similarity 1 Similarity 1 Similarity 1 Similarity 1 Similarity 1 Similarity 1 Similarity 1 Similarity 1 Similarity 1 Similarity 1 Similarity 1 Similarity 1 Similarity 1 Similarity 1 Similarity 1 Similarity 1 Similarity 1 Similarity 1 Similarity 1 Similarity 1 Similarity 1 Similarity 1 Similarity 1 Similarity 1 Similarity 1 Similarity 1 Similarity 1 Similarity 1 Similarity 1 Similarity 1 Similarity 1 Similarity 1 Similarity 1 Similarity 1 Similarity 1 Similarity 1 Similarity 1 Similarity 1 Similarity 1 Similarity 1 Similarity 1 Similarity 1 Similarity 1 Similarity 1 Similarity 1 Similarity 1 Similarity 1 Similarity 1 Similarity 1 Similarity 1 Similarity 1 Similarity 1 Similarity 1 Similarity 1 Similarity 1 Similarity 1 Similarity 1 Similarity 1 Similarity 1 Similarity 1 Similarity 1 Similarity 1 Similarity 1 Similarity 1 Similarity 1 Similarity 1 Similarity 1 Similarity 1 Similarity 1 Similarity 1 Similarity 1 Similarity 1 Similarity 1 Similarity 1 Similarity 1 Similarity 1 Similarity 1 Similarity 1 Similarity 1 Similarity 1 Similarity 1 Similarity 1 Similarity 1 Similarity 1 Similarity 1 Similarity 1 Similarity 1 Similarity 1 Similarity 1 Similarity 1 Similarity 1 Similarity 1 Similarity 1 Similarity 1 Similarity 1 Similarity 1 Similarity 1 Similarity 1 Similarity 1 Similarity 1 Similarity 1 Similarity 1 Similarity 1 Similarity 1 Similarity 1 Similarity 1 Similarity 1 Similarity 1 Similarity 1 Similarity 1 Similarity 1 Similarity 1 Similarity 1 Similarity 1 Similarity 1 Similarity 1 Similarity 1 Similarity 1 Similarity 1 Similarity 1 Similarity 1 Similarity 1 Similarity 1 Similarit

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                                                                                        125 TLLSSPTTNRRKILLSHPNSDLTFSLINTTPFGFTISRKSTHDVLFDATPDPTNPNTF-- 182
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                       ----SSLQCSNAIGKGYRLISMEKSPDDG---SFIGYLQVKQS
                                             SSVYGPDIQLLSITASLESNDRLRVRITDAKHRRWEIPDNILHRHQPPPPPPHSLSSLYR
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                                                                                                             KSRKSPVTVQE---ISGPELILIFTV---DPFSFAVRRSNGETIFNTS---SSDESFGE
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alpha-glucosidase (EC 3.2.1.20) precursor, lysosomal - human NyAlternate names: acid alpha-glucosidase; acid maltase-glucoamylase C;Species: Home sapiens (wan) C;Decies: Home sapiens (wan) C;Date: 21-May-1990 #sequence revision 05-Apr-1995 #text change 18-Jun-1999 C;Accession: A40577; A32609; Ā35698; S00831; S18847; I52309; S63526 R;Martiniuk, F.; Bodkin, M.; Tzall, S.; Hirschhorn, R.

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A Description: also has EC 3.1.2.3 activity; hydrolyzes alpha 1,4 and alpha 1,6 glycos A; Description: also has EC 3.1.2.3 activity; hydrolyzes alpha 1,4 and alpha 1,6 glycos A; Note: deficiency causes glycogen storage disease type II (Pompe's disease); Superfamily: lysosomal alpha-glucosidase; sucrase/isomaltase homology; trefoil homology (TRF) P; 82-130/Domain: trefoil homology (TRF) P; 82-130/Domain: sucrase/isomaltase homology <SIM>P; 69-70/Cleavage site: Gln-Ala (unidentified proteinase) #status experimental P; 82-109, 92-108, 103-127/Disulfide bonds: #status predicted F; 122-123/Cleavage site: Met-Gly (unidentified proteinase) #status experimental
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R;Hoefsloot, L.H.; Hoogeveen-Westerveld, M.; Kroos, M.A.; van Beeumen, J.; Reuser, A.J
EMBO 17, 1697-1704, 1988
A;Title: Primary structure and processing of lysosomal alpha-glucosidase; homology wit A;Reference number: S00831; MUID:89005058; PMID:3049072
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A; Residues: 70-99;123-126, VLL',130-145;204-215;230-249;332-345;349-370;394-401, 'R',40
A; Residues: 70-99;123-126, VLL',130-145;204-215;230-249;332-345;349-370;394-401, 'R',40
R; Lin, C.Y.; Shieh, J.J.
Biochem. Biophys. Res. Commun. 208, 886-893, 1995
A; Title: Identification of a de novo point mutation resulting in infantile form of Pom A; Reference number: 152309; MUID:95209708; PMID:7695647
A; Accession: 152309
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A; Matterns: 182/3; 231/2; 286/3; 319/1; 359/1; 398/3; 442/3; 479/3; 517/3; 546/1; 585/2
A; Note: GAA 1, GAA 2, and GAA 4 are common alleles in the normal population
C; Function:
                                                                                                                                                                                                                                                  A; Molecule type: DNA
A; Residues: 1-952 < MAR>
A; Note: order of example is incorrect
R; Martiniuk, F; Mehher, M; Taal, S; Meredith, G.; Hirschhorn, R.
DNA Cell Biol. 9, 85-94, 1990
A; Title: Sequence of the CDNA and S'-flanking region for human acid alpha-glucosidase, s with previous CDNA and amino acid sequences
A; Reference number: A32609; MUID:90262651; PMID:2111708
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A;Accession: S18847
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A.Molecule type: mRNA
A.Rosidues: 631-644,"1646-680 <RES>
A.Rosidues: 631-644,"1646-680 <RES>
A.Cross-references: GB:S76893; NID:g912786; PIDN:AAB33842.1; PID:g912787
A.Cross-references: GB:S76893; NID:g912786; PIDN:AAB33842.1; PID:g912787
A.Cross-references: GB:S76893; NID:g912786; PIDN:AAB33842.1; PID:g912787
A.Cross-references mutation of Asp-645 to His causes an infantile form of Pompe's distRibuler, M.; van der Ploeg, A.; Reuser, A.J.J.; Anson, D.S.; Hopwood, J.J.
BUT. J. Blochem. 234, 903-909, 1395
A.Title: Isolation and characterisation of a recombinant, precursor form of lysosomal A.Reference number: 863526; MUID:96163476; PMID:8575451
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A: Molecule type: mRNA
A; Residues: 1-952 cMA2.
A; Residues: 1-952 cMA2.
A; Cross-references: GB:M34424; NID:g182907; PIDN:AAA52506.1; PID:g182908
R; Martiniuk, F.; Bodkin, M.; Tzall, S.; Hirschhorn, R.
Am. J. Hum. Genet. 47, 440-445, 1990
                                                                                gene
                                                                      structural
DNA Cell Biol. 10, 283-292, 1991
A;Title: Isolation and partial characterization of the s
A;Reference number: A40577; MUID:91229698; PMID:1674202
A;Accession: A40577
A;Status: not compared with conceptual translation
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A;Residues: 68-74, X',76-79, X',81 <FUL>
C;Comment: In common with other lysosomal er
C;Comment: In common with other lysosomal er
Cprocessing at both amino and carboxyl ends.
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F;140,233/Binding site: carbohydrate (Asn) (covalent) #status experimental F;203-204/Cleavage site: Arg-Ala (unidentified proteinase) #status experimental F;390,470,492,652,882,925/Binding site: carbohydrate (Asn) (covalent) #status predicted F;518/Active site: Asp #status predicted
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JC4624 alpha-glucosidase (EC 3.2.1.20) - Rhizomucor circinelloides f. circinelloides

C; Species: Rhizomucor circinelloides f. circinelloides
C; Date: 10-May-1996 #sequence_revision 19-Jul-1996 #text_change 20-Jun-2000
C; Accession: 704624; PC4149
R; Sugimoco, M.; Suzuki, P.
J. Biochem. 119, 500-505, 1996
A; Title: Molecular cloning, sequencing, and expression of a cDNA encoding alpha-glucos A; Reference number: JC4624; MUD: 96271012; PMID: 8830045
A; Accession: JC4624
A; Molecule type: mRNA
A; Residues: 1-664 < SUG1>
A; Molecule type: mRNA
A; Residues: 1-664 < SUG1>
A; Molecule type: protein
A; Residues: 203-214;492-495;612-623;715-731;742-751;769-778 < SUG2>
A; Molecule type: protein
A; Residues: 203-214;492-495;612-623;715-731;742-751;769-778 < SUG2>
C; Comment: This enzyme is an exo-carbohydrase, and catalyzes the splitting of an alpha well as soluble starch.
C; Superfamily: lysosomal alpha-glucosidase; sucrase/isomaltase homology; trefoil homol C; Reywords: glycoprotein; glycosidase; hydrolase
F; 122-805/Domain: sucrase/isomaltase homology < SIM>
F; 187, 364, 406, 466, 500, 568, 734/Binding site: carbohydrate (Asn) (covalent) #status prec encoding alpha-glucos an alpha #status pred 299 241 359 264 SIAYTDLIGKPMMPSHWMLGWHHCRYGYPNIDKVBTVKRKYKEANIPLQTVWVDIDYMEE 323 TXDFTFDKVNFPQDRMIGLGEQLHKDGQNYVVMVDPAISANTTYEPYVRGTEMDVWIKNA 383 SRDHSSLGTTYQELYRWESVAASARKVLGIRYTLLPYFYTLMYEAQLNGIPIARPLFFSF 678
:|:|:: || || || || || || || || || || 360 YKDFTLDPVNFPLDKMKKFVNNLHKNGQKYVVILDPGISTNKTYETYIRGMKHDVFLKR- 418 NGKPYLGSVWPGPVYFPDFLKPSALTFWTDEIKRFLNLLPVDGLWIDMNEISNF---- 472 DGSDFIGSVWPGFTTFPDWWHPNATKYWNKEIIDFVDWLGVDGLWIDMNEPASFCLGSCG 443 ---ISSPPIPGSTLDNPPYKINNSGVMLPI 499 ||||||| : | | || ::||:||:|| || || GHWIGDNHSFWPYLKASIANILNPQMFGVSYSGADVCGFNSDTTEELCTRWEIGAFYPF 621 63 V--YGPDIQLLSITASLESNDRLRVRITDAKHRRWEIPDNILHRHQPPPPPPFHSLSSLYR 124 TLLSSPITNRRKILLSHPNSDLIFSLINTIPFGFTISRKSTHDVLFDATPDPTNPNTFLI 184 -----QIKHYVSPKHSNLDFQ-YTAKPFSFKVVRKDDKTTIFDTTNMP----LV 154 HPFYMDVRSSPVAGSTHGVLLLNSNGMDVEYTGNRITYKVIGGIIDLYFFAGPS--PGQV 300 VEQFTRVIGRPAPMPYWAFGFQQCRYGYHDVYELQSVVAGYAKAKIPLEVMWTDIDYMDA 444 SGKVDAGNOPYRWTYTEEEQAANHTRWEKELKAMGNPPGEERNLLYPKYAINNGAGNLS-FIDOYLHLTSSLPGTRAHIYGLGEHSKPTFQLAHNQTLTMRAADIPSSNPD---VNLYGS INKTIPPTAMHYGDIPEYNVHNLFGYLEARVTRAALIKLTEK-RPFVLSRSTFSGSGKYT AHWTGDNAATWNDLVYSIPSMLDFGLFGIPMVGADICGFLGNTTEELCRRWIQLGAFYPF 12 ILLVFLLQYLVAGISTSENDPEGVIGY---GYKVKS--VKVDSGTRRSLTALPQLVKNSS 98; Length 864; Indels 64 IDTFGKTIKDITVDVEYETEERLHVKISDKAKKQYLVPDSPLGFERP 31.4%; Score 1499; DB 2; 38.2%; Pred. No. 1.7e-98; 430/Active site: Asp #status predicted 562 619 g ò

Db 439 IFLRNPDRSLYVGNVMPGFTTFPDFTNYMTECLMNLSAAFGYNSSFPLPYSG 495 Qy 462 LMIDMNBISNF	OY 571 DLVYSIPSMLDFGLFGIPMVGADICGFLGNTTEELCRRWIQLGAFYPFSRDHSSLGTTYQ 630 ::::	RESULT 10 algorithms or the control of the control of the control of control of control of control of control of control of control of control of control of control of control of control of control of control of control of control of control of control of control of control of control of control of control of control of control of control of control of control of control of control of control of control of control of control of control of control of control of control of control of control of control of control of control of control of control of control of control of control of control of control of control of control of control of control of control of control of control of control of control of control of control of control of control of control of control of control of control of control of control of control of control of control of control of control of control of control of control of control of control of control of control of control of control of control of control of control of control of control of control of control of control of control of control of control of control of control of control of control of control of control of control of control of control of control of control of control of control of control of control of control of control of control of control of control of control of control of control of control of control of control of control of control of control of control of control of control of control of control of control of control of control of control of control of control of control of control of control of control of control of control of control of control of control of control of control of control of control of control of control of control of control of control of control of control of control of control of control of control of control of control of control of control of control of control of control of control of control of control of control of control of control of control of control of control of control of control of control of control of control of control of control
DD 622 ARNHNNNAAKDOEPYLWESTAEASRIAINTRYEMLPYFYTLFEESNRLGLGVWRPLIFEY 681 QY 679 PDDIKTYGISSQPLLGKGVMVSPVLKPGVVSVTAYFPRGNMFDLFDYTRSVTASTGR 735	FESULT 9 TSO267 probable family 31 glucosidase [imported] - fission yeast (Schizosaccharomyces pombe) C;Species: Schizosaccharomyces pombe C;Date: 09-Jun-2000 #sequence_revision 09-Jun-2000 #text_change 21-Jul-2000 C;Accession: T50267 R;Hunt, C.; Aves, S.; McDougall, R.C.; Rajandream, M.A.; Barrell, B.G. R;Hunt, C.; Aves, S.; McDougall, R.C.; Rajandream, M.A.; Barrell, B.G. A;Reference number: Z25031 A;Accession: T50267 A;Reference number: Z25031 A;Accession: T50267 A;Reference number: Z25031 A;Accession: T50267 A;Reference number: Z25031 C;Geretics: Prellminary; translated from GB/EMBL/DDBJ A;Residues: 1-995 cHUN- A;Residues: 1-995 cHUN- A;Residues: Byclus-AL133522; PIDN:CAB63549.1; GSPDB:GN0066; SPDB:SPAC922.02c C;Geretics: A;Reperimental source: strain 972h(-); cosmid c922 C;Geretics: A;Rep position: 1 C;Superfamily: Schwarniomyces glucan 1,4-alpha-glucosidase GAMI; sucrase/isomaltase home	Ouery Match Best Local Similarity 33.8%; Score 1444.5; DB 2; Length 995; Best Local Similarity 33.8%; Pred. No. 1.6e-94; Matches 339; Conservative 151; Mismatches 291; Indels 223; Gaps 29; MKKIPELALDILLYPLOYVAGISTSENO

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A; Experimental source: strain 972h-; cosmid c30D11
R; Pearson, D.; Churcher, C.M.
submitted to the EMBL Data Library, November 1995
A; Accession: $62559
A; Accession: $62559
A; Accession: $62559
A; Accession: $62559
A; Cross-references: EMBL: 267961
A; Residues: 1-384 < PEZ-
A; Cross-references: EMBL: 267961
R; Readson, D; Churcher, C.M.; Barrell, B.G.; Rajandream, M.A.; Waish, S.V.
A; Reference number: 221817
A; Reference number: 221817
A; Reference number: 221817
A; References: EMBL: 269228; PIDN: CAA93572.1; GSPDB: GN00066; SPDB: SPAC56F8.01
A; Residues: 352-993 < PEZ-
A; Cross-references: EMBL: 269228; PIDN: CAA93572.1; GSPDB: GN00066; SPDB: SPAC56F8.01
A; Reperimental source: strain 972h-; cosmid c56F8
C; Genetics:
A; Genetics:
A; Genetics: A; Map position: 1L
C; Superfamily: Schwanniomyces glucan 1, 4-alpha-glucosidase GAMI; sucrase/isomaltase ho
F; 165-384/Domain: sucrase/isomaltase homology (fragment) < SIM>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Matches 312; Conservative 170; Mismatches 287;
                                                                                                                                                                                                                                                                                                                                                                                                                                            28.9%; Score 1379; DB 2; 33.3%; Pred. No. 7.7e-90;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A;Molecule type: DNA
A;Residues: 1-385 <PEA>
A;Cross-references: EMBL:Z67961; PIDN:CAA91887.1; GSPDB:GN00066; SPDB:SPAC30D11.01c
                                                                                                                                                                      249 YKVGGQNKSHTIVKSSEAEPSQEYVSYSHGVFLRNAHGQEILLRDQKLIWRTLGGSVDLT 308
                                                                                                                                                                                                                                             369 YLWADIDYMHGYRNFDNDQHRFSYEEGEKFLNKLHAGGRRWVPIVDGALYIPNPENASDA 429
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  549 GAASQSAAASSTTTSAPYLRTTPTPGVRNVDHPPYVINHVQPGHDLSVHAISPNSTHSDG 608
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LGKGVMVSPVLKPGVVSVTAYFP---RGN-WFDLFDYTRSVTASTGRYVTLSAPPDHINV 748
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                                                                                                                                                                                                                                                                                                    VMWTDIDYMDAYKDFTLDPVNFPLDKMKKFVNNLHKNGQKYVVILDPGI-----STNKT 402
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    VWYDMAEVSSFCVGSCGTGNLSMNPAHPPFALPGEPGNVVYDYPEGFNITNATEAASASA 548
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ------ISSPPIPG-STLDNPPYKINNSGVMLPIINKTIPPTAMHYGD 513
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                                                                                                                                                                                                                                                                                                                                                                              YETYIRGMKHDVFLKR-NGKPYLGSVWPGPVYFDDFLKPSALTFWTDEIKRFLNLLPVDG 461
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  YRWESVAASARKVIGLRYTILPYFYTLMYEAQLNGIPIARPLFFSFPDDIKTYGISSQFL
                                                               LTSSLPGTRAHIYGLGEHSKPTFQLAHNQTLTMRAADIPSSNP-DVNLYGSHPFYMDVRS
                                                                                                     193 FVTLLP-EEYNLYGLGERMN-QLRLLENANLTLYAADI--ADPIDDNIYGHHAFYLDTRY
                                                                                                                                            SPVAGS------THGVLLLNSNGMDVEYTGNRITYKVIGGIIDLY
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A;Accession: T38598
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25 252 417 444 465 573 633 682 SSISTILTFNILGIPWVGADVCGYNGNTDEBLCARWMALGAFIPFYRNHNSLGSIPQEPF 741 81 LESNDRLRVRITJAKHRRWEIPDNILHRHQPPPPPPPHSLSSLYRTLLSSPTTNRRKIL-- 138 139 -LSHPNSDLTFSL----INTTPFGFTISRKSTHDVLFDATPDPTNPNTFLIFIDQYLHL 192 207 264 304 265 IGTINIYTSASHGVLMLSSNGMEVLLRSTYIKYRMIGGIIDLFVYSGSTVSPKYTIQQYV 324 364 325 QSIGTPTWQPYWSLGFQMSRWGYKTLSDLINMRSYLNASNIPTEGFWNDIDYMSEFRIFT 384 501 481 561 514 562 QYKATATSEKSHETPSSESLINGKPEFSINYPPYALDTDTETHDLAQFGVSPNATMHGNT 621 V-----AGSTHGVLLLNSNGMDVBYTGNRITYKVIGGIIDLYPPAGP--SPGQVVEQFT 365 LDPVNFPLDKMKKFVNNLHKNGQKYVVILDPGI-----STNKTYETYIRGMKHDVFLK 385 VNSTAFPPNQTLDFFRSLDESHQHYVPVLDPAIYAANPNKSADRTYYPYYSGFEDNIFIK 418 R-NGKPYLGSVWPGPVYFPDFLKPSALTFWTDEIKRFLNL------LPVDGLWID ||| ::| | | 502 MNEPTSFCIGSCGSDLLKLNPVHPPFSLPGDVDNKVYSYPEDFNATNTTEYKSVSRASQS 22 VAGISTSENDPEGVIGYGYKVKSVKVDSGTRRSLTALPQLVKNSS-VYGPDIQLLSITAS 67 VAQEPTLYESSRĞLSCPGYQARNI - - - SEYSYGVLAILELAGDACYAYGTDYPYLLLNVS 193 TSSLPGTRAHIYGLGEHSKPTFQLAHNQTLTMRAADIPSSNPDVNLYGSHPFYMDVRSSP 305 RVIGRPAPMPYWAFGFQQCRYGYHDVYELQSVVAGYAKAKIPLEVWWTDIDYMDAYKDFT -----TEDNPPYKINNSGVMLPIINKTIPPTAMHYGDI 515 PEYNVHNLFGYLEARVTRAALIKLTEK-RPFVLSRSTFSGSGKYTAHWTGDNAATWNDLV 574 YSIPSMLDFGLFGIPMVGADICGFLGNTTEELCRRWIQLGAFYPFSRDHSSLGTTYQELY Indels 168; Length 993;

321 QCRMCYDTIEKLSEVVENFKKFNIPLETIWSDIDYMDSYKDFTYDPHRFPLDEYRKFLDE 382 LHKONGCKTVVLLDPGISTNKTYETYIRGMKHDVFLKR-NGKPYLGSVWPGPVY 381 LHKONGHYVPILDAAIYVPNPNNATDNEYQFFYGNETDVFLKNPDGSLYIGAVWQ-VTL 434 FEDFLKESALTFWTDEIKRFLNLLPVGCANIDKNEISNFISSPPIP	737 719 797 779 856 839 905	Sucrose alpha-glucosidase (EC 3.2.1.48) / oligo-1,6-glucosidase (EC 3.2.1.10) - rabbit sucrose alpha-glucosidase (EC 3.2.1.10) - rabbit NiAlternate names: small intestinal sucrase/isomaltase (SI) C;Species: Oryctolagus cuniculus (domestic rabbit) C;Date: 03-Mar-1994 #sequence_revision 03-Mar-1994 #text_change 24-May-1996 C;Accession: A23445; B25987; A29463 R;Hunziker, W.; Spiess, M.; Semenza, G.; Lodish, H.F. Cell 46, 227-234, 1986 A;Title: The sucrase-isomaltase complex: primary structure, membrane-orientation, and A;Reference number: A23945; MUID:86245068; PMID:3755079 A;Holecule type: mRNA	A.Residues: 1-1827 <hun> A.Residues: 1-1827 <hun> R.Sjoestroen, H.; Noren, O.; Christiansen, L.A.; Wacker, H.; Spiess, M.; Bigler-Meier, FEBS Lett. 148, 321-325, 1982 A;Title: N-terminal sequences of pig intestinal sucrase-isomaltase and pro-sucrase-iso A;Reference number: A25887; MUID:83105704; PMID:7152027 A;Accession: B25987 A;Molecule type: protein A;Residues: 2-32, XXX, 36-38;1008, N, 1010-1014, E' <\$J2> R;Frank, G'; Brunner, J.; Jauser, H.; Wacker, H.; Semenza, G.; Zuber, H. R;Residues: 2-32, XXX, 36-38;1008, N, 1010-1014, E' <\$J2> R;Frank, G'; Brunner, J.; Jauser, H.; Wacker, H.; Semenza, G.; Zuber, H. R;Residues: 2-32, XXX, 36-38;1008, MUID:79086207; PMID:729784 A;Reference number: A29163; MUID:79086207; PMID:729784 A;Accession: A29163 A;Molecule type: protein A;Residues: 2, VNA', 6-32, XXX', 36-38 <fra> C;Comment: Carbohydrate analysis of the mature enzyme complex indicates both N- and O-C;Comment: Carbohydrate analysis of the mature dater cleavage</fra></hun></hun>
OY 634 RWESVAASARKVLGLRYTLLPYFYTLMYEAOLNGIPIARPLFFSFPDDIKTYGISSOFLL 693 742 RWASVAASARKVLGLRYTLLPYFYTLMYEAOLNGIPIARPLFFSFPDDIKTYGISSOFLL 693 742 RWASVAEASRSAIEIRYSLLPYWTLMHTASVDGTPWVRPLFFFPFQSILASVDKOFMI 801 OY 694 GKGWWVSPVLKPGVVSVTAYFPGNWFDLFDYTRSYTASTGRYVTLSAPPDHINVHI 750 is:	A; Reterence number: JN0102; MUID:91071592; PMID:1979298 A; Reterence number: JN0102 A; Residues: 1-958 «DOH» A; Residues: 1-958 «DOH» A; Residues: 1-958 «DOH» A; Cross-references: GB:M60207; GB:M34666; NID:g169845; PIDN:AAA33923.1; PID:g169846 A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Gene	184; Gaps 27; 184; Gaps 27; GVKQIPNIFNDSA 64 TTASLESNDRLRVR 90	158 237 210 260 321 381

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the 1,2-alpha-D-c
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C;Species: Rattus norvegicus (Norway rat)

C;Accession: T10799

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R;Chandrasena, G.; Osterholm, D.E.; Sunitha, PMID: 7821806

R;Chandrasena, G.; Osterholm, D.E.; Sunitha, PMID: 7821806

R;Chandrasena, G.; Osterholm, D.E.; Sunitha, PMID: 7821806

R;Chandrasena, G.; Osterholm, D.E.; Sunitha, PMID: 784659

R;Chandrasena, G.; Osterholm, D.E.; Sunitha, PMID: 784659

R;Chandrasena, G.; Osterholm, D.E.; Sunitha, PMID: 784659

R;Chandrasena, G.; Osterholm, D.E.; Sunitha, D.E.; Din: 773669

R;Chandrasena, D.G.; Din: 7821806

R;Chandrasena, D.G.; Din: 7821806

R;Chandrasena, D.G.; Din: 7821806

R;Chandrasena, D.G.; Din: 7821806

R;Chandrasena, D.G.; Din: 7821806

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R;Chandrasena, D.G.; Din: 7821806

R;Chandrasena, D.G.; Din: 7821806

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R;Chandrasena, D.G.; Din: 7821806

R;Chandrasena, D.G.; Din: 7821806

R;Chandrasena, D.G.; Din: 7821806

R;Chandrasena, D.G.; Din: 7821806

R;Chandrasena, D.G.; Din: 7821806

R;Chandrasena, D.G
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C.Function:
A.Gene: SI
C.Function:
A.Pescripption: sucrose alpha-glucosidase catalyzes the hydrolysis of the 1,2-alph
A.Pathway: carbohydrate digestion
C.Superfamily: sucrase/isomaltase, sucrase/isomaltase homology; trefoil homology
C.Keywords: carbohydrate digestion; glycosidase; hydrolase
F.199-846/Domain: sucrase/isomaltase homology <SIM>
F.199-846/Domain: trefoil homology <TRF>
                   SPGELFLDDGVEVTMGVNRGKWTFVKFIAASAKQTCIITSDVVSGEFAVSQKWVIDKVTI 844
                                                                                                                                                                                                                               AVGDFFWDDG-ETKDTVQNDNYILYTFAVSNNNLNITCTHBLYSEGTTLA----FQTIKI 880
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                                                                                                                                                                                                                                                                                                                                               LGLRKGTKINGYTVRTGAVTRKGDKSKLKS--TPDRKGEFIVAEISGLNLLLGREFKL 900
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                                                                                                                                                                               A Description: sucrose alpha-glucosidase catalyzes the hydrolysis of the 1,2-alpha-D-glu A; Pathway: carbohydrate digestion

A; Pathway: carbohydrate digestion

B; Superfamily: sucrase/isomaltase; sucrase/isomaltase homology; trefoil homology

C; Keywords: carbohydrate digestion; duplication; glycoprotein; glycosidase; hydrolase; m

F; 2-1007/Product: oligo-1,6-glucosidase (isomaltase chain) #status experimental <1SO>
F; F; 3-150Pomain: membrane associated #status predicted <TMM>
F; 43-65/Region: serine/threonine-rich

F; 43-65/Region: serine/threonine-rich

F; 43-65/Region: serine/threonine-rich

F; 43-65/Region: serine/threonine-rich

F; 43-65/Region: serine/threonine-rich

F; 43-65/Region: serine/threonine-rich

F; 43-65/Region: serine/threonine-rich

F; 51-109-137/Domain: sucrase/isomaltase homology <SIM>
F; 1008-1827/Product: sucrose alpha-glucosidase (sucrase chain) #status experimental <SUC

F; 108-1827/Product: sucrase/isomaltase homology <SIM>
F; 108-1827/Product: sucrase/isomaltase homology <SIM>
F; 108-1827/Product: sucrase/isomaltase homology <SIM>
F; 108-1827/Product: sucrase/isomaltase homology <SIM>
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F; 108-1827/Product: sucrase/isomaltase homology <SIM>
F; 108-1827/Product: sucrase/isoma
C;Function: <ISM>
A;Description: oligo-1,6-glucosidase catalyzes the hydrolysis of 1,6-alpha-D-glucosidic
A;Pathway: carbohydrate digestion
C;Function: <SUC>
A;Description: sucrose alpha-glucosidase catalyzes the hydrolysis of the 1,2-alpha-D-glu
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A;Description: oligo-1,6-glucosidase catalyzes the hydrolysis of 1,6-alpha-D-glucosidi A;Pathway: carbohydrate digestion . SiDescription: sucrose alpha-glucosidase catalyzes the hydrolysis of the 1,2-alpha-D-g A;Pathway: carbohydrate digestion . SiDescription: sucrase/isomaltase homology; trefoil homology C;Superfamily: sucrase/isomaltase homology; trefoil homology C;Keyworse: carbohydrate digestion; duplication; glycoprotein; glycosidase; hydrolase, F;2-1007/Product: oligo-1,6-glucosidase (isomaltase chain) #status experimental wATI>F;13-32/Domain: membrane associated #status predicted <PWMA.
                                                                                                                                                                                                                                                                                                  F;1008-1827/Product: sucrose alpha-glucosidase (sucrase chain) #status experimental </br>
F;1068-1827/Product: sucrose Alpha-glucosidase (sucrase chain) #status experimental </br>
F;1052-1734/Domain: sucrase/isomaltase homology <51M2></br>
F;107/Binding site: carbohydrate (Ser) (covalent) #status absent<br/>F;99,437,455,823,855,904,926,1235,1303,1340,1354,4403,1535,1572,1675,1748,1763,1815/Bi<br/>F;1007-1008/Cleavage site: Arg-lle (trypsin) #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               210
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                                                                                                                                                                                                                                 F;63-109/Domain: trefoil homology <TRF1>
F;189-840/Domain: sucrase/isomaltase homology <SIM>
F;931-977/Domain: trefoil homology <TRF2>
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A.Molecule type: mRNA
A.Molecule type: mRNA
A.Molecule type: mRNA
A.Molecule type: mRNA
A.Residues: 1-1827 < LAG.
A.Cross-references: EMBL:X63597; NID:g36644; PIDN:CAA45140.1; PID:g36645
R.Green, F.; Edwards, Y.; Hauri, H.P.; Povey, S.; Ho, M.W.; Pinto, M.; Swallow, D.
A.Title: 10-10410n of a CDNA probe for a human jejunal brush-border hydrolase, sucrase-i
A.Reference number: A27326; MUID:88112852; PMID:2962903
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           sucrose alpha-glucosidase (EC 3.2.1.48) / oligo-1,6-glucosidase (EC 3.2.1.10) [validated N/Alternate names: linit dextrinase; small intestinal sucrase/isomaltase (SI) [c;Species Homo sapiens (man) [C;Species Homo sapiens (man) [C;Date: 19-Nov-1988 #sequence revision 24-May-1996 #text change 08-Dec-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        the 5' structure of the human sucrase-isomald PMID:1353958
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A;Title: Expression of sucrase-isomaltase and dipeptidylpeptidase IV in human small
A;Reference number: A61136; MUID:91317403; PMID:1677636
                                                                                                                                                                                                       CRRWIQLGAFYPFSRDHSSLGTTYQE-LYRWESVAASARKVLGLRYTLLPYFYTLMYEAG 664
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 C;Date: 19-Nov-1988 #sequence_revision 24-May-1996 #text_change 08-Dec-2000
C;Accession: S36082; A27326; $24329; A61136
                        --TAMHYGDIPEYNVHNLFGYLEARVTRAALIKL-TEKRPFV
                                                    PPFTPGILDKVMYSKTLCMDAVQHWG--KQYDVHSLYGYSMAIATEQAVERVFPNKRSFI
                                                                                                                                                                                                                                                                                                                                                                                                                        Richantret, 1.; Lacasa, M.; Chevalier, G.; Ruf, J.; Islam, I.; Mantei, N.; Biochen, J. 285, 915-922, 1992
Affitle: Sequence of the complete cDNA and the 5' structure of the human su
A;Reference number: S24129; MUID:92359963; PMID:1333958
                                                                                                                                             597 LTRSTFGGSGRHANHWLGDNTASWEQMEWSITGMLEFGISCMPLVGATSCGFLADTTEEL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    778 VMSDCGASFGELFLDDGVEVTMGVNRGKMTFVKFIAASAKQTCIITSDVVSGEFAVSQKW
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                                                                                                              LSRSTFSGSGKYTAHWIGDNAATWNDLVYSIPSMLDFGLFGIPMVGADICGFLGNTTEEL
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C;Complex: the two product chains remain associated after cleavage
C;Function: <ISM>
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.Residues: 2-14,'F',16-20;1008-1015,'E',1017-1021,'TX',1024
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submitted to the EMBL Data Library, December 1991
A;Reference number: S36082
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A;Residues: 1-661,'F',663-931 <CHA>
A;Cross-references: EMBL:X63597
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A;Residues: 1-661,'X',663-678 <GRE>
A;Cross-references: GB:M22616
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             938 VIDKVTILGLRKGTK 852
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Search completed: October 27, 2003, 10:22:10 Job time: 27.6046 secs
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 ORGANISM: Spinach
US-10-043-418-3
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Sequence 2, Appli
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Sequence 125, Appli
Sequence 2, Appli
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Sequence 40, Appl
Sequence 12, Appl
Sequence 123, App
Sequence 122, Appl
Sequence 121, Appl
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4768
1 MKKKIPSLALGILLVFLLQY......VAEISGLNLLLGREFKLVJH 903
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1: /cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB.pep:*

2: /cgn2_6/ptodata/1/pubpaa/PCT_MBW_PUB_pep:*

3: /cgn2_6/ptodata/1/pubpaa/US06_NBW_PUB_pep:*

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9: /cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep:*

10: /cgn2_6/ptodata/1/pubpaa/US09E_PUBCOMB.pep:*

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12: /cgn2_6/ptodata/1/pubpaa/US09E_PUBCOMB.pep:*

13: /cgn2_6/ptodata/1/pubpaa/US10B_PUBCOMB.pep:*

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16: /cgn2_6/ptodata/1/pubpaa/US10B_PUBCOMB.pep:*

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18: /cgn2_6/ptodata/1/pubpaa/US60_PUBCOMB.pep:*
GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
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1 US-10-043-418-4

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2 US-10-032-189-125

US-10-032-189-42

2 US-10-032-189-44

2 US-10-032-189-44

2 US-10-032-189-123

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Maximum Match 100%
Listing first 45 summaries
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Maximum DB seq length: 2000000000
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DB 14; Length 903; 0; Indels

100.0%; Score 4768; 100.0%; Pred. No. 0; iive 0; Mismatches

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Sequence 132, Appl
Sequence 6, Appli
Sequence 7, Appli
Sequence 3, Appli
Sequence 10107, A
Sequence 1107, A
Sequence 12, Appli
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APPLICANT: Muslin, Elizabeth H.
APPLICANT: Muslin, Elizabeth H.
TITLE OF INVENTION: Modified barley alpha-glucosidase
FILE REFERENCE: 960296,97486
CURRENT APPLICATION NUMBER: US/10/043,418
CURRENT FILING DATE: 2002-06-25
PRIOR APPLICATION NUMBER: 60/260,787
PRIOR FILING DATE: 2001-01
NUMBER OF SEQ ID NOS: 7
SOFTWARE: Patentin Ver. 2.1
SEC ID NO 3.3
5 US-10-102-806-557
2 US-10-228-063-26
2 US-10-228-063-36
2 US-10-228-063-36
2 US-10-228-063-5
2 US-10-228-063-5
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3 US-09-423-126-4
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                                                                                                                          LPQLVKNSSVYGPDIQLLSITASLESNDRLRVRITDAKHRRWEIPDNILHRHQPPPPPH 117
                                                                                                                                         SLSSLYRTLLSSPTTNRRKILLSHPNSDLTFSLINTTPFGFTISRKSTHDVLFDATPDPT 177
                                                                                                                                                                                         122 PLSSLQHLPKPIPQNQPTTTVLSHPHSDLAFTLFHTTPFGFTIYRKSTHDVLFDATPIPS 181
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                                                                                          DB 14; Length 914;
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                                                  Matches 610; Conservative 122; Mismatches 166;
                          68.0%; Score 3243.5; DB 1 67.3%; Pred. No. 1.8e-292;
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                          Query Match
Best Local Similarity
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                                                                          SHPFYMDVRSSPVAGSTHGVLLLNSNGMDVEYTGNRITYKVIGGIIDLYFFAGPSPGQVV
                                                                                                                EQFTRVIGRPAPMPYWAFGFQQCRYGYHDVYELQSVVAGYAKAKIPLEVMWTDIDYMDAY
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Sequence 2, Application US/10043418

Publication No. US2020184662A1

GENERAL INFORMATION:

APPLICANT: Henson, Cynthia A.

APPLICANT: Hensin, Elizabeth H.

APPLICANT: Clark, Suzanne E.

TILLE OF INVENTION: Modified barley alpha-glucosidase:
FILE REFERENCE: 960266.97466

CURRENT APPLICATION NUMBER: US/10/043,418

CURRENT FILING DATE: 2002-06-25

PRIOR APPLICATION NUMBER: 60/260,787

PRIOR FILING DATE: 2001-01-10

NUMBER OF SEQ ID NOS: 7

SOFTHARE: PatentIn Ver: 2.1

SEQ ID NO 2

LENGTH: 914

TYPE: PRI

COPANITY:
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  837
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                                                                 SDCGASFGELFLDDGVEVTMGVNRGK--WTPVKFIAASAKQTCIITSDVVSGEFAVSQKW
                                                                                                       774 SRLENISGELFLDDGENLRMGAGGGNRDWTLVKFRCYVTGKSVVLRSEVVNPEYASKMKW
                                                                                                                                                838 VIDKVTILGLRKGTKINGYTVRTGAVTRKGDKSKLKSTPDRKG-EFIVAEISGLNLLLGR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Muslin, Elizabeth H.
APPLICANT: Clark, Stranne E.
TITLE OF UNENTION: Modified barley alpha-glucosidase
FILE REFERENCE: 960296.97486
CURRENT APPLICATION WUMBER: US/10/043,418
CURRENT FILING DATE: 2002-06-25
RIOR APPLICATION NUMBER: 60/260,787
PRIOR FILING DATE: 2001-01-10
NUMBER OF SEQ ID NOS: 7
SOFTWARE: Patentin Ver. 2.1
                                                                                                                                                                                                                                                                                                                                                US-10-043-418-1
Sequence 1, Application US/10043418
Publication No. US20020184662A1
GENERAL INFORMATION:
APPLICANT: Henson, Cynthia A.
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Best Local Similarity
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KFEMRL 899
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ORGANISM: Barley
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59.4%; Score 2830.5; DB 14; Length

Best Local Similarity 59.6%; Pred. No. 5.1e-254;

Matches 540; Conservative 138; Mismatches 205; Indels
                Publication No. US20020184662A1
GENERAL INFORMATION:
APPLICANT: Henson, Cynthia A.
APPLICANT: Huslin, Ellzabeth H.
APPLICANT: Clark, Suzanne E.
ITLE OF INVENTION: Modified barley alpha-glucosidase;
FILE REFERENCE: 960296.97486
CURRENT FILING DATE: 2002-06-25
FRIOR APPLICATION NUMBER: 60/260,787
FRIOR FILING DATE: 2001-01-10
NUMBER OF SEQ ID NOS; 7
SOFTWARE: PatentIn Ver. 2.1
Sequence 4, Application US/10043418
                                                                                                                                                                                                                                                                                                                             TYPE: PRT
ORGANISM: Arabidopsis
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PRIOR FILING DATE: 2000-12-20
PRIOR APPLICATION NUMBER: 60/269,940
PRIOR PILING DATE: 2001-02-20
PRIOR FILING DATE: 2001-03-08
PRIOR FILING DATE: 2001-03-08
PRIOR FILING DATE: 2001-03-08
PRIOR PRILING DATE: 2001-03-22
PRIOR FILING DATE: 2001-03-22
PRIOR PRILING DATE: 2001-03-29
PRIOR APPLICATION NUMBER: 60/299,840
PRIOR PILING DATE: 2001-04-11
PRIOR PELING DATE: 2001-04-11
PRIOR PILING DATE: 2001-04-13
PRIOR FILING DATE: 2001-04-13
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PRIOR FILING DATE: 2001-04-13
PRIOR FILING DATE: 2001-08-17
PRIOR PILING DATE: 2001-08-17
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                                                                                                IKLTEKRPFVLSRSTFSGSGKYTAHWTGDNAATWNDLVYSIPSMLDFGLFGIPMVGADIC
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APPLICANT: Smithson, Glennda
TITLE OF INVENTION: Proteins and Nucleic Acids Encoding Same
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CURRENT APPLICATION NUMBER: US/10/032,189
CURRENT FILING DATE: 2001-12-21
PRIOR APPLICATION NUMBER: 60/257,495
PRIOR FILING DATE: 2000-12-21
PRIOR APPLICATION NUMBER: 60/257,495
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; Sequence 125, Application US/10032189; Publication No. US20030170630A1; GENERAL INFORMATION:
; APPLICANT: Alsobrook II, John P; APPLICANT: Tchernev, Velizar T; APPLICANT: Spytek, Kimberly A; APPLICANT: Zerbusen, Bryan D; APPLICANT: Patturajan, Meera; APPLICANT: Patturajan, Meera; APPLICANT: Lepley, Denise M; APPLICANT: Lepley, Denise M; APPLICANT: Burgess, Catherine E
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Patturajan, Meera
Grosse, William M
Lepley, Denise M
Burgess, Catherine E
Shimkets, Richard A
Grosse, William M
Szekeres, Edward S
Vernet, Corine A.M.
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Gorman, Linda
Gangolli, Esha A
Fernandes, Elma R
Rieger, Daniel K
Edinger, Shlomit R
Gunther, Erik
Millet, Isabelle
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                                                                                                                                                                              Gaps
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) OTHER INFORMATION: Description of Artificial Sequence: Glycosyl; OTHER INFORMATION: hydrolases family 31
US-10-032-189-125
                                                                                                                        Length 707;
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                                                                                                                   39.4%; Score 1880; DB 12;
ilarity 53.7%; Pred. No. 1.1e-165;
Conservative 97; Mismatches 205;
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SCKYTAHWIGDNAATWNDLVYSIPSMLDFGLFGIPMVGADICGFLGNTTEELCRRWIQLG 613
                                                                                        AFYPFSRDHSSLGTTYQE--LYRWES-VAASARKVLGLRYTLLPYFYTLMYEAQLNGIPI 670
                                                                                                                                                                                                                                                                                                     ARPLFFSFPDDIKTYGISSQFLLGKGVMVSPVLKPGVVSVTAYFPRGNWFDLFDYTRSVT 730
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APPLICANT: MacDougall, John R
APPLICANT: Smithson, Glennda
TITLE OF INVENTION: Proteins and Nucleic Acids Encoding Same
FILE REFERENCE: 21402-228
CURRENT APPLICATION NUMBER: US/10/032,189
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APPLICATION NUMBER: 60/269,940
FILING DATE: 201-02-20
APPLICATION NUMBER: 60/274,192
FILING DATE: 2001-03-08
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PRIOR APPLICATION NUMBER: 60/257,495
PRIOR FILING DATE: 2000-12-21
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Publication No. US20030170630A1
GENERAL INFORMATION:
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Patturajan, Meera
Grosse, William M
Lepley, Denise M
Burgess, Catherine E
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Grosse, William M
Szekeres, Edward S
Vernet, Corine A.M.
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APPLICANT: Tchernev, Velizar I
APPLICANT: Liu, Xiaohong
APPLICANT: Spytek, Kimberly A
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Gangolli, Esha A
Fernandes, Elma R
Rieger, Daniel K
Gunther, Shlomit R
Millet, Isabelle
Sciore, Paul
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Ferenc L
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Patent No. US20010036635A1
GENERAL INFORMATION
GENERAL INFORMATION
APPLICANT: Park, Jason
APPLICANT: Park, Jason
APPLICANT: Schulz, Stephanie
TITLE OF INVENTION: Compositions And Methods For Identifying And Targeting Cancer (TITLE OF INVENTION: Campositions And Methods For Identifying And Targeting Cancer (URRENT APPLICATION NUMBER: US/09/819,247
CURRENT FILING DATE: 2001-03-27
PRIOR FILING DATE: 2000-03-27
PRIOR FILING DATE: 2000-03-27
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                     735 RYVTLSAPPDHINVHIQEGNILAMQGKAMTTQAARKTPFHLLVVMSDCGASFGELFLDDG
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                                                                                                                                          ESI--DIORGDYLLVQF---SANNNTLIGTEVVIGYYKNSTNLTLEKITILGV 698
                                                                                                           795 VEVTMGVNRGKWTFVKFIAASAKQTCIITSDVVSGEFAVSQKWVIDKVTILGL
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SOFTWARE: PatentIn version 3.0
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US-09-819-247-2
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LENGTH: 1827
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US-09-819-247-2
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690 ASQPVMRPLWVBFPDELKTFDMBDBYMLGSALLVHPVTEPKATTVDVFLPGSNEVW---Y 746
                                666 NGIPIARPLFFSFPDDIKTYGISSOFLLGKGVMVSPVLKPGVVSVTAYFPRGN--WFDLF 723
                                                                                                                                                                                                         781 DCGASFGELFLDDGVEVTMGVNRGKWTFVKFIAASAKQTCIITSDVVSGEFA----VSQ 835
                                                                                                                                                                                                                                          724 DYTRSVTASTGRYVTLSAPPDHINVHIQBGNILAMQ----GKAMTTQAARKTPFHLLVVMS
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APPLICANT: Ellerman, Karen
APPLICANT: MacDougall, John R
APPLICANT: Smithson, Glennda
TITLE OF INVENTION: Proteins and Nucleic Acids Encoding Same
FILE REFERENCE: 21402-228
CURRENT APPLICATION NUMBER: US/10/032,189
CURRENT APLICATION DATE: 2001-12-21
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PRIOR APPLICATION NUMBER: 60/257,495
PRIOR APPLICATION NUMBER: 60/257,495
PRIOR PLING DATE: 2000-12-21
PRIOR PELING DATE: 2000-12-20
PRIOR PELING DATE: 2001-02-94
PRIOR FILING DATE: 2001-02-09
PRIOR PELING DATE: 2001-03-08
PRIOR APPLICATION NUMBER: 60/274,192
PRIOR APPLICATION NUMBER: 60/279,840
PRIOR PELING DATE: 2001-03-22
PRIOR PELING DATE: 2001-03-29
PRIOR FILING DATE: 2001-03-29
PRIOR FILING DATE: 2001-04-11
PRIOR APPLICATION NUMBER: 60/299,840
PRIOR FILING DATE: 2001-04-11
PRIOR APPLICATION NUMBER: 60/299,840
PRIOR PILING DATE: 2001-04-11
PRIOR PELING DATE: 2001-04-13
PRIOR PILING DATE: 2001-07-31
                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 40, Application US/10032189
Publication No. US20030170630A1
GENERAL INFORMATION:
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Shimkets, Richard A
Grosse, William M
Szekeres, Edward S
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Gangolli, Esha A
Fernandes, Elma R
Rieger, Daniel K
Edinger, Shlomit R
Gunther, Erik
Miller, Isabelle
Sciore, Paul
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APPLICANT: Tchernev, Velizar T
APPLICANT: Liu, Xisobong APPLICANT: Spytek, Kimberly A
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Grosse, William M
Lepley, Denise M
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855 KCVVEXILVLGFRK 868
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Boldog, Ferenc L
Gorman, Linda
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PRIOR APPLICATION NUMBER: 60/277,826
PRIOR FILING DATE: 2001-03-22
PRIOR PAPPLICATION NUMBER: 60/299,840
PRIOR FILING DATE: 2001-03-29
PRIOR FILING DATE: 2001-04-19
PRIOR PAPLICATION NUMBER: 60/282,981
PRIOR FILING DATE: 2001-04-13
PRIOR PILING DATE: 2001-04-13
PRIOR PILING DATE: 2001-07-31
PRIOR APPLICATION NUMBER: 60/311,754
PRIOR FILING DATE: 2001-08-17
PRIOR FILING DATE: 2001-08-17
PRIOR FILING DATE: 2001-08-17
PRIOR FILING DATE: 2001-08-17
PRIOR FILING DATE: 2001-08-17
NUMBER OF SEQ ID NOS: 260
                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: PRT
ORGANISM: Homo sapiens
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LENGTH: 914
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---SFCSSVLINSFADQRGHYPS 854
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APPLICANT: Sciote, Faul
APPLICANT: Bellerman, Glenda
TITLE OF INVENTION: Proteins and Nucleic Acids Encoding Same
FILE REFERENCE: 21402-228
CURRENT APPLICATION NUMBER: US/10/032,189
CURRENT FILING DATE: 2000-12-21
PRIOR APPLICATION NUMBER: 60/259,1495
PRIOR APPLICATION NUMBER: 60/259,171
PRIOR APPLICATION NUMBER: 60/259,171
PRIOR APPLICATION NUMBER: 60/259,171
PRIOR PILING DATE: 2000-12-20
PRIOR FILING DATE: 2001-03-09
PRIOR FILING DATE: 2001-03-09
PRIOR PILING DATE: 2001-03-09
PRIOR PELING DATE: 2001-03-09
PRIOR PELING DATE: 2001-03-29
PRIOR PELING DATE: 2001-03-29
PRIOR PELING DATE: 2001-03-29
PRIOR PELING DATE: 2001-04-11
PRIOR PILING DATE: 2001-04-13
PRIOR PILING DATE: 2001-04-13
PRIOR PILING DATE: 2001-04-13
PRIOR PILING DATE: 2001-03-31
PRIOR PILING DATE: 2001-08-17
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PRIOR PILING DATE: 2001-08-17
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PRIOR PILING DATE: 2001-08-17
PRIOR PILING DATE: 2001-08-17
  805 TKGSSVGELYLDDGHSFQY-LHQKQFLHRKF---
                                                                                                                                                                                                               ; Sequence 44, Application US/10032189; Publication No. US20030170630A1; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Burgess, Catherine E
Shimkets, Richard A
Grosse, William M
Szekeres, Edward S
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Boldog, Ferenc L
Gorman, Linda
Gangolli, Esha A
Fernandes, Elma R
Rieger, Daniel K
Edinger, Shlomit R
Gunther, Erik
Millet, Isabelle
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Spytek, Kimberly A
Zerhusen, Bryan D
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APPLICANT: Tchernev, Velizar T
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Grosse, William M
Lepley, Denise M
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855 KCVVEKILVLGFRK 868
                                              836 KWVIDKVTILGLRK 849
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CRGANISM: Homo sapiens
US-10-032-189-44
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ----- DATPDPTNPN--- 180
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                                                                                                                                                                                                                                                                                                                                                                                                                                                  97 RRWEIPDNILHRHQPPPPPPPHSLSSLYRTLLSSPTTNR-----RKILLSHPNSDLTF 148
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             18: -----TFLIFID-----QYLHLTSSLPGTRAHIYGLGEHSKPTFQLAHNQTLTMRAAD 228
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         229 IPSSNPDV-----NLYGSHPFYMDVRSSPVAGSTHGVLLLNSNGM------DVE 271
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                                                                                                                                                                                                                                                           Query Match 17.8%; Score 848; DB 12; Length 914;
Best Local Similarity 27.9%; Pred. No. 2.2e-69;
Matches 255; Conservative 142; Mismatches 327; Indels 190; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                149 SLINTTPF-----GFTISRKSTHDVLF-----
                   PRIOR APPLICATION NUMBER: 60/313,331
PRIOR FILING DATE: 2001-08-17
NUMBER OF SEQ ID NOS: 260
SOFTWARE: PATENTIN VET: 2.1
PRIOR FILING DATE: 2001-08-17
                                                                                                                                                                TYPE: PRT
CORGANISM: Homo sapiens
US-10-032-189-40
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94 PRFEVPD-
                                                                                                                 SEQ ID NO 40
LENGTH: 914
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300 YTLTQMGPVAAKQKVRSRTHVHWMSESGIIDVFLLTGPTPSDVFKQYSHLTGTQAMPPLF 359
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|-------EQTMQKNAIHHGNWEHRELHNIYGFYHQNATAEGLIKRSKGKERPFVL 567
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                                                                                                                                                                                                                                                                133 H-ITANPFKVDLVSEEEVVISINSLGQLYFEHLQILHKQRAAKENEEETSVDTSQENQED 191
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                                                                              38 YGYKVKSVKVDSGTRRSLTALPQLVKNSSVYGPDIQLLSITASLESN-DRLRVRITDAKH 96
                                                                                                                 43 YRALLDSVTTDEDSTRF----QIINEAS----KVPLLAEIYGIEGNIFRLKINEETPLK 93
                                                                                                                                                         97 RRWEIPONILHRHQPPPPPPPPHSLSSLYRTLLSSPTTNR------RKILLSHPNSDLTF
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                                             Gaps
Query Match 17.8%; Score 847; DB 12; Length 912; Best Local Similarity 28.0%; Pred. No. 2.8e-69; Matches 256; Conservative 142; Mismatches 324; Indels 192;
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RESULT 10 US-10-032-189-123 ; Sequence 123, Application US/10032189 ;; Publication No. US20030170630A1

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GSVFVLL-----AHNPHRDLGIFWINAAETWVDISSNTAGKTLFGKNMDYLQGSGETP 348
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APPLICANT: Gargolli, Esha A
APPLICANT: Gangolli, Esha A
APPLICANT: Gangolli, Esha A
APPLICANT: Rieger, Daniel R
APPLICANT: Reiger, Daniel R
APPLICANT: Beinger, Daniel R
APPLICANT: Guncher, Erik
APPLICANT: Guncher, Erik
APPLICANT: MacDougalli, John R
APPLICANT: MacDougalli, John R
APPLICANT: MacDougalli, John R
APPLICANT: Smitchson, Glennda
TITLE OF INVENTION: Proteins and Nucleic Acids Encoding Same
CURRENT APPLICANT: Solore, 228
CURRENT APPLICANT: Solore, 228
CURRENT FILING DATE: 2001-12-21
PRIOR FILING DATE: 2001-12-21
PRIOR FILING DATE: 2001-02-20
PRIOR APPLICATION NUMBER: 60/259, 940
PRIOR PLILNG DATE: 2001-03-29
PRIOR FILING DATE: 2001-03-29
PRIOR PLILNG DATE: 2001-03-29
PRIOR PLILNG DATE: 2001-04-11
PRIOR PLILNG DATE: 2001-04-11
PRIOR FILING DATE: 2001-06-17
PRIOR FILING DATE: 2001-06-17
PRIOR FILING DATE: 2001-06-17
PRIOR FILING DATE: 2001-07-11
PRIOR FILING DATE: 2001-08-17
PRIOR FILING DATE: 2001-08-17
PRIOR PLILNG DATE: 2001-08-17
PRIOR FILING DATE: 2001-08-17
PRIOR PLILNG DAT
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Grosse, William M
Lepley, Denise M
Burgess, Catherine E
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Grosse, William M
Szekeres, Edward S
APPLICANT: Alsobrook II, John P
APPLICANT: Tcherney, Velizar T
APPLICANT: Liu, Xiaohong
APPLICANT: Spytek, Kimberly A
APPLICANT: Zerhusen, Bryan D
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Vernet, Corine A.M.
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Boldog, Ferenc L
Gorman, Linda
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US-10-032-189-123
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-----GIIDLYFFAGPSPGQVVEQFTRVIGRPAPMPYWAFGFQQCRYGYHDVYEL
                          349 QTDVRWMSETGIIDVFLLGPSISDVFRQXASLTGTQALPPLFSLGYHQSRWNYRDEADV
                                                                           334 QSVVAGYAKAKIPLEVMWIDIDYMDAYKDFTLDPVNFPLDKMKKFVNNLHKNGQKYVVIL
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Publication No. US20030170630A1
GENERAL INFORMATION;
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APPLICANT: Tchernev, Velizar T
APPLICANT: Liu, Xiaohong
APPLICANT: Liu, Xiaohong
APPLICANT: Surtusan, Meera
APPLICANT: Grosse, William M
APPLICANT: Grosse, William M
APPLICANT: Lepley, Denise M
APPLICANT: Burgess, Catherine E
APPLICANT: Shimkers, Richard A
APPLICANT: Shimkers, Richard A
APPLICANT: Shimkers, Richard A
APPLICANT: Scekers, Edward S
APPLICANT: Yernet, Corine A.M.
APPLICANT: Vernet, Corine A.M.
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Boldog, Ferenc L
Gorman, Linda
Gangolli, Esha A
Fernandes, Elma R
Rieger, Daniel K
Edinger, Shlomit R
Gunther, Erlk
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297 GSVPVLL-----AHNPHRDLGIFWLNAAETWVDISSNTAGKTLFGKMMDYLOGSGETP 349
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APPLICANT: Ellerman, Karen
APPLICANT: MacDougall, John R
APPLICANT: MacDougall, John R
APPLICANT: Smithson, Glennda
TITLE OF INVENTION: Proteins and Nucleic Acids Encoding Same
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CURRENT APPLICATION NUMBER: US/10/032,189
CURRENT FILING DATE: 2001-12-21
PRIOR APPLICATION NUMBER: 0/25/495
PRIOR APPLICATION NUMBER: 60/25/495
PRIOR FILING DATE: 2000-12-21
PRIOR FILING DATE: 2000-12-20
PRIOR FILING DATE: 2001-02-20
PRIOR FILING DATE: 2001-02-20
PRIOR FILING DATE: 2001-02-20
PRIOR FILING DATE: 2001-03-08
PRIOR FILING DATE: 2001-03-29
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PRIOR FILING DATE: 2001-08-17
PRIOR FILING DATE: 2001-08-17
PRIOR APPLICATION NUMBER: 60/313,331
PRIOR FILING DATE: 2001-08-17
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; ORGANISM: Homo sapiens
US-10-032-189-122
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85 VLLVLELQGLQXAMTRIRIDELEPRRP---RYRVPDVLVADPPTARLSVSGRDDNSVELT 141
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        336 FWLNAAETWVDISSNTAGKTLFGKMLDYLQGSG---ETPQTDIRWMSESGIIDVFLMLGP 392
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16.9%; Score 805; DB 12; Length 966;
Best Local Similarity 28.1%; Pred. No. 2.5e-65;
Matches 275; Conservative 133; Mismatches 369; Indels 200;
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PRIOR APPLICATION NUMBER: 60/283,656
PRIOR FILING DATE: 2001-04-13
PRIOR PAPLICATION NUMBER: 60/310,247
PRIOR FILING DATE: 2001-07-31
PRIOR FILING DATE: 2001-07-31
PRIOR FILING DATE: 2001-08-17
PRIOR FILING DATE: 2001-08-17
PRIOR FILING DATE: 2001-08-17
NUMBER OF SEQ ID NOS: 260
SOFTWARE: PATENTIN VET: 2.1
                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: PRT ORGANISM: Mus musculus
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       TGDNTAEWDHLKISIPMCLSLGLVGLSFCGADVGGFFKNPEPELLVRWYQMGAYQPFFRA 675
                                                                           HSSLGTTYOELYRWESVAAS-ARKVLGLRYTLLPYFYTLMYEAQLNGIPIARPLFFSFPD 680
                                                                                                                                           HAHLDTGRREPWLLPSQHNDIIRDALGQRYSLLPFWYTLLYQAHREGIPVMRPLWVQYPQ 735
                                                                                                                                                                                                                DIKTYGISSOFLLGKGVMVSPVLKPGVVSVTAYFP-RGN-WFDLFDYTRSVTASTGRY-- 736
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APPLICANT: MacDougall, John R
APPLICANT: Smithson, Glennda
TILE OF INVENTION: Proteins and Nucleic Acids Encoding Same
FILE REFERENCE: 21402-228
CURRENT APPLICATION NUMBER: US/10/032,189
CURRENT FILING DATE: 2001-12-21
PRIOR APPLICATION NUMBER: 60/254,495
PRIOR FILING DATE: 2000-12-20
PRIOR APPLICATION NUMBER: 60/259,171
PRIOR APPLICATION NUMBER: 60/269,940
PRIOR APPLICATION NUMBER: 60/269,940
PRIOR APPLICATION NUMBER: 60/279,826
PRIOR FILING DATE: 2001-03-08
PRIOR FILING DATE: 2001-03-08
PRIOR PLING DATE: 2001-03-08
PRIOR PLING DATE: 2001-03-08
PRIOR PLING DATE: 2001-03-22
PRIOR FILING DATE: 2001-03-29
PRIOR FILING DATE: 2001-03-29
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5. US20030170630A1
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Publication No. US20030170630A1
GENERAL INFORMATION:
APPLICANT: Tcherney, Velizar T
APPLICANT: Liu, Xiaohong
APPLICANT: Spytek, Kimberly A
APPLICANT: Spytek, Kimberly A
APPLICANT: Sertusen, Bryan D
APPLICANT: Grosse, William M
APPLICANT: Grosse, William M
APPLICANT: Lepley, Denise M
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Shimkets, Richard A
Grosse, William M
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Vernet, Corine A.M.
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Boldog, Ferenc L
Gorman, Linda
Gangolli, Esha A
Fernandes, Elma R
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Edinger, Shlomit R
Gunther, Erik
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Sciore, Paul
Ellerman, Karen
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                                                                                                                                                                                           Query Match
16.9%; Score 804; DB 12; Length 966;
Best Local Similarity 28.0%; Pred. No. 3.1e-65;
Matches 267; Conservative 131; Mismatches 351; Indels 206;
          PRIOR FILING DATE: 2001-08-17
NUMBER OF SEQ ID NOS: 260
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 120
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                                                                                                          TYPE: PRT
CRGANISM: Homo sapiens
US-10-032-189-120
                                                                                           LENGTH: 966
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758 MOGKA-MITQAARKIPFHLLVVMSDCGASFGELFLDDGVEVIMGVNRGKWIFVKFIAASA 816
                                                                                                                                                 817 KOTCIITSDVVSGEFAVSQKMVIDKVTILGLRKGTKINGYTVRTGAVTRKGD-KSKLKST 875
                                                                                                                                                                          890 SGSTLVSSSADPKGHLETPIW-IERVVIMGAGKPAAV-----VLQTKGSPESRLSFQ 940
                                                                                                        334 RWMRVRRSSDCMKDDPITLFVALSPQGTAQGELFLDDGHTFNY-QTRHEFLLRRF---SF
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APPLICANT: MacDougall, John R
APPLICANT: Mathon, Glenda
TITLE OF INVENTION: Proteins and Nucleic Acids Encoding Same
FILE REFERENCE: 21402-228
CURRENT APPLICATION NUMBER: US/10/032,189
CURRENT FILING DATE: 2001-12-21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRIOR APPLICATION NUMBER: 60/257, 495
PRIOR FILING DATE: 2000-12-21
PRIOR FILING DATE: 2000-12-20
PRIOR FILING DATE: 2000-12-20
PRIOR PELICATION NUMBER: 60/269, 940
PRIOR APPLICATION NUMBER: 60/20
PRIOR PLING DATE: 2001-02-20
PRIOR PELING DATE: 2001-03-08
PRIOR PELING DATE: 2001-03-08
PRIOR FILING DATE: 2001-03-29
PRIOR PILING DATE: 2001-03-29
PRIOR APPLICATION NUMBER: 60/279, 840
PRIOR PILING DATE: 2001-03-19
PRIOR PILING DATE: 2001-04-11
PRIOR PELING DATE: 2001-04-13
PRIOR PELING DATE: 2001-04-13
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                                                                                                                                                                                                                                                                                                                                                                        Sequence 120, Application US/10032189
Publication No. US20030170630A1
GENERAL INFORMATION:
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Grosse, William M
Lepley, Denise M
Burgess, Catherine E
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Grosse, William M
Szekeres, Edward S
Vernet, Corine A.M.
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Casman, Stacie J
Boldog, Ferenc L
Gorman, Linda
Gangolli, Esha A
Fernandes, Elma R
Rieger, Daniel K
Edinger, Shlomit R
Gunther, Erik
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APPLICANT: Tchernev, Velizar I
APPLICANT: Liu, Xiaohong
APPLICANT: Spytek, Kimberly A
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Sciore, Paul
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US-10-032-189-120
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                                                                                                                                                                                                                 117 HSLS-----SLYRTLLSSPTINRRKILLSHPNSDLTFSLINTTPFGPTISRKSTHDVLFD 171
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                                          10 LGILLVFLLQYLVAGISTSENDPEGVIGYGYKVKSVKVDSGTRRSLTALPQLVKNSSVYG 69
                                                                                  23 IGVCLGLTLAVDRSNFKTCEES----SPCKRQRSIRPGQSPYRALLDSLQL-----G
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APPLICANT: MacDougall, John R
APPLICANT: MacDougall, John R
APPLICANT: SMithson, Glennda
TITLE OF INVENTION: Proteins and Nucleic Acids Encoding Same
FILE REFERENCE: 21402-228
CURRENT APPLICATION NUMBER: US/10/032,189
CURRENT FILING DATE: 2001-12-21
PRIOR APPLICATION NUMBER: 60/257,495
PRIOR FILING DATE: 2000-12-21
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Pred. No. 8.7e-65;
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PRIOR FILING DATE: 2000-12-20
PRIOR FILING DATE: 2001-02-20
PRIOR PILING DATE: 2001-02-20
PRIOR PELING DATE: 2001-03-20
PRIOR APPLICATION NUMBER: 60/274,192
PRIOR APPLICATION NUMBER: 60/274,192
PRIOR FILING DATE: 2001-03-08
PRIOR FILING DATE: 2001-03-29
PRIOR PELING DATE: 2001-03-29
PRIOR PELING DATE: 2001-04-11
PRIOR APPLICATION NUMBER: 60/289,91
PRIOR PILING DATE: 2001-04-11
PRIOR APPLICATION NUMBER: 60/283,656
PRIOR PELING DATE: 2001-04-13
PRIOR PILING DATE: 2001-08-17
                                                                                                                                                Application US/10032189
o. US20030170630Al
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Shimkets, Richard A
Grosse, William M
Szekeres, Edward S
Vernet, Corine A.M.
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APPLICANT: Therrew, Velizar T
APPLICANT: Liu, Kiachong
APPLICANT: Spytek, Kimberly A
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Gunther, Erik
Millet, Isabelle
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Patturajan, Meera
Grosse, William M
Lepley, Denise M
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Fernandes, Elma R
Rieger, Daniel K
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Boldog, Ferenc L
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SEQ ID NO 124
LENGTH: 944
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Best Local Similarity
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; ORGANISM: Sus
US-10-032-189-124
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TLLSSPTTNR------RKILLSHPNSDLTFSLINTTPF------GFTISRKSTHDVL 169
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                                                                                                                                                                                                                                                            ------PNTFLIFID-----QYLHLISSLPGTRAHIYGLGEHSKPTFQLAHNQT 221
                                                                                                                                                                                                                                                                                                        240 GKAEKDEPGAWEETFKTHSDSKPYGPSSIGLDFSLHGFE-HLYGIPQHAE----SHQLK 293
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    Search completed: October 27, 2003, 10:38:15 Job time : 112.481 secs
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16.7%; Score 797.5; DB 12; Length 967;
Best Local Similarity 25.6%; Pred. No. 1.2e-64;
Matches 266; Conservative 156; Mismatches 365; Indels 251; Gaps
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APPLICANT: MacDougall, John R
APPLICANT: Smithson, Glennda
TITLE OF INVENTION: Proteins and Nucleic Acids Encoding Same
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CURRENT APPLICATION NUMBER: US/10/032,189
CURRENT APPLICATION NUMBER: US/10/032,189
CURRENT PILING DATE: 2001-12-21
PRIOR APPLICATION NUMBER: 60/258,171
PRIOR FILING DATE: 2000-12-20
PRIOR FILING DATE: 2001-02-20
PRIOR APPLICATION NUMBER: 60/269,940
PRIOR FILING DATE: 2001-02-20
PRIOR APPLICATION NUMBER: 60/269,940
PRIOR APPLICATION NUMBER: 60/279,840
PRIOR FILING DATE: 2001-03-29
PRIOR FILING DATE: 2001-03-29
PRIOR FILING DATE: 2001-03-29
PRIOR FILING DATE: 2001-03-29
PRIOR FILING DATE: 2001-03-29
PRIOR FILING DATE: 2001-04-11
PRIOR APPLICATION NUMBER: 60/283,656
PRIOR FILING DATE: 2001-04-13
PRIOR APPLICATION NUMBER: 60/283,656
PRIOR FILING DATE: 2001-04-13
PRIOR APPLICATION NUMBER: 60/383,656
PRIOR FILING DATE: 2001-04-13
PRIOR APPLICATION NUMBER: 60/311,754
PRIOR PILING DATE: 2001-04-13
PRIOR PILING DATE: 2001-04-13
PRIOR PILING DATE: 2001-04-13
PRIOR PILING DATE: 2001-04-13
PRIOR PILING DATE: 2001-08-17
PRIOR APPLICATION NUMBER: 60/313,331
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Sequence 38, Application US/10032189
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Grosse, William M
Lepley, Denise M
Burgess, Catherine E
Shimkets, Richard A
Grosse, William M
Szekeres, Edward S
Vernet, Corine A.M.
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Gangolli, Esha A
Fernandes, Elma R
Rieger, Daniel K
Edinger, Shlomit R
Gunther, Erik
Millet, Isabelle
Sciore, Paul
                                                                  APPLICANT: Alsobrook II, John P
APPLICANT: Therriew, Velizar T
APPLICANT: Liu, Xiaohong
APPLICANT: Spytek, Kimberly A
                      Publication No. US20030170630A1
GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                Casman, Stacie J
Boldog, Ferenc L
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GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
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US-09-437-054A-8
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US-08-897-843A-1
US-08-633-770A-2
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US-08-633-770A-1
US-08-633-770A-1
US-08-633-768A-1
US-09-275-608-3
US-09-275-608-4
US-09-275-608-4
US-09-237-608-4
US-09-231-28-331
US-09-016-366A-12
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                                                                                             YGSHPFYMDVRSSPVAGSTHGVLLLNSNGMDVEYTGNRITYKVIGGIIDLYFFAGPSPGQ 298
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                                                                                                                                  VVEQFTRVIGRPAPMPYWAFGFQQCRYGYHDVYELQSVVAGYAKAKIPLEVMWTDIDYMD 358
                                                                                                                                                                       AYKDFILDPVNFPLDKMKKFVNNLHKNGQKYVVILDPGIST---NKTYETYIRGMKHDVF 415
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                                                                    ---LVFRDKYLEVTSALPAGRASLYGLGEHTKSSFRLRHNDSFTLWADIGASYYJVL
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                               PNTFLIFIDQYLHLTSSLPGTRAHIYGLGEHSKPTFQLAHNQTLTMRAADIPSSNPDVNL
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APPLICANT: Kinney, Anthony J.
TITLE OF INVENTION: Plant Alpha-Glucosidase II
FILE REFERENCE: BB1273 US NA
CURRENT APPLICATION NUMBER: US/09/437,054A
CURRENT FILING DATE: 2001-05-14
PRIOR APPLICATION NUMBER: 60/107,909
PRIOR PILING DATE: 1998-No. 6316698ember-10
NUMBER OF SEQ ID NOS: 19
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VGEEFEL 871
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                                                                                                   Gape
Ouery Match
17.4%; Score 831; DB 4; Length 914;
Best Local Similarity 28.7%; Pred. No. 1e-68;
Matches 242; Conservative 133; Mismatches 348; Indels 120;
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                                                                                                                                                                           APPLICANT: Blum, Paul H.
TITLE De INVENTION: Hyperthermophilic Alpha-Glucosidase Gene and Its UTITE De INVENTION: Hyperthermophilic Alpha-Glucosidase Gene and Its UFILE REFERENCE: N1231-200
CURRENT APPLICATION NUMBER: US/09/376,343
CURRENT FILING DATE: 1999-08-18
EARLIER APPLICATION: 040-18
NUMBER: OF SEQ ID NOS: 4
SCFTWARE: PatentIn Ver: 2.0
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14.2%; Score 676; DB 4; Length 693;
Best Local Similarity 27.0%; Pred. No. 2.3e-54;
Matches 189; Conservative 130; Mismatches 286; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ; TYPE: PRT
; ORGANISM: Sulfolobus solfataricus
US-09-376-343-2
                                                                            ; Sequence 2, Application US/09376343; Patent No. 6506592; GENERAL INFORMATION:
           RESULT 4
US-09-376-343-2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WTFVKFIAASAKQTCIITSDVVSGEFAVSQKWVIDKVTILGLRKGTK 852
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Patent No. 6316698
GENERAL INCRMATION:
APPLICANT: Allen, Stephen M.
APPLICANT: Allen, Stephen M.
APPLICANT: Rinney, Anthony J.
TITLE OF INVENTION: Plant Appla-Glucosidase II Homologs:
FILE REFERENCE: BBL273 US NA
CURRENT FILING DATE: 2001-05-14
CRIENT APPLICATION NUMBER: 60/107,909
PRIOR FILING DATE: 1998-No. 6316698ember-10
NUMBER OF SEQ ID NOS: 19
SOTTWARE: Microsoft Office 97
SEQ ID NO 17
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LENGTH: 919
TYPE: PRT
CORGANISM: Solanum tuberosum
US-09-437-054A-17
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US-09-437-054A-17
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APPLICANT: Bojsen, Kireten
APPLICANT: Yu, Sunkun
APPLICANT: Yu, Sunkun
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APPLICANT: Yu, Sunkun
APPLICANT: Yu, Jan
APPLICANT: Christensen, Tove
APPLICANT: Marcussen, Jan
APPLICANT: Marcussen, Jan
TITLE OF INVENTION: PURIFICATION GENE CLONING AND EXPRESSION IN MICROORGANISMS
NUMBER OF SEQUENCES: 12
ADDRESSEE: Knobbe, Martens, Olson & Bear
372 LDKMKKFVNNLHKNGQKYVVILDPGISTNKTYETYIRGMKHDVFLK-RNGKPYLGSVWPG 430
                               --QPLNMLEHLDSKRRNVVAIVDPHIKVDSGYRVHEELRNHGLYVKTRDGSDYEGWCWPG 500
                                                                                                                                                                                                                      600 NITEBLORRWIQLGAFYPFSRDHSSLGTTYQELYRW----ESVAASA-----RKVLGL 648
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                                                                                          431 PVYFPDFLKPSALTFWTDEIKRFLNLLPVDG------LWIDMNEISNFISSPPIPGS 481
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                                                                                                                         541 -KRPFVLSRSTFSGSGKYTAHWTGDNAATWNDLVYSIPSMLDFGLFGIPMVGADICGFLG
                                                                                                                                                                                    482 TLDNPPYKINNSGVMLPIINKTIPPTAMHYGDIPEYNVHNLFGYLEARVTRAALIKLTE-
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APPLICATION NUMBER: US/08/633,770A
FILING DATE: July 8, 1996
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/EP94/03398
FILING DATE: OCT-15-1994
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STREET: 620 Newport Center Drive 16th Floor
CITY: Newport Beach
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; Sequence 2, Application US/08633770A; Patent No. 5908760
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COMPUTER: IBM Compatible
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US-08-633-770A-2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            208 ETQEKAEKDEPGAWEETFKTHSDSKPYGPTSVGLDFSLPGME-HVYGIPEHADSLRLKVT 266
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       267 EGGEPYRLYNLDVFQYELNNP-MALYGSVPVILAHSFHRDLGIFWLNAAETWVDISSNTA 325
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GST-HGVLL--LNSNGMDVEYTGNRITYKVIGGIIDLYFFAGPSPGGVVEQFTRVIGRPA 311
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      312 PMPYWAFGFQQCRYGYHDVYELQSVVAGYAKAKIPLEVMWTDIDYMDAYKDFTLDPVNFP 371
                                                                                GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Delee, Albert B.; Loftus, Douglas; Appella, Ettore
TITLE OF INVENTION: CDNA CLONE FOR WURINE TUMOR PEPTIDE VACCINE
TITLE OF INVENTION: REJECTION ANTIGEN GPIIO AND TUMOR PEPTIDE VACCINE
NUMBER OF SEQUENCES:
ADDRESSEE: Diane R. Meyers
ADDRESSEE: Diane R. Meyers
ATRET: 600 Grant Street, 42nd Floor
CITY: PA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   52 RRSLTALPQLVKNSSVYGPDI-----QLLSITASLE----SNDRLRVRITDAKHR-RW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 13.5%; Score 643.5; DB 4; Length 938; Best Local Similarity 25.3%; Pred. No. 4.4e-51; Matches 247; Conservative 137; Mismatches 361; Indels 231;
                                                                                                                                                                                                                                                                                                                                                                                       MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER: US/08/897,843A FILING DATE:
                                       Sequence 1, Application US/08897843A
Patent No. 6514493
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Embryo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CLASSIFICATION: 424
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          : 938 amino acids
amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     N-terminal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ORGANISM: Mus musculus
DEVELOPMENTAL STAGE: E
TISSUE TYPE: Embryo
CELL LINE: NIH 3T3
                                                                                                                                                                                                                                                                                                                                                                        COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TOPOLOGY: linear
MOLECULE TYPE:
HYPOTHETICAL: NO
ANTI-SENSE: NO
FRAGMENT TYPE: N-tel
ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                              15219
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GENERAL INFORMATION:

APPLICANT: Bojsen, Kirsten
APPLICANT: Yu, Shukun
APPLICANT: Yu, Shukun
APPLICANT: Yu, Shukun
APPLICANT: Kaagh, Karsten
APPLICANT: Marcussen, Jan
TITLE OF INVENTION: ALPHA-1,4-GLUCAN LYASE FROM A FUNGUS, ITS
TITLE OF INVENTION: PURIFICATION GENE CLONING AND EXPRESSION IN MICRORGANISMS
TITLE OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:
ADDRESSEE: Knobbe, Martens, Olson & Bear
                                                         863
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         -----GPDIQLLSITASLESNDRLRVRITDA-KHRRWEIPD 103
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           155 RIQVVRTLTPLKDPYPIPNVAAABARVSDKVVWQTSPKTFRKNL---HPQ------201
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       154 TPFGFTISRKSTHDVLFDATPDPTNPNTFLIPIDQYLHLTSSLPGTRAHIYGLGE---- 208
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        4 KIPSLALGILLVF-----LLQYLVAGISTSENDPEGVIGYGYKVKSVKVDSGTRRSLTA 57
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ---APE
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                                | : | | : | | : | | 815 G-ENRDVEGGSVINYTARIV----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               10.0%; Score 476; DB 2; Length 1066; 21.4%; Pred. No. 3e-35;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PatentIn Release #1.0, Version #1.25 (EPO)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         E: Knobbe, Martens, Olson & Bear
620 Newport Center Drive 16th Floor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Ouery Match
10.0%; Score 476; DE
Best Local Similarity 21.4%; Pred. No. 3e-3
Matches 209; Conservative 135; Mismatches
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APPLICATION NUMBER: US/08/633,770A
FILING DATE: July 8, 1996
CLASSIFICATION 435
FRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/EP94/03398
FILING DATE: CCT-1194
ATTORNEY/AGENT INFORMATION:
NAME: Altman, Daniel E
REGISTRATION NUMBER: 34,115
                                                                                                                                                                                                                                                             Sequence 1, Application US/08633770A
Patent No. 5908760
                                                                                                 744 DH-----INVHIQEGNIL 756
                                                                                                                                 |: : |:|| |:
864 DYNLFHNVVPVYIREGAII 882
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TELECOMMUNICATION INFORMATION:
TELEPHONE: 714-760-0404
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              : Diskette
IBM Compatible
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         58 LPQLVKNS-SVY-----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE CHARACTERISTICS
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MEDIUM TYPE: Diskett
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STREET: 620 Newport
CITY: Newport Beach
STATE: CA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          OPERATING SYSTEM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            amino acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     201
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                162 RKSTHOVLFDATPDPTNPNTFLIFIDQYLHLTSSLPGTRAHIYGLGE-----HSKPTF- 214
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ----HKMLKDIVLDIIKPG--------HGEYVGWGEMGGIEFMKEPTFM 238
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              -----QLAHNQTLTMRAADIPSSNPDVNLYGSHPFYMDVRSSPVAGSTHGVLLLNSNGM 268
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           239 NYFNFDNMQYQQVYAQGALD--SREP---LYHSDPFYLDVNSNPEHKNITATFIDNYSQI 293
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           269 DVEYTGNRITYKVIG---GIIDLYFFAGPSPGQVVEQFTRVIGRPAPMPYWAFGFQQCRY 325
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       326 GYHDVYELQSVVAGYAKAKIPLEVMWTDIDYMDAYKDFTLDPVNFPLDKMKKFVNNLHKN 385
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     412 GIKCSTNITPVISIRDRPNGYSTLNEGYDKKYFIMDDRYTEGTSGDPQNVRYSFYGGGNP 471
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               412 ----HDVFLKRN-----GKPYLGSVWPG-----PVYFPDFLKPSALTFWT 447
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DEIKRFLNLLPVDGLWIDMNEISNFISSPPIPGSTLDNPPYKINNSGVMLPIINKTIPPT 507
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         508 AMHYGDIPEYNVHNL----FGYLEARVTRAALIKLTEKRPFVLSRSTFSGSGKYTAHWTG 563
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           634
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                635 DNASTWEFWKISVSQVLSLGLNGVCIAGSDTGGFEPARTEIGEEKYCSPELLIRWYTGSF 694
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ---WESVAASARKVLGLRYTLLPY 655
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                755 LYDCMFQNVVDGMPLARSMLLTDTEDTTFFNESQKFLDNOYMAGDDILVAPILHSRNEVP 814
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ------DLFDYTRSVTASTGRYVTLSAPP 743
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        53 RSLTALPQLVKNSSVYGPDIQLLSITASLESNDRLRVRITDA-KHRRWEIPDNI----L
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                163 TPLVJPFPIPNVANATARVADKVVWQTSPKTFRKNL---HPQ-------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      584 AIESWALYSYNLHKATFHGLGRLESR------KNKRNFILGRGSYAGAYRFAGLWTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 656 FYTLMYEAQLNGIPIARPLFFSFPDDIKTYG----ISSOFLLGKGVMVSPVLK----P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                      Ouery Match 10.2%; Score 487; DB 2; Length 1070; Best Local Similarity 22.6%; Pred. No. 2.8e-36; Matches 194; Conservative 121; Mismatches 306; Indels 238;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   386 GOKYVVILDP-----GIST----NKTY----ETYIRGMK-----
NAME: Altman, Daniel E
REGISTRATION NUMBER: 34,115
REFRENCE/DOCKET NUMBER: DYOUG.001APC
TELEPHONE: 714-760-0404
TELEFAX: 714-760-0502
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               706 GVVSVTAYFPR-GNWF------
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                                                                                                                                                                                                    INFORMATION FOR SEQ ID NO: 2: SEQUENCE CHARACTERISTICS: LENGTH: 1070 amino acids TYPE: amino acid TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                 MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                            US-08-633-770A-2
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80 SLESNDRLRVRITDAKHRRWEIPDNILHRHQPPPPPPHSLSSLYRTLLSSPTTNRRKILL 139
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYETYIRGMKHDVFLKRN-----GKPYLGSVWPG-----PVYFPDFLKPSA 442
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        140 SHPNSDLTFSL------INTTPFGFTISRKSTHDVLFDATPDPTNPNT-----FL 183
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                                                                                                                                                       MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: Windows
OPERATING SYSTEM: Windows
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/275,608
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/EP95/02172
APPLICATION NUMBER: 08/836,156
FILING DATE: 15-APR-1997
APPLICATION NUMBER: PCT/EP94/03397
FILING DATE: 15-OCT-1994
ATTORNEY/AGENT INFORMATION:
NAME: Altman, Daniel E
REGISTRATION NUMBER: 34,115
REFERNCE/DOCKET NUMBER: 34,115
REFERNCE/DOCKET NUMBER: DYOU9.001C1
TELECOMMUNICATION INFORMATION:
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LENGTH: 1092 amino acids
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STRANDEDNESS: single
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HOLECULE TYPE: protein
US-09-275-608-3
                                                                                                       COMPUTER READABLE FORM: MEDIUM TYPE: Diskett
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                                                                                                                                                                   209 -HSKPTF-----QLAHNQTLIMRAADIPSSNPDVNLYGSHPFYMDVRSSPVAGSTHGV 260
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                                                      ---HGEYVGWGEMGGIQ 230
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APPLICANT: YU, Shukun
APPLICANT: YU, Shukun
APPLICANT: YU, Shukun
APPLICANT: YU, Shukun
APPLICANT: MARCUSEN, Jan
APPLICANT: MARCUSEN, Jan
TITLE OF INVENTION: TS USE IN THE PRODUCTION OF 1,5-ANHYDROFRUC
TITLE OF INVENTION: TOSE
NUMBER OF SEQUENCES: 21
CORRESPONDENCE ADDRESS:
ADDRESSEE: Knobbe, Martens, Olson & Bear
STREET: 620 Newport Center Drive 16th Floor
CITY: Newport Beach
STATE: CA
                                                -----HKMLKDTVLDIVKPG-----
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Patent No. 6541237
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                               -YKINNSGVMLPIINKTIPPTAMHYGDIPEYNVHNLFGYLEARVTRAALI-----KLTE- 540
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                                                            643 NWKSYHPQVLV----TDMRYGAEYGREPMVSQRNIHAYTLCESTRREGIVGNADSLTKF
                                                                                            541 KRPFVLSRSTFSGSGKYTAHWTGDNAATWNDLVYSIPSMLDFGLFGIPMVGADICGFL--
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APPLICANT: BOJGEN, KIRSTEN
APPLICANT: BOJGEN, KIRSTEN
APPLICANT: MAGH, KARSTEN
APPLICANT: MACH, KARSTEN
APPLICANT: NIELSEN, JOHN
APPLICANT: MACUSSEN, JOHN
TITLE OF INVENTION: ALPHA-1, 4-GLUCAN LYASE FROM
TITLE OF INVENTION: A FUNGUS INFECTED ALGAE, ITS PURIFICATION
MUMBER OF SEQUENCES: 25
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REFERENCE/DOCKET NUMBER: DYOU7.001APC
TELECOMMUNICATION INFORMATION:
TELEPHONE: 714-760.0404
TELEFAX: 714-760.
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CURRENT APPLICATION DATA:
APPLICATION NAMEE: US/08/633,768A
FILING DATE: 02-JUL-1996
CLASSIFICATION: 435
PRIOR APPLICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 1, Application US/08633768A
Patent No. 6013504
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APPLICATION NUMBER: 9321301.5
FILING DATE: 15-OCT-1993
ATTONNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ZIP: 92660
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM COMPALIDE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELEX:
INFORMATION FOR SEQ ID NO: 1:
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REGISTRATION NUMBER: 3
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ADDRESSEE: Knobbe, M
                                                                                                                                                                                                                                                                                                                                                                                                              808 FVKFIAA 814
                                                                                                                                                                                                                                                                                                                                                                                                                                            993 VISVKAA 999
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196 LPGT-----RAHIYGLGEHS---KPTF------QLAHNQTLTMRAADIP 230
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      403 YETYIR-----GMKHDVFLKRNGKPYLGSVWPG-----PVYFPDFLKPSALTFWTD 448
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        449 EIKRFLNLLPVDGLWIDMNEISNFISSPPIPGSTLDNPPYKINNSGVMLPIIN----- 501
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   757 AM-----QGKAMTIQAARKTPFHLLVVMSDCGASFGELFLDDGVEVTMGVNRGKWTPVK 810
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         246 VNKNFRNDAVKQEGFYGAGEVNCKYQDTYILERTGIAMTNYNYDNLNYNQWDLRPPHHDG 305
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     272 YTGNRITYKVIGGIIDLYFFAGPSPGQ--VVEQFTRVIG-------RPAPMPYWAFG 319
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              364 YMGAQY-----GPFDQHFVYGAGGGMECVVTAFSLLQGKEFENOVLNKRSVMPFKYVFG 417
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        320 FOQCRYGYHDV-----YELQSVVAGYAKAKIPLEVMWTDIDYMDAYKDFTL--- 365
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         418 FFOGVFGTSSLLRAHMPAGENNISVEEIVEGYONNNFPFEGLAVDVDMODNLRVFTTKGE 477
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ------DPVN-----PPLDK------MKKFVNNLHKNGQKYVVILDPGISTNKT 402
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       -----KTIPP----TAMHY---GDIPEYNVHNLFGYLEARVTRAALI-----KLTE-K 541
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             633 SNGQYNWKTYHPQVLVTDMRYENHGREPMVTQRNIHAYTLCESTRKEGIVENADTLTKFR 692
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     602 TE-----ELCRRWIQLGAFYPFSRDH----SSLGTTYQELYRWESVAASARKVL 646
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               647 GLRYTLIPYFYTLMYEAQLNGIPIARPLFFSFPDDIKTYGISSOFLL----GKGVMVSPV 702
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         813 EFRYRWGBVLYTAMYQNAAFGKPIIKAASMYNNDSNVRRAQNDHFLLGGHDGYRILCAPV 872
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LKPGVVSVTAYFP-RGNWFDL---FDYTRSVTASTG--RYVTLSAPPDHINVHIQEGNIL 756
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         873 VWENSTERELYLPVLTQWYKFGPDFDTKPLEGAMNGGDRIYNYPVPQSESPIFVREGALL 932
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      542 RPFVLSRSTFSGSGKYTAHWTGDNAATWNDLVYSIPSMLDFGLFGIPMVGADICGFLGNT 601
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SSNPD--VNLYGSHP-------FYMDVRSSPVAGSTHGVLLLNSNGMDVE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    478 FWTANRVGTGGDPNNRSVFEWAHDKGLVCQTNITCFLRN-DNEGQDYEV----NQTLRE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               532 RQLYTKNDSLTGTDFGMTDD----GPSDAYIGHLDYGGGVECDALFPDWGRPDVAEWWGN
                                                                                                                                                                                                                                                                                                                                                                                                                                                146 LIF----SLINTTPFGFTISRKSTHDVLFD----ATPDPTNPNTFLIFIDQ-YLHLTSS
                                                                                                                                                                                                                                                                                         Query Match 7.4%; Score 352.5; DB 3; Length 1088; Best Local Similarity 23.0%; Pred. No. 1.3e-23; Matches 200; Conservative 107; Mismatches 347; Indels 215;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   811 FIAA--SAKQTCIITSD----VVSGEFAV 833
                                      1088 amino acids
SEQUENCE CHARACTERISTICS
                                                                                                            single
                                                                                                                                                                             MOLECULE TYPE: protein
                              LENGTH: 1088 aminc
TYPE: amino acid
STRANDEDNESS: sing
TOPOLOGY: linear
                                                                                                                                                                                         ; MOLECULE TENUS-08-1
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738 -TLSAPPDHINVHIQEGNILAMQ-----GKAMTTQAARKTPFHLLVVMSDCGASFGELF 790
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              526 LEARVTR----AALIKLTE-KRPFVLSRSTFSGSGKYTAHWTGDNAATWNDLVYSIPSK 579
                                                                                                                    791 LDDGVEVTMGVNRGKMTFVKFIAASAKQTCIITSDVVSGEFAV-SQKWVID---KVTILG 846
469 ISNFISSPPIPGSTLDNPPYKINNSGVMLPIINKTIPPTAMHY----GDIPEYNVHNLFGY 525
                                                                                                                                                                                                                                                                                                                                                              688 -SSQFLL----GKGVMVSPVLKPGVVSVTAYFP-RGNWFDL---FDYTRSVTASTGRYV- 737
                                        520 VGDAVDTRSPYGWPNENDP---SNGRYNWKSYHPOVLVTDMRYENHGREPMFTQRNMHAY
                                                                                                                                                                                                                                                                      628 TYGELYRWESVAASARKVLGLRYTLLPYFYTLMYEAQLNGIPIARPLFFSFPDDIKTYGI
                                                                                                                                                                                580 LDFGLFGIPMVGADICGFLGNTTEELCR----RWIQLGAFYPFSRDH-----SSLGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GENERAL INFORMATION:
APPLICANT: YU, Shukun
APPLICANT: YSHUKUN
APPLICANT: VSHUKUN
APPLICANT: WARCUSSEN, KITELEN
APPLICANT: MARCUSSEN, Jan
TITLE OF INVENTION: ALPHA-1, 4-GLUCAN LYASE AND
TITLE OF INVENTION: ITS USE IN THE PRODUCTION OF 1,5-ANHYDROFRUC
TITLE OF INVENTION: TOSE
NUMBER OF SEQUENCES: 21
CORRESPONDENCE ADDRESS:
ADDRESSEE: Knobbe, Mattens, Olson & Bear
STREET: 620 Newport Center Drive 16th Floor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SOFTWARE: FactSED FOR Windows SOFTWARE: FactSED for Windows Version 2.0b CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/275,608
FILLING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NAME: Altman, Daniel E
REGISTRATION NUMBER: 34,115
REFERENCE/DOCKET NUMBER: DYOU9.001C1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PCT/EP95/02172
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FILING DATE: 15-OCT-1994
KTTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER: PCT/EP95/03
FILING DATE: 06-JUN-1995
APPLICATION NUMBER: 08/836,156
FILING DATE: 15-APR-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        US-09-275-608-4; Sequence 4, Application US/09275608; Patent No. 6541237
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     847 LRKGTKINGYTVRTGA 862
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ZIP: 92660
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRIOR APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          331 ---YELQSVVAGYAKAKIPLEVYWTDIDYMDAYKDFTLDPVNFPLDKMKKFVNNLHKNGQ 387
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           423 --YLGSVWPG-----PVYFPDFLKPSALTFWTDEIKRFLNLLPVDGLWIDM-----NE 468
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     333 SGNSDEQY--SYGWFMDNVSQTYMNT--GGTSWNCGEENLAYMGAQC-----GPFDQHF 382
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   443 GNNISVOEIVEGYGSNNFPLEGLAVDVDMQQDLRVFTTKIEFWTANKVGTGGDSNNKSVF 502
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EWA--HDKGLVCQTNVTCFLRNDNGGADYEVNQTLREKGLYTKNDSLTNTNFGTTNDGFS 560
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          231 SSNPDVNLYGSHPFYMDVRSSPVAGSTHGVLLLNSNGMDVEYTGNRITYKVIGGIIDLYF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     388 KYVVILDPGISTNKTYETYIR----GMKHDV----------FLKRNGKP-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    291 FAGPSPG--QVVEQFT-----RVIGRPAPM-FYWAFGFQQCRYGYHDV----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                       APPLICANT: YU, SHUKUN
APPLICANT: YU, SHUKUN
APPLICANT: KRAGH, KARSTEN
APPLICANT: BOJKO, MAJA
APPLICANT: BOJKO, MAJA
APPLICANT: MIELSEN, JOHN
APPLICANT: MARCUGSEN, JAN
TITLE OF INTENTION: ALPHA-1,4-GLUCAN LYASE FRON
TITLE OF INTENTION: A FUNGUS INFECTED ALGAE, ITS PURIFICATION
NUMBER OF SEQUENCES: 25
CORRESPONDENCE ADDRESS:
ADDRESSE: Knobbe, Martens, Olson & Bear
STREET: 620 Newport Center Drive 16th Floor
CITY: Newport Beach
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 7.4%; Score 351; DB 3; Length 1091; Best Local Similarity 23.2%; Pred. No. 1.8e-23; Matches 171; Conservative 114; Mismatches 319; Indels 132;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NAME: Altman, Daniel E
REGISTRATION NUMBER: 34,115
REFERENCE/DOCKET NUMBER: DYOU7.001APC
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SOFTWARE: FastEEQ Version 1.5
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/633,768A
FILING DATE: 02-UUL-1996
CLASSIFICATION: 435
              Sequence 2, Application US/08633768A
Patent No. 6013504
GENERAL INFORMATION:
APPLICANT: YU, SHUKUN
APPLICANT: BOJSEN, KIRSTEN
APPLICANT: RAAGH, KARSTEN
APPLICANT: BOJSEN, MAJA
APPLICANT: NIELSEN, JOHN
APPLICANT: MARCUSSEN, JAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE: 15-0CT-1993
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LENGTH: 1091 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           : 714-760-0404
714-760-9502
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-633-768A-2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       OPERATING SYSTEM:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FILING DATE: 02 CLASSIFICATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                 92660
  US-08-633-768A-2
                                                                                                                                                                                                                                                                                                                                                                                                         COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                 CITY: )
STATE:
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417 KRNGKPYLGSVWPGPVYFPDFLKPSALTFWTDEIKRFLNLLP----VDGLWIDMNEISNF 472
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                                                                                                                                                                                                                                                                                                                                                                                                                              131 -LSPVDPA----NPKPDDRDFAKEVAIGVKALKTDVAWVGSGYSFGLDGL-AKADAMMTQ 184
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          533 AALIKLIEKRPFVLSRSTFSGSGKYTAHWIGD-NAATWNDLVYSIPSMLDFGLFGIPMVG 591
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              242 SDMDGIFGGGNPIVNTRDFQWKAFTPIQLNMDGWGANPKTPFSFDQQTTAINRAYNKQKT 301
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      652 -LLPYFYTLMYEAQLNGIPIARPLFFSFPDDIKTYG--ISSQFLLGKGVMVSPVLKPGVV 708
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              302 MLMPYNYTASAQSVFDGKPMVRGLFLDYPNIPEAYTDLVKYEYLWGDNFLVAPIYQN--- 358
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              592 ADICGFLGNTTEELCRRWIQLGAFYPFSRDHSSLGTTYQELYRWESVAASARKVLGLRYT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                      42;
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                                                                                                                                                                                                     4.2%; Score 199; DB 4; Length 390; 22.8%; Pred. No. 5.8e-10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 10, Application US/09437054A

Parent No. 611669B

GENERAL INFORMATION:
APPLICANT: Kinney, Anthony J.
TITLE OF INVENTION: Plant Alpha-Glucosidase II Homologs
TITLE OF INVENTION: Plant Alpha-Glucosidase II Homologs
TITLE OF INVENTION: Plant Alpha-Glucosidase II Homologs
CURRENT APPLICATION NUMBER: US/09/437,054A
CURRENT FILING DATE: 2001-05-14
PRIOR FILING DATE: 1998-No. 6316698ember-10
NUMBER OF SEQ ID NOS: 19
SOFTWARE: Microsoft Office 97
                                                                                                                                                                                                                                                    Indels
                                                                                                                                                                                                                                                  53; Mismatches 159;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            709 SVTAYFPRGN------WFDLF 723
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      - TAADEKGNDVRNGIYLPDKQQVWIDYY 385
    CURRENT FILING DATE: 2000-08-08
NUMBER OF SEQ ID NOS: 422
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 331
                                                                                        LENGTH: 390
TYPE: PRT
ORGANISM: Lactobacillus rhamnosus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: PRT
ORGANISM: Triticum aestivum
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Matches 45; Conservative
                                                                                                                                                                                                                                                  75; Conservative
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UNSURE
                                                                                                                                                                                                                             Best Local Similarity
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US-09-437-054A-10
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US-09-437-054A-10
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        366 DPVNFPLDKMKKFVNNLHKNGQKYVVILDPGI--STNKTYETYIRGMKHDVFLKRNGKPY 423
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     190 RPAFWTANKVGEGGDPNNKSVFEWA--HDRGLVCQTNVT-------CFLKNEKNPY 236
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               237 EVNQSLREKQLYTKSDSLDNIDFGTTPDGPSDAYIGHLDYGGGVECDALFPDWGRPDVAQ 296
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          445 FWTDEIKRFLNLLPVDGLWIDM-----NEISNFI---SSPPIPGSTLDNPPYKINNSG 494
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      495 VMLPIINKTIPPTAMHYGDI----PEYNVHNLFGYLEARVTRAALI-----KLTE-KRPFV 545
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               353 YMWKSYHPQVLVTDMRYDDYGRDPIVTQRNLHAYTLCESTRREGIVGNADSLTKFRRSYI 412
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LSRSTFSGSGKYTAHWTGDNAATWNDLVYSIPSMLDFGLFGIPMVGADICGFLGN---- 600
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        76 DLAYMGAQC-----GPFJQHFVYEAGDGLEDVVTAFSYLQGKEYENQGLNIRSAMPPKY
                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                           Query Match 7.0%; Score 335; DB 4; Length 570; Best Local Similarity 24.4%; Pred. No. 1.8e-22; Matches 122; Conservative 71; Mismatches 188; Indels 118;
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TITLE OF INVENTION: Polynuclectides, materials incorporating
TITLE OF INVENTION: them and methods for using them.
FILE REPERRORS: 11000.104301
CURRENT APPLICATION NUMBER: US/09/634,238
                                                                                                                                                                                                                                                                                                                                                                                  269 DVEYTGNRITYKVIGGIIDLYFF--AGPSPGQVVEQFTRVIG-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 331, Application US/09634238 Patent No. 6544772
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Havukkala, Ilkka J.
Bloksberg, Leonard, N.
Lubbers, Mark W.
Dekker, James
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O'Toole, Paul W.
TELECOMMUNICATION INFORMATION:
                                                                                                                                LENGTH: 570 amino acids
TYPE: amino acid
STRANDEDNESS: single
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                                                                                        INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                    TELEPHONE: 714-760-040
TELEFAX: 714-760-9502
                                                                                                                                                                                                 TOPOLOGY: linear
MOLECULE TYPE: protein
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                                                                                                                                                                                                             958 RNTFABVIGLSPGVTYYFKVFAVSHGRESKPLTAQQTTKLDAPINLQFVNETDSTVLVRW 1017
                                                                                                                                                                                                                                                                                               1018 TPPRAQITGYRLTVGLTRRGQPRQYNVGPSVSKYP-------LRNLQPAS 1060
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1179 NLHLEANPOTGVLTVSWERSTTPDITGY---RITTTPTNGQQGNSLEEVVHADQSSCTFD 1235
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  272 YTGNRITYKVI--GGIIDLYFFA----GPSPGQVVEQFTRVIGRPAPMPYWAFGFQQCRY 325
                                                                                                                                                                                                                                                          406 ----YIRGMKHDVFLKRNGKPYLGSVWPGPVYFPDFLKPSALTFWTDEIKRFLNLLPVD 460
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               508 AMHYGDIPEYNV------HNLFGYLEARVTRAAL----IKLTEKRPFVLSRSTFS 552
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               605 LCRRWIQLGAFYPFSRDHSSLGTTYQELYRWESVAASARKVLGLRYTLLPYFYTLMYEAQ 664
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   665 LNGIPIARPLFFSFPDDIKTYGISSQFLLGKGVMVSPVLKPGV---VSVTAYFPRGNWFD 721
                                                                                      GYHDVYELQSVVAGYAKAKIPLEVMWTDIDYMDAYKDFTLD--PVNFPLDKMKKFVNNLH 383
                                                                                                                ---- TNKTYET---- 405
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                                     860 ETANSVTLSDLQPGVQXNITIYAVEENQESTPVVIQQETTGTPRSDTVP-----
                                                                                                                                                                                                                                                                                                                                            461 GLWIDMNEISNFISSPPI-----PGSTLDNPPYK-----
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TITLE OF INVENTION: HYBRID CROSS-LINKING PROTEINS
NUMBER OF SEQUENCE: 14
CORRESPONDENCE ADDRESS:
ADDRESSEE: ZymoGenetics, Inc.
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4225 Roosevelt Way, N.E.
                                                                                                                                                                        384 KNGOKYVVILDPGIS-----
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COMPUTER READABLE FORM:
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CITY: Se
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                                                                                                                   64 KSVSVYLPGXXLWYDLRNGSPYKGSVSHK-----LQVSEDSIPXFQRSGTIVPRKDRFR 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        160 GDEP------QYLDLPSTATSVNIPDLLPGRKYIVNVYQISEDGEQSLILSTSQTTAP 811
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648 LRYTLLPYFYTLMYEAQLNGIPIARPLFFSFPDDIKTYGISSOFLLGKGVMVSPVLKPGV 707
                          708 VSVTAYFPRGN-WFDLFD---YTRSVTASTGRYVTLSAPPDHINVHIQEGNILAMQG--K
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Similarity 18.2%; Pred. No. 0.037;
30; Conservative 114; Mismatches 324; Indels 373;
                                                                                                                                                                                                                                                                                                               Sequence 2, Application US/08551356
Patent No. 5830700
GENERAL INFORMATION:
APPLICANT: Irani, Meher
TITLE OF INVENTION: HYBRID CROSS-LINKING PROTEINS
CORRESPONDENCES: 14
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Patentin Release #1.0, Version #1.25
                                                                                                                                                                   762 AMTIQAARKIPFHLLVVMSDCGASFGELFLDDG 794
                                                                                                                                                                                              APPLICATION NUMBER: US/08/349,762
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APPLICATION NUMBER: US/08/551,356
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FILING DATE: APPLICATION NUMBER: US/07/998,273
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1: 4225 Roosevelt Way, N.E.
Seattle
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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TELEPHONE: 206-547-8080 ext 322
TELEFAX: 206-548-2329
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2.7%; So
Best Local Similarity 18.2%; Pr
Matches 180; Conservative 114;
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REGISTRATION NUMBER: 33-246
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        INFORMATION FOR SEQ ID NO: 2: SEQUENCE CHARACTERISTICS:
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PRIOR APPLICATION DATA:
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MEDIUM TYPE: Floppy
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1179 NLHLEANPOTGVLTVSWERSTTPDITGY---RITTTPTNQQQGNSLEEVVHADQSSCTFO 1235
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     958 RNIFAEVIGLSPGVIYYFKVPAVSHGRESKPLIAQQIIKLDAPINLQFVNEIDSIVLVRW 1017
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  125 TLLSSPTINRRKILLSHPNSDL---TFSLINTIPFGFTISRKSTHD-----VLFDATPD 175
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  700 TSTSTPVTSNTVTGETTPFSPLVAISESVTEITASSFVVSWVSASDTVSGFRVEYELSEE 759
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    272 YTGNRITYKVI--GGIIDLYFFA----GPSPGQVVEQFTRVIGRPAPMPYWAFGFQQCRY 325
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  326 GYHDVYELQSVVAGYAKAKIPLEVMWTDIDYMDAYKDFTLD--PVNFPLDKMKKFVMNLH 383
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             176 PTNPNTFLIFIDQYLHLTSS-----LPGTR--AHIYGLGEHSKPTFQLAHNQTLTX
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         860 ETANSVILSDLQPGVQYNITIYAVEENQESTPVVIQQETIGTPRSDTVP-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
2.7%; Score 130.5; DB 5; Length 2446;
Best Local Similarity 18.2%; Pred. No. 0.037;
Matches 180; Conservative 114; Mismatches 324; Indels 373; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                461 GLWIDMNEISNFISSPPI-----PGSTLDNPPYK-------
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: SYSTEM: PC-DOS/MS-DOS
SOTTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US93/12687
FILING DATE: CLASSIFICATION DATA:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/998,271
FILING DATE: 31-DEC-1992
ATTONNEY/AGENT INFORMATION:
NAME: PARKET INFORMATION:
REFRENCE/COCKET NUMBER: 92-26PC
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION OF 2:
SEQUENCE CHRAACTERISTICS:
LENGTH: 206-547-8080 ext 322
INFORMATION FOR SEQ ID NO: 2:
SEGUENCE CHRAACTERISTICS:
LENGTH: 2466 amino acids
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ; TYPE, amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
PCT-US93-12687-2
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đ	1279TDSSIGLRWTPLNSSTIIGYRITVVAA	1305
ò	E G	721
qq	1306 GEGIPIFEDFVYSSVGYYTVTGLEPGIDYDISVITLINGGE 1346	1346
ò	722 LFDYTRSVTASTGRYVTLSAPPDHINVHIQEGNILAMQGKAMTTQ 766	992
qc	1347SAPTILIQQTAVPPPIDLRFTNIGPDTMRVTWAPPPSIDLINFLVRYSPVKNEE 1400	1400
ઠે	767 AARKTPFHLLVVMSDCGASFGELFLDDGVEVTMGVNRGKWTFVKFI	812
qq	1401 DVAELSISPSDNAVVLTNLLPGTEYVVSVSVYEQHESTPLRGRQK 1446	1446
ò	813 AASAKQTCIITSDVVSGEFAVSQKWVIDKVTILGLRKGTKINGYTVRTGAVTRKGDKSKL 872	872
Ω̈́	1447 TGLDSPTGIDFSDITANSFTVHWIAPRATITGYRIRHHPEHFSGRPREDRVPHSRNSI	1504
ζ	873 KSTPDRKGEFIVAEISGLNLLLGRE 897	
qa	1505 TLINLTPGTEYVSIVALNGREESPLLIGQQ 1535	
Searcl Job t:	Search completed: October 27, 2003, 10:26:47 Job time : 22.3223 secs	

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                                 GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
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Maximum Match 100%
Listing first 45 summaries
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Gapop 10.0 , Gapext 0.5
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Maximum DB seq length: 200000000
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4768
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution. SUMMARIES

		Description		Common buckwheat a	Buckwheat alpha-ql	Common buckwheat a	Buckwheat alpha-ql	Barley alpha-gluco	Potato alpha-gluco	Mouse ischaemic co	Endomyces fibulige	Aspergillus oryzae
		ID		AAU97731	ABB09151	AAU97732	ABB09152	AAW59040	AAY51670	ABB57174	AAY49895	AAW15191
		DB	-	23	23	23	23	19	21	23	20	18
		re Match Length DB I		901	901	901	901	877	682	953	963	985
do.	Query	Match		60.5	60.5	59.7	59.7	50.8	48.2	31.4	29.9	29.6
		Score		2884	2884	2847	2847	2422.5	2297.5	1499	1427.5	1410.5
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Glycosyltransferas Aspergillus niger An enzyme with sug Glucoamylase encod Sequence of glucoa Human hST protein Human sucrase isom Novel human diagno Alpha galactosidas Human NOV11b prote Human NOV11b prote Human NOV11b prote Human nov10hydrate Carbohydrate-assoc Soybean alpha-gluc Peteto alpha-gluc Peteto alpha-gluc Soybean alpha-gluc Fuctato alpha-gluc Fuctato alpha-gluc Fuctato alpha-gluc Fuctato alpha-gluc Futato alpha	Drosophila melanog Plasmid pNOV4831 m MalA fusion proteis S. solfataricus ma Plasmid pNOV4839 m Human ORFX ORF259 O Alpha-glucosidase Alpha-le glucosidase Alpha-le glucomas Human mDDT SEQ ID Novel human enzyme Human diagnostic a M.vulgaris anglanostic a Alpha-1,4-glucan l	le #1. dase gene, and a glucosidase -
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10 1401.5 111 1401.5 112 1375.5 114 1375.5 115 1318.5 116 1318.5 1173.6 1173.6 1173.6 1173.6 1173.6 1173.6 1173.6 1173.6 1173.6 1173.6 1173.6 1173.6 1173.6 1173.6 1173.6 1173.6 1173.6 1173.6 1173.6 1173.6 1173.6 1173.6 1173.6 1173.6 1173.6 1173.6 1173.6 1173.6 1173.6 1173.6 1173.6 1173.6 1173.6 1173.6 1173.6 1173.6 1173.6 1173.6 1173.6 1173.6 1173.6 1173.6 1173.6 1173.6 1173.6 1173.6 1173.6 1173.6 1173.6 1173.6 1173.6 1173.6 1173.6 1173.6 1173.6 1173.6 1173.6 1173.6 1173.6 1173.6 1173.6 1173.6 1173.6 1173.6 1173.6 1173.6 1173.6 1173.6 1173.6 1173.6 1173.6 1173.6 1173.6 1173.6 1173.6 1173.6 1173.6 1173.6 1173.6 1173.6 1173.6 1173.6 1173.6 1173.6 1173.6 1173.6 1173.6 1173.6 1173.6 1173.6 1173.6 1173.6 1173.6 1173.6 1173.6 1173.6 1173.6 1173.6 1173.6 1173.6 1173.6 1173.6 1173.6 1173.6 1173.6 1173.6 1173.6 1173.6 1173.6 1173.6 1173.6 1173.6 1173.6 1173.6 1173.6 1173.6 1173.6 1173.6 1173.6 1173.6 1173.6 1173.6 1173.6 1173.6 1173.6 1173.6 1173.6 1173.6 1173.6 1173.6 1173.6 1173.6 1173.6 1173.6 1173.6 1173.6 1173.6 1173.6 1173.6 1173.6 1173.6 1173.6 1173.6 1173.6 1173.6 1173.6 1173.6 1173.6 1173.6 1173.6 1173.6 1173.6 1173.6 1173.6 1173.6 1173.6 1173.6 1173.6 1173.6 1173.6 1173.6 1173.6 1173.6 1173.6 1173.6 1173.6 1173.6 1173.6 1173.6 1173.6 1173.6 1173.6 1173.6 1173.6 1173.6 1173.6 1173.6 1173.6 1173.6 1173.6 1173.6 1173.6 1173.6 1173.6 1173.6 1173.6 1173.6 1173.6 1173.6 1173.6 1173.6 1173.6 1173.6 1173.6 1173.6 1173.6 1173.6 1173.6 1173.6 1173.6 1173.6 1173.6 1173.6 1173.6 1173.6 1173.6 1173.6 1173.6 1173.6 1173.6 1173.6 1173.6 1173.6 1173.6 1173.6 1173.6 1173.6 1173.6 1173.6 1173.6 1173.6 1173.6 1173.6 1173.6 1173.6 1173.6 1173.6 1173.6 1173.6 1173.6 1173.6 1173.6 1173.6 1173.6 1173.6 1173.6 1173.6 1173.6 1173.6 1173.6 1173.6 1173.6 1173.6 1173.6 1173.6 1173.6 1173.6 1173.6 1173.6 1173.6 1173.6 1173.6 1173.6 1173.6 1173.6 1173.6 1173.6 1173.6 1173.6 1173.6 1173.6 1173.6 1173.6 1173.6 1173.6 1173.6 1173.6 1173.6 1173.6 1173.6 1173.6 1173.6 1173.6 1173.6 1173.6 1173.6 1173.6 1173.6 1173.6 1173.6 1173.6 1173.6 1173.6	708 5 708 5 84 681.5 85 67.5 87 681.5 87 681.5 87 681.5 87 681.5 87 681.5 87 681.5 87 681.5 88 645.5 88	Common buckwh Fagopyrum esc Fagopyrum esc JP2002065273-05-MAR-2002. 31-AUG-2000; 31-AUG-2000; 31-AUG-2000; 4 AUG-2000; AL-AUG-2000; AL-
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tes 559; Conserv
                 LLVGRNFKL
                                                                             ABB09151 standard;
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         The invention relates to a recombinant vector containing alpha-glucosidase gene derived from buckwheat. A transformant containing the recombinant vector can be used for preparing alpha-glucosidase by culturing the transformant and isolating alpha-glucosidase from the culture. This sequence represents a buckwheat alpha-glucosidase protein.
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                                                                                                                                                           14 LLLAATLLFCSLFVV-----SESGEVVGYGYRVVRAKVDSSS-NTLTAFLKLINASSL
                                                                                                                                                                                        YGPDIQLLSITASLESNDRLRVRITDAKHRRWEIPDNILHR-----HQPPPPPHSLSS
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                                                                                                60.5%; Score 2884; DB 23; Length 901; 61.5%; Pred. No. 4.5e-237;
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                                                                                                                                                                    Buckwheat; alpha-glucosidase; enzyme; Fagopyrum esculentum Moeench;
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                                                                                                                            Buckwheat alpha-glucosidase protein SEQ ID NO:1
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Fagopyrum esculentum Moeench.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       590 TTTEELCRRWIQLGAFYPFSRDHSDNLSEPQELTQWGSVTESARKVLGLRYRLLPYYYTL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    8 LALGILLVFLLQYLVAGISTSENDPEGVIGYGYKVKSVKVDSGTRRSLTALPQLVKNSSV
                                                                                                                                                                                                                                                                                                                                                                                                                                  YGPDIQLLSITASLESNDRLRVRITDAKHRWEIPDNILHR-----HQPPPPPHSLSS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  181 TFLIFIDQYLHLTSSLPGTRAHIYGLGEHSKPTFQLAHNQTLTMRAADIPSSNPDVNLYG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SHPFYMDVRSSPVAGSTHGVLLLNSNGMDVBYTGNRITYKVIGGIIDLYFFAGPSPGQVV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EQFTRVIGRPAPMPYWAFGFQQCRYGYHDVYELQSVVAGYAKAKIPLEVMWTDIDYMDAY
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                470 DSPLDNPPYVINNSGGRRPINEKTIPVSSVHYGNVSDYNVHNLYGYLEATATNVALKKVT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           600 NITEELCRRWIQLGAFYPFSRDHSSLGTTYQELYRWESVAASARKVLGLRYTLLPYFYTL
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                                                                                                                                                                                                                                                                                                               Length 901;
  and
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A recombinant vector containing alpha-glucosidase gene, a transformant useful for preparation of alpha-glucosidase
                                                                                                                                                                                                                                                                                                          ch 59.7%; Score 2847; DB 23; Il Similarity 60.7%; Pred. No. 6.6e-234; 552; Conservative 128; Mismatches 185;
                                                                        2; Page 8-9; 18pp; Japanese,
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DSPLDNPPYVINNSGGRRPINEKTIPVSSVHYGNVSDYNVHNLYGYLEATATNVALKKVT 529
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                                                                                     EQFTRVIGRPAPMPYWAFGFQQCRYGYHDVYELQSVVAGYAKAKIPLEVMWTDIDYMDAY 360
                                                                                                    KDFTLDPVNPPLDKMKKFVNNLHKNGQKYVVILDPGISTN-KTYETYIRGMKHDVFLKRN 419
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        836 KWVIDKVTILGLRKGTKINGYTV----RTGAVTRKGDKSKLKSTPDRKGEFIVAEISGLN 891
172 VGLVFKDQYIQLSSSLPADRSNLYGIGEHTKPTFRLARNQTLTLWNADIASYNVDLNLYG 231
                                                                                                                                                                                                  GKPYLGSVWPGPVYFPDFLKPSALTFWTDEIKRFLNLLPVDGLWIDMNEISNFISSPPIP 479
                            SHPFYMDVRSSPVAGSTHGVLLLNSNGMDVEYTGNRITYKVIGGIIDLYFFAGPSPGQVV
                                               GSTLDNPPYKINNSGVMLPIINKTIPPTAMHYGDIPEYNVHNLFGYLBARVTRAALIKLT
                                                                                                                                                                                                                                                                                                                 EKRPFVLSRSTFSGSGKYTAHWTGDNAATWNDLVYSIPSMLDFGLFGIPMVGADICGFLG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                FDLFDYTRSVTA-STGRYVTLSAPPDHINVHIQEGNILAMQGKAMTTQAARKTPFHLLVV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MSDC--GASFGELFLDDGVEVTMGVNRGKWTFVKFIAASAKQTCI-ITSDVVSGEFAVSQ
                                                                                                                                                                                                                                                                                                                                                                          NTTEELCRRWIQLGAFYPFSRDHSSLGTTYQELYRWESVAASARKVLGLRYTJLPYFYTL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Alpha-glucosidase, barley, starch grain hydrolysis, alpha-amylase,
glucoamylase, industry, germplasm, hydrolytic enzyme.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Barley alpha-glucosidase protein.
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                             YGPDIQLLSITASLESNDRLRVRITDAKHRRWEIPDNILHR-----HQPPPPPPHSLSS 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LYRILLSSPITNRRKILLSHPNSDLIFSLINTIPFGFIISRKSTHDVLFDA-TPDPINPN 180
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                KWVIDKVTILGLRKGTKINGYTV----RTGAVTRKGDKSKLKSTPDRKGEFIVAEISGLN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 8 LALGILLVFLLQYLVAGISTSENDPEGVIGYGYKVKSVKVDSGTRRSLTALPQLVKNSSV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The present sequence represents an alpha-glucosidase isolated from buckwheat (Fagopyrum esculentum Moeench). The alpha-glucosidase gene can be used for the preparation of alpha-glucosidase derived from
                                                                                                                                                                                                                                                                                     Buckwheat; alpha-glucosidase; enzyme; Fagopyrum esculentum Moeench;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      44;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Local Similarity 60.7%; Pred. No. 6.6e-214; included 552; Conservative 128; Mismatches 185; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        59.7%; Score 2847; DB 23; 60.7%; Pred. No. 6.6e-234;
                                                                                                                                                                                                                                                        protein SEQ ID NO:2
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                                                                                                                                                                                                                                                                                                                                                                        1..31
/label= signal
32..901
/label= alpha_glucosidase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 buckwheat-derived alpha-glucosidase
                                                                                                                                                                                                                                                                                                                                                           Location/Qualifiers
                                                                                                                                                                      ABB09152 standard; Protein; 901 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (NISO ) NIPPON SHOKUHIN KAKO
                                                                                                                                                                                                                                                          Buckwheat alpha-glucosidase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     31-AJG-2000; 2000JP-0262102
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                                                                                                                                                                                                                               (first entry)
                                                                    LLLGREFKL 900
                                                                                      Fagopyrum esculentum.
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Matches
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This invention describes a novel potato alpha-glucosidase (I). (I) is used to produce transgenic plants (or plant or bacterial cells) that used to produce transgenic plants (or plant or bacterial cells) that produce starch with modified degrees of branching, amplose/amplopertin cartio, phosphate content, starch granule size and/or sidechain structure, and thus altered physical and chancial properties. This starch is used for all usual applications, particularly in preparation of foods. Dackaging materials and disposable articles, but also for hydrolysis to glucose (for manufacture, in adhesives; for treating textiles; for soil paper/pulp manufacture; in adhesives; for treating textiles; for soil catabilization; as wenting agent in pharmaceuticals and cosmetics; as additive for rubber, building materials, leather and in casting; as floctulant for soil or coal slurries; and in polymers, as simple filler or reactive component, e.g. in polymersen, we simple filler produced using plants that contain (I) are easily hydrolyzed, reducing the requirement for expensive enzymes. This sequence represents the
LVVMSDCGASFGELFLDDGVEVTMGVNRGK#TFVKF--IAASAKQTCIITSDVVSGEFAV 833
                                                                                                                                                                     SQKWVIDKVTILGLRKGTKINGYTVRTGAVTRKGDKSKLKSTPDRKGBFIVAEISGLNLL 893
                                                                                                                                                                                                                                                                SRTLVISKVVLMGHRSPAAPKKLTVHVNSAEVEASSSAGTRYQNAGGLGGVAHIGGLSLV 864
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Alpha-glucosidase; potato; transgenic plant; starch; branching; amylose; amylogectin; granule size; sidechain; food; packaging; hydrolysis; paper; pulp; adhesive; soil stabilization; wetting agent; plant protection; fertilizer.
                                                                                                      686 AĞRWYRLYDYSLAVATRTGKHYRLPAPADTVNVHLTGĞTILPLQQSALTTSRARRTAFHL
                                                               RGNWFDLFDYTRSVTASTGRYVTLSAPPDHINVHIQEGNILAMQGKAMTTQAARKTPFHL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 New nucleic acid encoding potato alpha-glucosidase, used to produce transgenic plants that contain modified starch
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Potato alpha-glucosidase protein fragment.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAY51670 standard; Protein; 682
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                                                                                                                                                                                                                                                                                                              LGREFKL 900
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VGEEFEL 871
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                                                                                                                                                                                                                                                                               This sequence represents a novel barley alpha-glucosidase protein. Recombinant alpha-glucosidase can be used to increase the rate of starch grain hydrolysis when used together with alpha-amylase or can supplement glucoamylase in industrial starch hydrolysis systems. Useful DNA sequence characteristics from this enzyme can be identified which can be used as hybridisation probes for identifying germplasm with high levels of efficient hydrolytic enzymes.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          267
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  119 LSSLYRTLLSSPTTNRRKILLSHPNSDLTFSLINTTPFGFTISRKSTHDVLFDATPDPTN 178
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          55; Gaps
                                                                                                                                                                   DNA encoding barley alpha-glucosidase protein - useful for producing recombinant protein to increase rate of starch grain hydrolysis when used with alpha amylase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 877;
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al Similarity 53.6%; Pred. No. 1.3e-197;
486; Conservative 132; Mismatches 234; Indels
                          (WISC ) WISCONSIN ALUMNI RES FOUND
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                                                               Skadsen RW, Tibbot BK,
                                                                                                        WPI; 1998-347329/30
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                                                                                                                      2002-034733/04
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 WO200188188-A2
                                                                                                  shikawa K,
                     22-NOV-2001
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                                                                                        230 PSSNPDVNLYGSHPPYMDVRSSPVAGSTHGVLLLNSNGMDVEYTGNRITYKVIGGIIDLY
                                                                                                           PSQHHPIQLHRPPALHRGYSFRYFAGVSHGVLLLSSNGMDIVYTGDRISYKVIGGLIDLY
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 potato alpha-glucosidase protein described in the method of the
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                                                  Length
                                                                  418; Conservative 109; Mismatches 144; Indels
                                                  21;
                                                48.2%; Score 2297.5; DB 2.62.0%; Pred. No. 4.1e-187;
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The present invention describes a method for examining ischaemic conditions, comprising measuring the expression levels of particular genes (I) in a test sample or determining the expression profile of a gene group in the sample comprising genes selected from (I). The method is useful for examining the ischaemic condition (e.g. compression expression levels of particular genes (ABI92202 to ABI99912, encoding the protein sequences in ABB57020 to ABB9912, encoding the protein sequences in ABB57020 to ABB97314) or by determining the expression profile of a gene group comprising these genes are used as an indicator when screening for ischaemic condition-improving drugs or therapeutics for ischaemic condition improving drugs or therapeutics for ischaemic condition related sequence, which are used in the exemplification of the present invention.
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                                                                                                                                                                                                                                 Examining the ischemic condition (e.g. occlusive ischemia) by measuring expression levels of particular genes defined in the specification or by determining the expression profile of a gene group comprising these
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31.4%; Score 1499; DB 23;
Best Local Similarity 37.9%; Pred. No. 1.3e-118;
Matches 336; Conservative 136; Mismatches 317;
Takahashi Y, Nagata T,
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98 YGYDFDYLNLSVEYQSDDRLNVHI
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                      GDIPEYNVHNLFGYLEARVTRAALIKLTEKRPFVLSRSTFSGSGKYTAHWTGDNAATWND 571
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                                                                                                                                                                                  744 LLWGPALLITPVLEPGKTEVTGYFPKGTWYNMQVVSVDSLGTLPSPSSASSFRSAVQSKG 803
HXQVPFDGMWLDMNEPSNFVRGSQQGCPNNELENPPY---XPGVVGGILQAATICASSHQ 563
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The present sequence represents Endomyces fibuliger (also called Saccharomycopsis fibuligera) glucoamylase GLA2. The invention describes the recombinant GLA2 enzyme, which is useful for hydrolysing carbohydrate-containing materials, especially materials containing rice carbohydrates. The glucoamylase is used to produce glucose and alcohol from starch containing raw materials. GLA2 is useful for hydrolysing
                                                                                                                                                                                                                     FLSTHYNLHNLYGLTEALASSRALVKTRGTRPFVISRSTFSGHGRYAGHWTEDVRTSWEH
                                                                                ESLAV-LEHGAYTLVTF---SAKONTIVNKLVRVTKEGAELQ---LKEVTVLGVA----
                                                                   LVYSIPSMLDFGLFGIPMVGADICGFLGNTTEELCRRWIQLGAFYPFSRDHSSLGTTYOE
                                                                                                                                                            FLIGKGVMVSPVLKPGVVSVTAYFPRGNWFDL-------FDYTRSVTASTG
                                                                                                                                                                                                         RYVTLSAPPDHINVHIQEGNILAMQGKAMTTQAARKTPFHLLVVMSDCGASFGELFLDDG
                                                                                                                                                                                                                                                      VEVTMGVNRGKWTFVKFIAASAKQTCIITSDV-VSGEFAVSQKWVIDKVTILGLRKGTKI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Endomyces fibuliger; glucoamylase; GLA2; hydrolysis; carbohydrate; glucose; alcohol; starch; leguminous plant; cooked; oleaginous plant; roasted; cereal; soya; wheat; rice.
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                                                                                                                                                                                                                                                                                                  NGYTVRTGAVTRKGDKSKLKSTPDRKGEFIVAEISGLNLLLGREFKL 900
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                                                                                                                                                                                                                                                                                                                                                                                                                                                    Endomyces fibuliger glucoamylase GLA2 protein.
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                                                                                                                                                                                                                                                                                                                                                                                 AAY49895 standard; Protein; 963
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carbohydrate containing materials e.g. mixtures of a source of proteins and a source of carbohydrates, especially a mixture of leguminous plant or of a cooked oleaginous plant and of a cooked or roasted cereal source e.g. a mixture of soya or cooked beans and of cooked or roasted wheat or rice.
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                                                                                                                                                                                                                           Query Match 29.9%; Score 1427.5; DB 20; Length 963; Best Local Similarity 34.7%; Pred. No. 1.8e-112; Matches 343; Conservative 165; Mismatches 310; Indels 171;
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461

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249 YKVGGQNKSHIIVKSSEAEPSQEYVSYSHGVFLRNAHGQEILLRDQKLIWRTLGGSVDLT 308
                                -----THGVLLLNSNGMDVEYTGNRITYKVIGGIIDLY 289
                                                                                                                                                     549 GAASQSAAASSTTTSAPYLRTTPTPTPGVRNVDHPPPYVINHVQPGHDLSVHAISPNSTHSDG 608
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489 VWYDMAEVSSFCVGSCGTGNLSMNPAHPPFALPGEPGNVVYDYPEGFNITNATEAASASA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SITASLESNDRLRVRIT----DAKHRRWEIPDNILHRHOPPPPPPPHSLSSLYRTLLSSPT 131
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 -----LSEELVPRPK 141
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         142 ASQN----ASVPQSDFVVSWSNEPSFNFKVIRKATGDVLFN-----TKGST-LVYENQFIE 192
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           192 LTSSLPGTRAHIYGLGEHSKPTFQLAHNQTLTMRAADIPSSNP-DVNLYGSHPFYMDVRS 250
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   75
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LVAGISTSENDPEGV - - - - IGYGYKVKSVKVDSGTRRSLTALPQLVKN - SSVYGPDIQLL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TNRRKILLSHPNSDLTFSLINTTPFGFTISRKSTHDVLFDATPDPTNPNTFLIFIDQYLH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    tch 29.6%; Score 1410.5; DB 18; Length 985; al Similarity 34.3%; Pred. No. 5.2e-111; 333; Conservative 153; Mismatches 291; Indels 195; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Aspergillus oryzae contains two novel enhancer elements: one designated "enhancer-B") corresponds to the consensus sequence CGGNNATITA and the other (designated "enhancer-C") is of sequence CCAATCAGCGT. By inserting at least one of the enhancer elements into a promoter region which is functional in fungi, the activity of the promoter is enhanced Using such improved promoters, a gene of interest can be expressed efficiently in transformed fungi. The present sequence is encoded by the agdA gene.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Fungal DNA enhancer element - used to transform other host fungus
e.g Aspergillus oryzae, to produce large quantities of a gene
product
                                                                                                                                                                                                                                                                                                                                                                                                                                   Fungus; fungal; enhancer element; promoter; recombinant protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The promoter region of the alpha-glucosidase (agdA) gene of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TLTVEYQAKDRLNIQIVPTYFDASNASWYI ------
: ::|| ::||| 937 ENNTIF----VTGLDDQTEDGAFAKQFKL 961
                                                                        877 DRKGEFIVAEISGL -----NLLLGREFKL 900
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Disclosure; Page 14-19; 25pp; Japanese.
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                                                                                                                                                                                                                                          AAW15191 standard; Protein; 985
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(OZEK-) OZEKI KK.
                                                                                                                                                                                                                                                                                                                                         (first entry)
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Best Local Similarity
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                                                                                                                                                                                                                                                                                          AAW15191;
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29;
                                       QELYRWESVAASARKVLGLRYTLLPYFYTLMYEAQLNGIPIARPLFFSPPDDIKTYGISS 689
                                                                            785
666 WSMYYSISQALSFSLFGIPMFGADTCGFNGNSDEELCNRWMQLSAFFPFYRNHNELSTIP 725
                                                                                                                                          HINVHIQEGNILAMQGKAMTTQAARKTPFHLLVVMSDCGASFGELFLDDGVEV----TMG 800
                                                                                                                                                                                                                                                                           VN------RGKWTFVKFIAASAKQTCIITSDVVSGEFAVSQKWVIDKVTILGLR 848
                                                                                                                                                                                                                                                                                                              -----KERNPLANVIVLGVN 936
                                                                                                                  QFLLGKGVMVSPVLKPGVVSVTAYFP---RGN-WFDLFDYTR-SVTASTGRYVTLSAPPD 744
                                                                                                                                                                                                                                  844 HIPVYVRGGNILPMGEPALTTREARQTPWALLAALGSNGTASGQLYLDDGESIYPNATLH 903
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                                                                21 LVAGISTSENDPEGV----IGYGYKVKSVKVDSGTRRSLTALPQLV-KNSSVYGPDIQLL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DNA encoding truncated variants of Aspergillus glucosyltransferase is claimed. Deletion from the N- or C-terminal reduces Grase extivity of the protein. Specifically, glucoamylase with reduced Grase activity can be prepared. The full-length Grase structural gene was isolated as a 4.3kb Sphl fragment from chromosomal DNA of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    29,4%; Score 1401.5; DB 14; Length 985; 33,4%; Pred. No. 3.le-110;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Glucoamylase prepn. with reduced glucosyl-transferase activity using microorganism transformed using plasmids including DNA fragments having deletion of N-end or C-end of Aspergillus glucosyl-transferase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Glase, glucoamylase, GAase, recombinant production; truncated, N-terminal deletion; C-terminal deletion.
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                                                                                                                                                                                                                                                                                                                                                        849 K---GTKINGYTVRTGAVT 864
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N-PSDB; AAQ50982.
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| SWYDMSEVSSFCVGSCGTGNLTLNPAHPSFLLPGEPGDIIYDYPEAFNITNATEAASAS 545
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      289 YFFAGPSPGQVVEQF-TRVIGRPAPMPYWAFGFQQCRYGYHDVYELQSVVAGYAKAKIPL 347
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYETYIRGMKHDVFLKR-NGKPYLGSVWPGPVYFPDFLKPSALTFWTDEIKRFLNLLPVD 460
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            191 HLTSSLPGTRAHIYGLGEHSKPTFQLAHNQTLTMRAADIPSSNP-DVNLYGSHPFYMD-- 247
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         -----VRSSPVAGS-----THGVLLLNSNGMDVEYTGNRITYKVIGGIIDL 288
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         306 TEYSGPAPADVTRQYLTSTVGLPAMQQYNTLGFHQCRWGYNNWSDLADVVANFEKFEIPL 365
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              348 EVMWIDIDYMDAYKDFILDPVNFPLDKMKKFVNNLHKNGQKYVVILDPGI----STNK 401
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         47 LIANI ---- DDPQAADAQSVCPGYKASKVQHNS---RGFTASLQLAGRPCNVYGTDVESL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   76 SITASLESNDRLRVRI ----TDAXHRRWE-IPDNILHRHQPPPPPPPHSLSSLYRTLLSSP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                       29.4%; Score 1401.5; DB 14; Length 985; 33.4%; Pred. No. 3.1e-110; tive 160; Mismatches 287; Indels 205; Gaps
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                                                                                                                                                                                              Prepn. of glucosyl:transferase - using glucosyl:transferase gene
from recombinant DNA of Aspergillus niger
                                                                                                                                                                                                                                                                                          Glycosyltransferase was prepared from a culture of A. niger containing recombinant DNA encoding GTase (AAQ50468). GTase can lobtainted effectively using this method and in larger quantities. The probes (AAQ50466-67) were used to detect transformants containing the GTase gene.
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92JP-0101760
                                       92JP-0101760
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               327; Conservative
                                                                            (AMAN ) AMANO PHARM KK (UOZU/) UOZUMI T.
                                                                                                                                      WPI; 1993-364282/46.
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27-MAR-1992;
                                       27-MAR-1992;
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N-PSDB; AAX04639.
                                                                                                                                                                                                                                                                                                                                            922 AA;
                                                                            Acremonium sp
                                                                                                                                                                         (KIRI ) KIRIN
                                                                                               JP11009276-A.
             09-APR-1999
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                                                                                    -----SVSQSDLFVSWSNEPSFNFKVIRKATGDALF----STEGTVLVYENOFI
                                                                                                                 190 EFVTALP-EEYNLYGLGEH1-TQFRLQRNANLTIYPSD--DGTPIDQNLYGQHPFYLDTR
                                                                                                                                                        246 YYKGDRQNGSYIPVKSSEADASQDYISLSHGVFLRNSHGLEILLRSQKLIWRTLGGGIDL
                                                                                                                                                                               YFFAGPSPGQVVEQF-TRVIGRPAPMPYWAFGFQQCRYGYHDVYELQSVVAGYAKAKIPL
                                                                                                                                                                                          EYIWIDIDYMHGYRNFDNDQHRFSYSEGDEFLSKIHESGRYYVPIVDAALYIPNPENASD
                                                                                                                                                                                                                                                                  426 AYATYDRGAADDVFLKONPDGSLYIGAVWPGYTVFPDWHHPKAVDFWANELVIWSKKVAFD
                                                                                                                                                                                                                                                                                                                                             AGASSQAAATATTSTSVSYLRTTPTPGVRNVEHPPYVINHDQEGHDLSVHAVSPNATHV
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SITASLESNDRLRVRI----TDAKHRRWE-IPDNILHRHQPPPPPPPPHSLSSLYRTLLSSP
                                                                                                      HLTSSLPGTRAHIYGLGEHSKPTFQLAHNQTLTMRAADIPSSNP-DVNLYGSHPFYMD--
                                                                                                                                           -----VRSSPVAGS-----THGVLLLNSNGMDVEYTGNRITYKVIGGIIDL
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                                                100 TLSVEYQDSDRLNIQILPTHVDSTNASWYFLSENLV-----PRPKASLNA-
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AAW88044 standard; Protein; 922

AAW88044;

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The present sequence represents a sugar transferase protein of Acremonium sp. 54G13. The protein preferably catalyses the glucose transfer of an alpha-1 right arrow 3 bond or the glucose transfer of an alpha-1 right arrow 3 and an alpha-1 right arrow 4 bond to a sugar receptor by reacting with a substrate selected from starch and its decomposition
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     217
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                273 TGNRITYKVIGGIIDLYFFAGPSPGQVVEQFTRVIGRPAPMPYWAFGFQQCRYGYHDVYE 332
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LOSVVAGYAKAKI PLEVMWTDI DYMDA YKDFTLDPVNF PLDKMKKF VNNLHKNGOKYVVI 392
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   VDPAIAYVES-GTLDRGLDDDVFLLRSNGSVWLGVVWPGVTVFPDWFAENITQYWNNEFA 413
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FNITRADIDEVLEDISA-----ASIVFESQYLRLRISIP-IDPYLYGLGAHNDPMRLES
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       39 GYKVKSVKV-DSGTRRSLTALPQLVKNSSVYGPDIQLLSITASLESNDRLRVRITDAKHR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FTISRKSTHDVLFDATPDPTNPNTFLIFIDQYLHLTSSLPGTRAHIYGLGEHSKPTFQLA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Matches 324; Conservative 140; Mismatches 311; Indels 169;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            New sugar transferase gene and enzyme - useful for catalysing transfer of an alpha-1 right arrow 3 bond to a sugar receptor
                                                                   transferase
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                                                      Acremonium sp. $4013; glucose transfer; sugar sugar receptor; starch.
An enzyme with sugar transferase activity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Claim 1; Pages 13-17; 20pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                         97JP-0163110
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                                                                                                              ICGFLGNTTEELCRRWIQLGAFYPFSRDHSSLGTTYQELYRWESVAASARKVLGLRYTLL 653
                                                                                                                                                  PYFYTLMYEAQLNGIPIARPLFFSFPDDIKTYGISSQFLLGKGVMVSPVLKPGVVSVTAY 713
                                                                                                                                                              FPRGNWFDLFDY--TRSVTASTGRYVTLSAPPDHINVHIQEGNILAM-QGKAMTTQAARK 770
                                                                                                                                                                                               TPFHLLVVMSDCGASFGELFLDDGVEVTMGVNRGKWTFVKFIAASAKQTCIITSDVVSGE 830
                                                                                                                                                                                                                                    --IPGSTL 483
                                         DNPPYKINNSGVMLP-----IINKTIPPTAMHYGDIPEYNVHNLFGYLEARVTRAAL 535
                                                           LYPEYAIHNKAAFRDDWNADKGGISNKTVNTNVIHONGLAEYDVHNLYGAMMSSASRDAM 593
                                                                            -IKLTEKRPFVLSRSTFSGSGKYTAHWTGDNAATWNDLVYSIPSMLDF-GLFGIPWVGAD 593
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The expression cassette may contain a regulon (R), a signal peptide
                                                                                                                                                                                                                                                                                                                                                                                                       Schwanniomyces yeast cells; expression cassette; glucoamylase; marker gene; regulon; signal peptide; terminator; autonomously replicating sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Transformed Schwanniomyces yeast cells - contg. an expression cassette contg. regulon, DNA coding for foreign protein and
                                                                                                                                                                                                                                                                        FAVSOKWVIDKVTILGLR-KGTKINGYTVRTGAVTRKGDKSKLK 873
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Disclosure; Fig 2B(1-9); 59pp; English
                                                                                                                                                                                                                                                                                                                         AAR07575 standard; protein; 958 AA
                                                                                                                                                                                                                                                                                                                                                                                       Glucoamylase encoded by GAM1 gene.
                                                                                                                                                                                                                                                                                                                                                                                                                                           Schwanniomyces occidentalis
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                                                                                                                                                                                                                                                                                                                                                            (updated)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    262 LLNSNGMDVEYTGNRITYKVIGGIIDLYFFAGPSPGQVVEQFTRVIGRPAPMPYWAFGFQ 321
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           OCRYGYHDVYELQSVVAGYAKAKIPLEVMWTDIDYMDAYKDFTLDPVNFPLDKMKKFVNN 381
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              603 EELCRRWIQLGAFYPFSRDHSSLGTTYQELYRWESVAASARKVLGLRYTLLPYFYTLMYE 662
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            64
                                                                                                                                                                                                                                                                                                                                                                                                 R, S, F and T may be modified by insertions, deletions or substitutions such that biological activity is retained or improved.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               37 -----GYGYKVKSVKVDSGTRRSLTALPQLVKNSSVYGPDIQLLSITASLESNDRLRVR
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                                                                                                                                             S contains all or part of one of the sequences represented in AAQ06383-87.
Fis e.g. a cellulase, interleukin, insulin-like-growth factor, interferon etc.
T is pref. all or part of the terminator of this sequence (bp 2875-3120).
GAM1 acts as selective marker for the vector carrying the expression
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
S), a foreign protein sequence (F) and a terminator (T)
and/or S and/or T are derived from the glucoamylase gene
sequence (S), a foreign protein sequence (F) and a terminator (T) of which R and/or S and/or T are derived from the glucoamylase gen of S. occidentalis.
R is pref. a 1.3 kb BamHI-PvuII fragment (bases -1 to -320 of this
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Cuery Match 28.8%; Score 1375.5; DB 11; Length 958; Best Local Similarity 33.4%; Pred. No. 4.9e-108; Matches 332; Conservative 142; Mismatches 316; Indels 203;
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WFDLFDYTRSVTASTGRYVTLSAPPDHINVHIQEGNILAMQGKAMTTQAARKTPFHLLVV
                                                                                                                        LDNDGKAQGSLYLDDGESLVVDSS-----LLVSFSVSDNTLSASP--SGDYKADQP--
                               AQINGIPIARPLFFSFPDDIKTYGISSOFLLGKGVMVSPVLKPGVVSVTAYFPRGN----
                                                                                                         779 MSDCGASFGELFLDDGVEVTMGVNRGKWTFVKFIAASAKQTCIITSDVVSGEFAVSQKWV
                                                SHTTGLPILRAFSWQFPNDRSLSGVDNQFFVGDGLVVTPVLEPGVDKVKGVFPGAGKEEV
                                                                                                                                                                                                                                                                                    genomic DNA of Schwanniomyces
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 958;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                     G.
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28.8%; Score 1374; DB 9;
Best Local Similarity 33.8%; Pred. No. 6.6e-108;
Matches 328; Conservative 142; Mismatches 315;
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                                                                                                                                                                                                                                                                                   Sequence of glucoamylase encoded by castellii.
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(first entry)
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                                                                                                                                                                   LANVTILGV -----
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starch to ethanol
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12-DEC-1990
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AAW74090
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This sequence is the human hSI protein. The invention relates to purified proteins (1) that bind specifically to at least one of the gastro-intestinal (31) tract receptors human intestinal castro-intestinal cas
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                                                                                                                                                                                                                Gastro-intestinal transport receptor; binding protein; hSI; HPT1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         New proteins that bind specifically to receptors in the gastro-intestinal tract and related nucleic acid - chimaeras and antibodies, used to deliver therapeutic or diagnostic agents to, through, the gastrointestinal tract, e.g. insulin or leuprolide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Cagney GM, Carter JM, Singleton J;
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Omahony DJ, Patterson CA,
                                                                                                                                   hSI protein sequence
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                                                                        305 FIQPTPIVTYRVTGGILDFYILLGDTPEQVVQQYQQLVGLPAMPAYWNLGFQLSRWNYKS 364
                                                                                                                                                                      VVILDPGISTNK----TYETYIRGMKHDVFLKRN--GKPYLGSVWPGPVYFPDFLKPSA 442
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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SUMMARIES	ID	Q9LYF8	022444	Q9LLY2	Q8VWV9	Q9AVC3	7Y7260	Q9ZP26	OPLEC9	925760	Q9ZP04	Q9LZT7	073626	Q9MYM4	Q81WE7	QBBGI6	091245
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30.6	30.5	29.8	28.4	56.9	26.8	26.5	25.0	22.6	19.2	18.9	18.5	18.4	18.4	18.4	18.4	18.3	18.2	18.1	18.1	18.0	18.0	17.9	17.9	17.9	17.5	17.5	17.5	17.3
1453.5	1449	1417	1350	1278.5	1272.5	1261	1187	1072	914.5	900	877.5	876.5	876	875.5	875.5	898	864	862	861.5	855	854.5	851.5	851.5	851	833	832	831.5	820
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Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
eurosids II; Brassicales; Brassicaceae; Arabidopsis.
NCBI_TaxID=3702;
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MEDLINE-98045620; PubMed=9411456;
MEDLINE-98045620; PubMed=9411456;
MONCHOE J.D., Hall B.D., Gough C.M., Stephen A.L.;
MONCHOE Sequence of an alpha-glucosidase gene (Ac. AF014806) from Arabidopsis thaliana (PGR97-141).";
Plant Physiol. 115:863-863 [1997).
InterPro: JPR000322; Glyco hydro 31.
Pfam: PF01055; Glyco hydro 31.
PROSITE: PS00129; GLYCOSYL_HYDROL_F31_1; 1.
PROSITE: PS001029; GLYCOSYL_HYDROL_F31_2; 1.
Glycosidase; Hydrolase.
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EMBL; BTOO1222; AAN72233.1;
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EMBL; PSO0129; GLYCOSYL_HYDROL_F31.2;
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"Purification, enzymatic characterization, and nucleotide sequence of
a high-isoelectric-point alpha-glucosidase from barley malt.";
EMBL, AF118226, AAF76254.1;
InterPro: PR0000322; Glyco-hydro-31.
InterPro: IPR0000322; Glyco-hydro-31.
InterPro: IPR000325; No Masse
Pfam; PF01055; Glyco-hydro-31; 1.
PROSITE; PS00129; GLYCOSYL HYDROL F31_1; 1.
PROSITE; PS000129; GLYCOSYL HYDROL F31_2; 1.
PROSITE; PS000129; MG MTASE; 1.
SEQUENCE 879 AA; 96558 MM; AF9235ECE7D15844 CRC64;
                                                                                                                                                                                                                                                                    SRSTFVSSGKYTAHWTGDNAAKWEDLAYSIPGILNFGLFGIPMVGADICGFSHDTTEELC
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01-0CT-2000 (TrEMBLrel. 15, Created)
01-0CT-2000 (TrEMBLrel. 15, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
High pl alpha-glucosidase.
Hordeum vulgare (Barley).
Bukaryota: Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Dematophyta: Magnoliophyta; Liliopsida; Poales; Poaceae; Pooideae;
Triticeae; Hordeum.
NCBL TAXID-4513;
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SEQUENCE FROM N.A.
STRAULNECV. Igri;
MEDLINE=20267959; PubMed=10806244;
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                                                                                                                                                                    VIGKSVVLRSEVVNPEYASKMKMSIGKVTFVGPEN---------VENVKTYEV 854
                                                                                                                                                                                                             815 SDGKKVRLVSQVESGSYGLSQGWVVEKLMILGLSKSHLSSQIAFQLDGKPFTSSSFTYSV 874
696 ALKQGAVAVDAYFPAGNWFDLFNYSFAVGGDSGKHVRLDTPADHVNVHVREGSIVAMQGE
                                                                                                              31 GAGHRMISVFEFDDGSGFVANLELITGTEIYGPDISPLRMIARYDSDDRLHVHITDSIHA
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NCBI_TaxID=145481,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Hiwatashi Y., Nishiyama T., Hasebe M.;

"Establishment of gene- and enhancer-trap systems of the mo physcomitrella patens.";

Physcomitrella patens.";

Submitted (MAK-2001) to the EMBL/GenBank/DDBJ databases.

EMBL; AB057452; BAB39467.1;

Interpro; IPR001064; Crystallin.

Interpro; IPR001054; Crystallin.

Pfam; PF01055; Glyco_hydro_31; 1.

PROSITE; PS00125; CRYSTALLIN BETAGAMA, 1.

PROSITE; PS00129; GLYCOSYL HYDROL F11.1; 1.

PROSITE; PS00107; GLYCOSYL HYDROL F11.2; 1.
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                                                                                                                                                                                                                                                                                   OP-----LSTSARQSQGGAIMELNGLALPVGRNIDL
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Last annotation update)
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llarity 47.4%; Pred. No. 9.7e-144;
Conservative 150; Mismatches 257;
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Best Local Si
Matches 428;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DPSSD------LVFTLHNTTPFGFSVSRRSSGDILFDTSPDSSDSNTYFIFKDQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 180 FLQLSSALPENRSNLYGIGEHTK-RSFRLIPGETMTLWNADIGSENPDVNLYGSHPFYMD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          VRGSKGNEEAGTTHGVLLLNSNGMDVKYEGHRITYNVIGGVIDLYVFAGPSPEMVANQYT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GQVWPGAVYFPDFLNPKTVNFWADEISHFHQMVPVDCLWIDMNEISNFCSGKCSIPTNRS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       458 CPGTGFPWECCLDRTNITATRWDVPPYKINASGTQVPLGFKTIATSSVHYNGVLEYDAHS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FGMFGMPMVGADICGFYPDTTEELCGRWIQLGAFYPFSRDHSNLASKROELYLWDSVAKS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        72 SLNLHVSLETSERLRIRITDSSQQRWEIPETVIPRAGNHSPRRFSTEEDGGNSPENNFLA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        299 ELIGRPAPMPYWSFGFHQCRYGYKNVSDLEYVVDGYAKAGIPLEVMWTJIDYMDGYKDFT
                                                                                                                                                                                                                                                                                                                                                                                                                                               tch 46.3%; Score 2201.5; DB 10; Length 910; al Similarity 46.6%; Pred. No. 4.3e-149; A39; Conservative 148; Mismatches 247; Indels 109; Gaps
               Pinus pinaster (Maritime pine).
Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Coniferopsida, Coniferales, Pinaceae, Pinus.
NCBI_TaxID=71647;
                                                                                                                                       TISSUE=Etiolated hypocoty;
Sanchez M., Gianzo C., Sampedro J., Revilla G., Zarra I.;
Sanchez M., Gianzo C., Sampedro J., Revilla G., Zarra I.;
"Changes in alpha-xylosidase gene expression during intact and induced growth of pine hypocotyls";
Submitted (NOV-2001) to the EMBL/GenBank/DDBJ databases.

R EMBL; AF448201; AA440152.1;
R InterPro; IPR001022; Glyco-hydro_31.
R InterPro; IPR001029; HLH basic.
Pfam; PF01055; Glyco hydro_31; 1.
R PROSITE; PS001029; GLYCOSYL_HYDROL_F31_1; 1.
R PROSITE; PS00701; GLYCOSYL_HYDROL_F31_2; 1.
R PROSITE; PS00038; HLH_1; 1.
                                                                                                       [17]
SEQUENCE FROM N.A.
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386 ILDPGIGVD-SSYGTYNRGMEADVFIKRN-GEPYLGEVWPGKVYFPDFLNPAAATFWSNE 443 	444 IKMFQBILPLDGLWIDMNELSNFITSPLSSGSSL	479 DPPYKINNSGDKRPINNKTVPATSIHFGNISEYDAHNLYGLLEAKATHQAVVDITGKRPF 538	539 ILSRSTFVSSGKYTAHWIGDNAAKWEDLAYSIPGILNFGLFGIPWVGADICGFSHDTTEE 598 [599 LCRRWIQLGAFYPFARDHSSLGTARQELYLWDSVASSARKVLGLRWRLLPHLYTLMYEAH 658 	659 VSGNPIARPLFFSFPQDTKTYEIDSQFLIGKSIMVSPALKQGAVAVDAYFPAGNWFDLFN 718		777 ENISGELFLDDGENLRMGAGGGNRDWTLVKFRCYVTGKSVVLRSEVVNPEYASKMKWSIG 836 1911 1	837 KVTFVGFEN-VENVKTYEVRTSBRLRSPRISLIKTVSDNDDPRFLSVEVSKLSLLVGKKF 895		Y E	7 2	095777; 01.MAY-2000 (TrEMBLrel. 13, Created)		XYLI ON F2405.20. Arabidopsis thaliana (Mouse-ear cress). Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids II; Parssicales; Brassicaceae; Arabidopsis. NCBI TaxID=3702;		Sampedro J., Steiro C., Villa T.G., Revilla G., Zarra I.; "Cloning and expression pattern of an alpha-xylosidase gene from			Vysotskaia V.S., Schwartz J.R., Yu G., Toriumi M., Lenz C., Liu S., Lee J.M., Li J., Gonzalez A., Liu A., Liu K., Vaysberg M., Sakano H.,			
<i>≿</i> 93	S S	යි යි	장 음	\$ A	& 8	۶ ک	Cy Sp	ې م	음 성	Ω	991	AC PT	DI BE	8888888	R R P	RA	R.	X X X	8 8 8	225	4 7 7	RL

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           452
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           113 RRFSTEEDGGNSPENNFLADPSSDLVFTLHNTTPFGFSVSRRSSGDILFDTSPDSSDSNT 172
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A Kim C.J., Chen H., Cheuk R., Shinn P., Bowser L., Carninci P.,
A Chan M.M., Chang C.H., Dale J.M., Hayashizaki Y., Hsuan V.W.,
A Ishida J., Jones T., Kamiya A., Karlin-Neumann G., Kawai J., Lam B.,
R.A Lee J.M., Lin J., Miranda M., Narusaka M., Nguyen M., Onodera C.S.,
R.A Tang C.C., Toriumi M., Wong C., Wu H.C., Yamada K., Yu G., Yuan S.,
R.A Tang C.C., Toriumi M., Wong C., Wu H.C., Yamada K., Yu G., Yuan S.,
R. Shinozaki K., Davis R.W., Theologis A., Ecker J.R.;
R. Shinozaki K., Davis R.W., Theologis A., Ecker J.R.;
Shinited (DEC 2020) to the EMBL/GenBank/DDBJ databases.
BRBL; AR14078; AAD49987.1; --
DR EMBL; AR068075; AAD49987.1; --
DR EMBL; AR068075; AAD49987.1; --
DR EMBL; BY002675; AA091591.1; --
BRBL; BY002675; AA011591.1; --
BRBL; RY00575; AA011591.1; --
BR EMBL; RY00575; Glyco.hydro.31.1; 1.
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SEQUENCE FROW N.A.
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SEQUENCE FROW N.A.
Gordsmith A.D., Hayashzaki Y.,
Bowser L., Carninci P., Dale J.M., Goldsmith A.D., Hayashzaki Y.,
Ishida J., Jamap P.X., Jones T., Kamiya A., Karlin-Neumann G.,
Kawai J., Lam B., Lee J.M., Lin J., Lin S.X., Miranda M., Narusaka M.,
Nayyen M., Onodera C.S., Palm C.J., Phan P.K., Quach H.L., Sakurai T.,
Satou M., Seki M., Southwick A., Tang C.C., Toriumi M., Yamada K.,
Yamamura Y., Yu G., Yu S., Shinozaki K., Davis R.W., Theologis A.,
Ecker J.R.;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            44.6%; Score 2120.5; DB 10; Length 915; 44.8%; Pred. No. 2.8e-143;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Best Local Similarity 44.8%; Pred. No. 2.8e-143;
Matches 422; Conservative 166; Mismatches 277; Indels
                                                                                                                                                                                                                                                                                                                    "Arabidopsis cDNA clones.";
Submitted (SEP-2001) to the EMBL/GenBank/DDBJ databases.
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124 915 ALPHA-XYLOSIDASE.
915 AA: 102398 MW; 28F9610D8D7EA657 CRC64;
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116 ISG------SELIFS-YTTDPFTFAVKRRSNHETLFNTT-----SSLVFKDQ 155
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     DITTLRLFVKHETDSRLRVHITDAKQQRWEVPYNLLPREQPPQVGKVIGKSRKSPITVQE 115
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                                                                                                                                                                                                                                                                                                                                           271
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             634
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                                                                                                                                                                      180 FLQLSSALPENRSNLYGIGEHTK-RSFRLIPGETMTLWNADIGSENPDVNLYGSHPFYMD
                                                                                                                                                                                                       VRGSKGNEEAGTTHGVLLLNSNGMDVKYEGHRITYNVIGGVIDLYVFAGPSPEMVMQYT
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                                                                                                                                                                                                                                                                                                                                                                                               ELIGRPAPMPYWSFGFHQCRYGYKNVSDLEYVVDGYAKAGIPLEVMWTDIDYMDGYKDFT
                                                                                                                                                                                                                                                                                                                                                                                                                               QLIGRPAPMPYWSLGFHQCRWGYHNLSVVEDVVDNYKKAKIPLDVIWNDDDHMDGHXDFT
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Solanum tuberosum subsp. tuberosum.

Subraryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Asteridae; lamiids; Solanales; Solanaceae; Solanum.

NCBI_TaxID=90692;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Last sequence update)
Last annotation update)
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MEDLINE-2129583; PubMed=1140218;
Sampedro J., Sielro C., Revilla G. Gonzalez-Villa T., Zarra I.;
Cloning and Expression Pattern of a Gene Encoding an alpha-Xylosidase
Active against Xyloglucan Oligosaccharides from Arabidopsis.";
Plant Physiol. 126:910-920(2001).
EMBL; AF087483; AAD05539.1;
InterPro IRRO0322; Glyco hydro 31.
PROSITE; PS00129; GLYCORYL_HYDROL_F31_1; 1.
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Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
eurosids II; Brassicales; Brassicaceae; Arabidopsis.
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116 907 ALPHA-XYLOSIDASE.
907 AA; 101647 MW; 58ABBD235366CS88 CRC64;</pre>
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           ---- ENVENVKTYEVRISERLRSPRISLIKTVSDNDDP
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Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           63;
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                                                                                                                                                                                                                                                                                                                                                                      01-07T-2000 (TrEMBLrel. 15, Created)
01-0CT-2000 (TrEMBLrel. 15, Last sequence update)
01-0CT-2002 (TrEMBLrel. 22, Last annotation update)
EST AU092739(C53221) corresponds to a region of the predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STRAIN=CV. Nipponbare;
Sasaki T., Matsumoto T., Yamamoto K.;
"Oryza sativa nipponbare(GA3) genomic DNA, chromosome 1,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     clone:POSO4H10.";
Submitted (JUN-2000) to the EMBL/GenBank/DDBJ databases.
EMBL; AP002526; BAA99366.1; -
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Pfam; PF01055; Glyco hydro 31; 1.
PROSITE; PS00129; GLYCOSYL_HYDROL F31 1; 1.
SEQUENCE 929 AA; 102550 MW; 536ElD0B9D7F97BF
                                                                                                                                                                                                      903 KSMMLDIKGLELPIGKNFAMSWKM 926
                                                                                                                                                                       RFLSVEVSKLSLLVGKKFEMRLRL 901
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P SEQUENCE FROM N.A.

C STRAIN=cv. Record; TISSUE=Tuberising stolon tip;

STRAIN=cv. Record; TISSUE=Tuberising stolon tip;

MEDILINE=21362238; PubMed=11469591;

T Taylor M.A., Ross H.A., McRae D., Wright F., Viola R., Davies H.V.;

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44.0%; Score 2089.5; DB 10; Length
Best Local Similarity 44.6%; Pred. No. 4.9e-141;
Matches 412; Conservative 156; Mismatches 275; Indels
                                                                                                                                                                                                                                                                                                                              928 AA; 104687 MW; CEAC8634F6ED1820 CRC64;
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Best Local Similarity
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PVCKNFVMSWKM 933
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Q9LZT7
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                                                                                                                                                                                                                                                                                                                                                     ELGSYSLOKGLLIEKLSVLGLEGTGRDLAVHVDGANATAIATSRPYFAGAEAELHGHRDV 897
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
SEQUENCE FROM N.A.
STRAIN-CV. tall climbing mixed; TISSUE-Cotyledon;
Crombie H.J., Chengappa S., Jarman C., Sidebottom C., Reid G.;
"Molecular characterisation of a xyloglucan oligosaccharide-acting alpha-D-xylosidase from the cotyledons of nasturtium (Tropaeolum majus
823 VNPEYASKMKWSIGKVTFVGFE-----NVENVKTYEVRTSERLRSPRISLIKTVSD-
                                                                                    QAVVDITGKRPFILSRSTFVSSGKYTAHWTGDNAAKWEDLAYSIPGILNFGLFGIPMVGA
                                                                                                                                   DICGESHDTTEELCRRWIQLGAFYPFARDHSSLGTARQELYLWDSVASSARKVLGLRWRL
                                                                                                                                                                                  LPHLYTLMYEAHVSGNPIARPLFFSFPQDTKTYEIDSQFLIGKSIMVSPALKQGAVAVDA
                                                                                                                                                                                                                                  YFPAGNWFDLFNYSFAVGGDSGKHVRLDTPADHVNVHVREGSIVAMQGEALTTRDARKTP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Tropaeolum majus (Common nasturtium).

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
eurosids II; Brassicales; Tropaeolaceae; Tropaeolum.
                                    ----SGSSLDDPPYKINNSGDKRPINNKTVPATSIHFGNISEYDAHNLYGLLEAKATH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-MAY-1999 (TrEMBLrel. 10, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      935 ALPHA-D-XYLOSIDASE.
104937 MW; 22DE6901E9CE19BD
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InterPro; IPR000322; Glyco hydro 31.
Pfam; PF01055; Glyco hydro 31; 1.
PROSITE; PS00129; GLYCOSYL_HYDROL_F31_1; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            43.1%; Score 2049;
45.1%; Pred. No. 46
                                                                                                                                                                                                                                                                                                                                                                               NDDPRFLSVEVSKLSLLVGKKFEM 897
                                                                                                                                                                                                                                                                                                                                                                                                    EGHKKSVMVEVGGLALPLGKSFTM 921
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRELIMINARY;
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935
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                                     473
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             421
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SIGNAL
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Q9Z204
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ELVPVDGL#IDMNEDLEFLFWEMINPQGKQCPTGEGPGWICCLDCKNITKTRWDEPPYKI 508
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PGIAVNSSYGTYORGLANDVFIKYBGEPFLAQVWPGAVNFPDFLNPKTVDWWGDEVRRFH 448
                                                                                                                                                                                                                                                                                                                                                                         YVVDGYAKAGIPLEVMWTDIDYMDGYKDFTLDPVNFPEDKMQSFVDTLHKNGQKYVLILD 388
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    -----SSLDDPPYKI 484
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NLFLDKDELPEMKLGNGYS--TYVEFYATLNGGAVKVWSQVQEGKFALDNGWSIEKVTVL 866
                                                                                                                                                                                                                                                                                                                                  HRITYNVIGGVIDLYVFAGPSPEMVMNQYTELIGRPAPMPYWSFGFHOCRYGYKNVSDLE 328
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         QLGAFYPFARDHSSLGTARQELYLWDSVASSARKVLGLRMRLLPHLYTLMYEAHVSGNPI 664
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ARPLFFSFPQDTXTYEIDSQFLIGKSIMVSPALKQGAVAVDAYFPAGNWFDLFNYSFAVG 724
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GFEN------VENVKTYEVRTSERLRSPRISLIKTVSDNDDPRFLSVEVSKLSL 889
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EKQRMEVPYNLLPR--EQPP---VVEANDRBIPGKNLITVSEISGSELIFSYRPRDRFGF
                                                                                                                                              PGETMTLWNADIGSENPDVNLYGSHPFYMDVRGSKGNEEAGTTHGVLLLNSNGMDVKYEG
                                                                                                                                                                                                                                                                          PNDPYTLYTMDVSAINLNADSYGSHPMYMDLRNVGGEAYA---HAVLLLNSNGMDVFYRG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DVVERYKNAKI PLDVI WNDDDHMDGKKDFTLNTKNY PRPOLLAFLDKSIGIGMKYIVIID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NNSGDKRPINNKTVPATSIHFGNISEYDAHNLYGLLEAKATHQAVVDITGKRPFILSRST
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SQQRWEIPETVIPRAGNHSPRRFSTEEDGGNSPENNFLA - - - DPSSDLVFTLHNTTPFGF
                                                                                                             SVSRRSSGDILFDTSPDSSDSNTYFIFKDQFLQLSSALPENRSNLYGIGEHTK-RSFRLI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GDSGKHVRLDTPADHVNVHVREGSIVAMQGEALTTRDARKTPYQLLV---VASRLENISG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FVSSGKYTAHWTGDNAAKWEDLAYSIPGILNFGLFGIPMVGADICGFSHDTTEELCRRWI
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Eukaryota, Viridiplantae; Streptophyta, Embryophyta; Tracheophyta;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-0CT-2000 (TrEMBLrel. 15, Created)
01-0CT-2000 (TrEMBLrel. 15, Last sequence update)
01-0TW-2002 (TrEMBLrel. 21, Last annotation update)
Hypothetical 95.9 kDa protein.
F16L2 150.
Arabidopsis thaliana (Mouse-ear cress).
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Gaps

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TVVGYGYVVRSVGVDSNRQVLTAKLDLIKPSSVYAPDIKSLNLHVSLETSERLRIRITDS

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411; Conservative 150; Mismatches 291; Indels

544 568

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GDILFDTSPDSSDSNTYFIFKDQFLQLSSALPENRSNLYGIGEHTKRSFRLIPGETMTLW 216
  --OVVAFPAGASEGYASGKL 715
                                                                                                                         KMKWSIGKVTFVGFENVENVKTYEVRTSERLRSPRISLIKTVSDNDDPRFLSVEVSKLSL 889
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EIPETVIPRAGNHSPRRFSTEEDGGNSPENNFLADPSSDLVFTLH-NTTPFGFSVSRRSS 156
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             217 NADIGSENPDVNLYGSHPFYMDVRGSKGNEEAGTTHGVLLLNSNGMDVKYE-GHRITYNV 275
                                                                                                                                               774 KGTWKVSEILLNGSSISNETKTIEVSSKEQM-----YVVGSEDEGESKSFMVELKGLEM 827
                                                                      116 FLDDDELPEMKLGNGKS--TYIDFYASVGNESVKIWSQVKBGQFALSQGLVIEKVIVLGL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             39 YVVRSVGVDSNRQVLTAKLDLIKPSSVYAP-DIKSLNLHVSLETSERLRIRITDSSQQRW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EVP-LEVPRVTKRA-----ENP-----INSLEISQDPFGVLLRRQGT
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maltase
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    86;
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its mRNA in acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Kunita R., Nakabayashi O., Wu J.Y., Hagiwara Y., Mizutani M.,
Pennybacker M., Chen Y.T., Kikuchi T.;
"Molecular cloning of acid alpha-glucosidase cDNA of Japanese
(coturnix coturnix japonica) and the lack of its mRNA in acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 932;
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"Genomic sequenses of ggaal and ggaa2.";
Schmitted (WAR-2002) to the EMBL/GenBank/DDBJ databases.
EMBL; AB0009567; BAA25884.1;
EMBL; AB081289; BAC15595.1;
HSSP; P04155; 1PS2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                InterPro; IPR000322; Glyco hydro_31.
InterPro; IPR000322; Glyco hydro_31.
InterPro; IPR000519; P_trefoil.
Pfam; PF00089; Lirefoil.; 1.
SMART; SM00018; PD; 1.
SMART; SM00018; PD; 1.
SROSTIE; PS00129; GLYCOSYL, HYDROL_F31_1; 1.
SEQUENCE 932 AA; 104689 PM; BGZE182F03DE3F61 CRC64;
                                        784 FLDDGENLRMGAGGGNRDWTLVKFRCYVTGKSVVLRSEVVNPBYA-
                                                                                                                                                                                                                                                                                                                                                                                                               Last sequence update)
Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Matches 329; Conservative 122; Mismatches 239;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               deficient quails.";
Biochim. Biophys. Acta 1362:269-278(1997)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          32.7%; Score 1552; 42.4%; Pred. No. 2e
670 KNGRLFTLPAPFNVVNVHLYQNAILPMQ-
                                                                                                                                                                                                                                                                                                                                                                                            Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE=98201735; PubMed=9540858;
                                                                                                                                                                                                                                                                                                                                                                                                             01-AUG-1998 (TrEMBLrel. 07, 01-MAR-2003 (TrEMBLrel. 23,
                                                                                                                                                                                                                                                                                                                                                                                          07,
                                                                                                                                                                                                                                  PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                        01-AUG-1998 (TrEMBLrel.
                                                                                                                                                                                                                                                                                                                                                                                                                                                      Acid alpha glucosidase.
GAAI OR GAAI.
                                                                                                                                                                                                         890 LVGKKFEMRLRL
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                                                                                                                       830
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                                                                                                                                                                                                                                                                                                             RESULT 12
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PMPYWSL------VVKD---VVDNYQKAKIPLDVIWNDADYMDGYKDFTLDLVNFP 330
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PMPYWSFGFHQCRYGYKNVSDLEYVVDGYAKAGIPLEVMWTDIDYMDGYKDFTLDPVNFP 365
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EDKMQSFVDTLHKNGQKYVLILDPGIGVDSSYGTYNRGMEADVFIKRNGEPYLGEVWPGK 425
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               331 HAKLLSFLDRIHKMGMKYVVIKDPGIGVNASYGVYQRGMASDVFIKYEGKPFLAQVWPGP 390
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                                                                                                      Mewes H.W.
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Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
                                                                                                                                                                                                                                                                                                                                                                                          Length 855;
                                                                                                                                                       SEQUENCE FROM N.A.

B. SEQUENCE FROM N.A.

E. Stablished (APR-2000) to the EMBL/GenBank/DDBJ databases.

Submitted (APR-2000) to the EMBL/GenBank/DDBJ databases.

B. Bubl; AL162459; CAB82818.1;

B. FIND 18701055; GIYCO, Hydro 31.

B. Fram; PRO1129; GIYCO, Hydro 31.

B. PROSITE; PS00129; GIYCO, Hydro 31.

B. PROSITE; PS00129; GIYCO, Hydro 31.

B. PROSITE; PS00129; GIYCOSYL-HYDROL_F31_1; 1.

RW Hypothetical protein.

SEQUENCE 855 AA; 95858 MW; 54CB7AB35BB1C50E CRC64;
                                                                                                Jordan N., Bangert S., Wiedelmann R., Voss H., Unseld M., Rudd S., Lemcke K., Mayer K.F.X., Quetier F., Salanoubat M Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases.
                   eurosids II; Brassicales; Brassicaceae; Arabidopsis.
                                                                                                                                                                                                                                                                                                                                                                                    Query Match

41.1%; Score 1952; DB 10;
Best Local Similarity 43.8%; Pred. No. 3.2e-131;
Matches 399; Conservative 144; Mismatches 263;
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                                    NCBI_TaxID=3702;
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                                                                           336 KACIPLEVMWIDIDYMDGYKDFILDPVNFPEDKMQSFVDTLHKNGQKYVLILDPGIGVDS
                                                                                                                                                                                   PFDGLWIDMNEPSNFM - - - - - DGSEEGCPPGELDSPPYTPAVLGNS - - - - LTAKTVCAS
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O1-OCT-2000 (TrEMBLrel. 15, Created)
O1-OCT-2000 (TrEMBLrel. 15, Last sequence update)
O1-MAR-2003 (TrEMBLrel. 23, Last annotation update)
Acidic alpha-glucosidase.
Acidic alpha-glucosidase.
Bos taurus (Bovinae).
Eukaryota, Metazoa; Chordata, Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.

WEDLINE=20188772; PubMed=10723725;

Dennis J.A., Moran. C., Healy P.U.;

"The bovine alpha-glucosidase gene: coding region, genomic sand mutations that cause bovine generalized glycogenosis.";

Mamm. Genome 11:206-212(2000).

EMBL; AF171666; AAF81637.1;

HSSP; P01359; 2PSP.
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InterPro; IPR000322; Glyco hydro 31.
InterPro; IPR000519; P_trefoil.
Pfam; PF01005; Glyco hydro 31; 1.
Pfam; PF00008; trefoil; 1.
SMART; SM00018; PD; 1.
PROSITE; PS00129; GLYCOSYL HYDROL F31 1; 1.
PROSITE; PS000025; PIRRFOIL; 1.
SEQUENCE 937 AA; 104756 MM; B7E9A2D66BAF5026 CRC64;
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                                                                                                                                                             ---APLFFADQFLQLSTSLPS--QHITGLAEHLGSLMLSTNWTKITLWNRDIAPE-PNVN 277
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807 HIIPMGGPALTTTESRKQHMALAVALTASGEAQGELFWDDGESLGVLDGG---DYTQLIF 863
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031WAR7.
01-WAR2-2003 (TrEWBLrel. 23, Last sequence update)
01-MAR-2003 (TrEWBLrel. 23, Last sequence update)
01-MAR-2003 (TrEWBLrel. 23, Last annotation update)
Glucosidase, alpha, acid (Pompe disease, glycogen storage disease type
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Query Match 32.0%; Score 1518.5; DB 6; Length 937; Best Local Similarity 38.3%; Pred. No. 5.1e-100; Matches 336; Conservative 136; Mismatches 290; Indels 115;
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                                                                                                                                                       Query Match 31.9%; Score 1514.5; DB 4; Length 952; Best Local Similarity 38.1%; Pred. No. 1e-99; Matches 336; Conservative 137; Mismatches 302; Indels 107; Gaps
     Eukarycta; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mamalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
                                                                                          Strausberg R.;
Submitted (NOV-2002) to the EMBL/GenBank/DDBJ databases.
EMBL; BC040431; AMH40431.1; -.
SEQUENCE 952 AA: 105323 MM; 6E2717BF7201F469 CRC64;
                                                                    SEQUENCE FROM N.A.
TISSUE=Duodenum;
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Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus.
NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match 31.7%; Score 1508; DB 11; Length 953; Best Local Similarity 37.9%; Pred. No. 3e-99; Matches 335; Conservative 138; Mismatches 312; Indels 100
                         VPVSNPTXSP-----DIKVLDICV---SLIMGEQF 947
VRTSERLRSPRISLIKTVSDNDDPRFLSVEVSKLSLLVGKKF
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631 SVASSA-RKVLGLRWRLLPHLYTLMYEAHVSGNPIARPLFFSFPODTKTYFIDSOFLIGK 689	689 ETAQQAMRKAFALRYALLPYLYTLFHRAHVRGDTVARPLFLEFPEDPSTWSVDRQLLWGP 748	690 SIMVSPALKGAVAVDAYFPAGNWFDLFNYSFAVGGDSGKHVRL 733	749 ALLITPVLEPGKTEVTGYFPKGTWYNMQMVSVDSLGTLPSPSSASSFRSAVQSKGGWLTL 808	734 DTPADHVNVHVREGSIVAMGGEALTTRDARKTPYQLLVVASRLENISGELFLDDGENLRM 793	809 EAPLDTINVHLREGYIIPLQGPSLTTTESRKQPMALAVALTASGEADGELFWDDGESLAV 868	794 GAGGGNRDWTLVKFRCYVTGKSVVLRSEVVNPEYASKMKWSIGKVTFVGFENV-ENVKTY 852	869 LERGAYTLVTFSAKONTIVNKLVRVTKEGAELGLREVTVLGVATAPTQVLSN 920	853 EVRTSERLRSPRISLIKTVSDNDDPRFLSVEVSKLSLLVGKKFEM 897	921 GIPVSNFTYSPDNKSLAIPVSLLMGELFQI 950
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Search completed: October 27, 2003, 10:31:06 Job time : 65.7052 secs

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903 AA; 100880 MW; 5B054E27C20EC33A CRC64;
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004931 beta vulgar
043763 hordeum vul
P10253 homo sapien
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P56526 aspergillus
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074254 candida alb
P14410 homo sapien
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02263 uncus muri
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1 MSSLHWFPNIFIVVVVPFSL......EVSKLSLLVGKKFEMRLRLT
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                                                     PNIFIVVVVFFSLR---SSQVVLEEEESTVVGYGYVVRSVGVDS-NRQVLTAKLDLIKPS
                                                                               PSLALGILLVFLLQYLVAGISTSENDPEGVIGYGYKVKSVKVDSGTRRSLTALPOLVKNS
                             Gaps
                            23;
  Length 903
tch 59.6%; Score 2830.5; DB 1; Length al Similarity 59.6%; Pred. No. 1.8e-183; 540; Conservative 138; Mismatches 205; Indels
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its most by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                             Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
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                                                                                                                                                                                                                                                                                                                                                                           "Chemical modification and amino acid sequence of active site
                                                                                                                                                                            SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.
STRAIN=CV. NK-152;
MEDLINE=9731863; PubMed=9178565;
MEDLINE=9731863; PubMed=9178565;
MEDLINE STRAIN S., Chiba S.;
"Cloning and sequencing of a CDNA encoding alpha-glucosidase
                                                                                                                                                                                                                                                                                                                                                                                          sugar beet alpha-glucosidase.";
Biosci. Bacchenl. Biochem. 59:459-463(1995).

-i. PUNCTION: HIGH ACTIVITY FOR ALPHA-GLUCAN.

-i. CATALYTIC ACTIVITY: Hydrolysis of terminal, non-reducing linked D-glucose residues with release of D-glucose.

-i. PTM: THE N-TERMINUS IS BLOCKED.

-i. PTM: THE N-TERMINUS TO FAMILY 31 OF GLYCOSYL HYDROLASES.
                                                                                                                                                                                                                                                                                                                                          Iwanami S., Matsui H., Kimura A., Ito H., Mori H., Honma M.,
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                                                                                                      Spermatophyta; Magnollophyta; eudicotyledons; core er Caryophyllidae; Caryophyllales; Chenopodiaceae; Beta. NCBI_TaxID=161934;
               15-JUL-1998 (Rel. 36, Created)
15-JUL-1998 (Rel. 36, Last sequence update)
30-MAX-2000 (Rel. 39, Last annotation update)
Alpha-glucosidase precursor (EC 3.2.1.20) (Maltase).
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Pfam: PF01055; Glyco hydro 31: 1.
PROSITE; PS00129; GLYCOSVL-HYDROL.F31 1: 1.
PROSITE; PS001707; GLYCOSYL-HYDROL.F31 2: 1.
Hydrolase; Glycosidase; Glycoprotein; Signal.
                                                                                                                                                                                                                                                                           iosci. Biotechnol. Biochem. 61:875-880(1997)
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                                         LIYXDQYLQLSSSLPAQQAHLYGLGEHTKPTFQLAHNQILTLWNADIASFNRDLNLYGSH
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putative alpha-glucosidase gene from barley.";
Plant Mol. Biol. 30:229-241(1996).
-!- CATALYTIC ACTIVITY: Hydrolysis of terminal, non-reducing 1,4-
linked D-glucose residues with release of D-glucose.
-!- TISSUE SPECIFICITY: HIGH LEVELS SEEN IN THE ALEURONE AND SCUTELLUM
AFTER GERMINATION, WHILE LOW LEVELS ARE OUND IN DEVELOPPING SEEDS.
-!- DEVELOPMENTAL STAGE: LEVELS INCREASE STEADILY THROUGHOUT
IMBIBITION REACHING MAXIMUM LEVELS AT DAY 7. DURING GERMINATION,
LEVELS INCREASE FROM DAY 2, REACH MAXIMUM LEVELS AT DAY 3 AND
DECLINE AFTER DAY 5.
-!- INDUCTION: BY GIBBERELLIN A3 (GA).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          279 PAPMPYWSFGFHQCRYGYLNVSDLBRVVARYAKARIPLEVMWTDIDYMDGFKDFTLDRVN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ----PGTAHGVLLLSSNGMDVLYGGSYVTYKVIGGVLDFYFFAGPNPLAVVDQYTQLIAR
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BY SIMILARITY.

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InterPro; IPR000322; Glyco_hydro_31.
Pfam; PP01055; Glyco_hydro_31: 1.
PROSITE; PS00129; GLYCOSYL_HYDROL_P31_1; 1.
PROSITE; PS00707; GLYCOSYL_HYDROL_P31_2; 1.
Hydrolase; Glycosidase; Glycoprotein; Signal.
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16-JUL-1998 (Rel. 36, Last annotation update)
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17-JUL-1998 (Rel. 36, Last annotation update)
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SEQUENCE FROM N.A. STRAIN-cv. Morex; TISSUE=Aleurone; MEDLINE=96178863; PubMed=8616248;

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                                                                                                                                                                                                              "Human lysosomal alpha-glucosidase. Characterization of the catalytic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Martiniuk F., Bodkin M., Tzall S., Hirschhorn R.; Identification of the base-pair substitution responsible for a human acid alpha glucosidase allele with lower 'affinity' for glycogen (GAA) and transient gene expression in deficient cells.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           VARIANTS GSD-II ARG-643 AND TRP-725.
MEDIINE-94004908; PubMed-8401535;
Hermans M.M.P., Kroos M.A., de Graaff E., Oostra B.A., Reuser A.J.J.;
"Two mutations affecting the transport and maturation of lygosomal alpha-glucosidase in an adult case of glycogen storage disease type
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    "Identification of a missense mutation in an adult-onset patient with
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Martiniuk F., Mehler M., Bodkin M., Tzall S., Hirschhorn K., Zhong
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE=55327152; PubMed=7603530;
Reuser A.J.J., Kroos M.A., Hermans M.M.P., Bijvoet A.G.A.,
Perbeet M.P., van Diggelen O.P., Kleijer W.J., van der Ploeg A.T.;
"Glycogenosis type II dacid maltase deficiency).";
Muscle Nerve 3:861-869(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE-9135380; PubMed-1652892;
Zhong N., Martiniuk F., Tzall S., Hirschhorn R.;
Tdentification of a missense mutation in one allele of a patient
with Pompe disease, and use of endonuclease digestion of
PCR-amplified RNA to demonstrate lack of mRNA expression from the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            "Identification of a point mutation in the human lysosomal alpha-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      "Human lysosomal alpha-glucosidase: functional characterization
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         glucosidase gene causing infantile glycogenosis type II.";
Biochem. Biophys. Res. Commun. 179:919-926(1991).
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                                                                                                            MEDLINE=91310614; PubMed=1856189;
Hermans M.M.P., Kroos M.A., van Beeumen J., Oostra B.A.,
                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE=93168114; PubMed=8435067;
Hermans M.M.P., Wisselaar H.A., Kroos M.A., Oostra B.A.,
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Biochem. J. 289:687-693(1993).
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J. Biol. Chem. 266:13507-13512(1991).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              the glycosylation sites.";
Biochem. J. 289:681-686(1993).
       J. 272:493-497 (1990).
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                                                                                                                CRRWIQLGAFYPFARDHSSLGTARQELYLWDSVASSARKVLGLRMRLLPHLYTLMYEAHV
                                                                                                                                                                                                                                                  CGRWIQLGAFYPFSRDHSAIFTVRRELYLWPSVAASGRKALGERYQLEPYFYTLMYEAHM
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                                                                        LSRSTFVSSGKYTAHWTGDNAAKWEDLAYSIPGILNFGLFGIPMVGADICGFSHDTTEEL
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MEDLINE=89005068; PubMed=3049072;
MFOLINE=89005068; PubMed=3049072;
MFOLINE-MOGGOOSOEN WESTERVEID M., Kroos M.A., van Beeumen J.,
Reuser A.J.J., Oostra B.A.;
"Primary structure and processing of lysosomal alpha-glucosidase;
"Intransy structure and processing of lysosomal alpha-glucosidase;
EMBO J. 7:1697-1704(1988)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE=90262651; PubMed=2111708; Meredith G., Hirschhorn R.; Martiniuk F., Mehler M., Tzall S., Meredith G., Hirschhorn R.; Maguence of the cDNA and 5'-flanking region for human acid alphaglucosidase, detection of an intron in the 5' untranslated leader sequence, definition of 18-bp polymorphisms, and differences with previous cDNA and amino acid sequences.";
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P10253; Q14351; Q16302;
O1-MAR-1989 (Rel. 10, Created)
O1-FBE-1991 (Rel. 17, Last sequence update)
28-FSB-2003 (Rel. 41, Last annotation update)
Lysosomal alpha-glucosidase precursor (EC 3.2.1.20) (Acid maltase).
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo
NCBI_TaxID=9606;
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    'Glycogen storage disease type II: genetic and biochemical analysis
                                                                                                       Beesley C.E., Child A.H., Yacoub M.Y.;
"The identification of five novel mutations in the lysosomal acidalpha-(1,4) glucosidase gene from patients with glycogen storage
                                                                                                                                                                                                                                                                                                                                                         Indels 107;
                     of novel mutations in infantile patients from Turkish ancestry Hum. Mutat. 11:209-215(1998).
                                                                                                                                                                                                                                                                                                                DB 1; Length 952;
                                                                                                                                                                                                                                                                         Raben N., Lee E., Lee L., Hirschhorn R., Plotz P.H.;
                                                                                                                                                                                                                                                                                                              Query Match 32.0%; Score 1520.5; DB 1; Best Local Similarity 38.2%; Pred. No. 7.2e-95; Matches 337; Conservative 137; Mismatches 301;
                                                                [23]
VARIANT GSD-II GLY-VAL-PRO-VAL-SER-ASN-925 INS
                                                                                                                                                                                                                                                    MEDLINE=99202470; PubMed=10189220;
                                                                                                                                                                                         Hum. Mutat. 11:413-413(1998).
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MEDLINE-95072571; PubMed=7981676;
Hite M.L., Chen A.S., Brooks S.S., Grix A., Hirschhorn R.;
"A de novo 13 nt deletion, a newly identified C647W missense mutation and a deletion of exon 18 in infantile onset glycogen storage disease
                                         VARIANTS ILE-816 AND ILE-927.
MEDINE-9325406; PubMed-8486380;
MEDINE-93252406; PubMed-8486380;
METHORNS M.M.P., Svetkey L.P., Oostra B.A., Chen Y.T., Reuser A.J.J.;
"The loss of a polymorphic glycosylation site caused by Thr-927--->Ile
is linked to a second polymorphic Val-816-->Ile substitution in
Jysosomal alpha-glucosidase of American blacks.";
Genomics 16:300-301(1993).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE-95187163; PubMed=7881422;
Hermans M.W. P., de Graaff E., Kroos M.A., Mohkamsing S., Eussen B.J., Joosse M., Willemsen R., Kleijer W.J., Oostra B.A., Reuser A.J.J.;
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hum. Mol. Genet. 3:2213-2218(1994).
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MEDILNE=95233437; PubMed=7717400;
BOOCKCOL C.F., Exelbert R., Nicastri C., Nichols R.C., Miller F.W.,
Plotz P.H., Raben N.;
"Leaky splicing mutation in the acid maltase gene is associated with
delayed onset of 910090000sis type II.";
Am. J. Hum. Genet. 56:887-897(1995).
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                                                                                                                                                                                                                                               Huie M.L., Hirschhorn R., Chen A.S., Martiniuk F., Zhong N., "Mutation at the catalytic site (M519V) in glycogen storage disease type II (Pompe disease)."; Hum. Mutat. 4:291-293(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            VARIANTS GSD-II ARG-299; LYS-903 DEL AND VARIANTS HIS-199; ARG-223
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Lin C.-Y., Shieh J.-J.; and a de novo point mutation resulting in infantile form of Pompe's disease.; Biochem. Biophys. Res. Commun. 208:886-893(1995).
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Martiniuk P.,
"Acid alpha-glucosidase deficiency: identification and expression
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Kleijer W.J., Reuser A.J.J.;
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VARIANTS GSD-II ASN-645; TRP-647; SER-648; GLN-672 AND TRP-672
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Hum. Genet. 97:496-499(1996).
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MEDLINE=98180719; PubMed=9521422;
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VARIANT GSD-II VAL-519.
MEDLINE=95170739; PubMed=7866409;
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MEDLINE=96431168; PubMed=8834250;
Cell Biol. 10:681-687(1991)
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                                                                                                                                    LIGRPAPMPYWSFGFHQCRYGYKNVSDLEYVVDGYAKAGIPLEVMWTDIDYMDGYKDFTL 359
                                                                                                                                                           DPVNFPEDKMQSFVDTLHKNGQKYVLILDPGIGVDSSYGTYNRGMEADVFIKR-NGEPYL 418
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                                                                       -----GKAHGALLMNAHGMDVITTEGRITYKVIGGILDFYFPAPKSGKPNDLSIAYTD
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STRAIN-BALB/C; TISSUE-Liver;
Ding J.H., Yang B.Z., Reuser A.J.J., Roe C.R.;
Submitted (SPP-1996) to the EMBL/GenBank/DDBJ databases.
-:- FUNCTION: ESSENTIAL FOR THE DEGRADATION OF GLYGOGEN TO GLUCOSE
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01-NOV-1997 (Rel. 35, Last sequence update)
30-MSY-2000 (Rel. 39, Last annotation update)
Lysosomal alpha-glucosidase precursor (EC 3.2.1.20) (Acid maltase)
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      -!- CATALYTIC ACTIVITY: Hydrolysis of terminal, non-reducing linked D-glucose residues with release of D-glucose.
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-!- SIMILARITY: Contains 1 P-type (trefoil) domain.
-!- SIMILARITY: BELONGS TO FAMILY 31 OF GLYCOSYL HYDROLASES.
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01-NOV-1997 (Rel. 35, Last sequence update)
15-SEP-2003 (Rel. 42, Last annotation update)
Alpha-glucosidase precursor (EC 3.2.1.20) (Maltase).
Mucor javanicus.
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InterPro; IPR00322; Glyco_hydro_31.
Fran; PF01055; Glyco_hydro_31; 1.
PROSITE; PS00129; GLYCOSYL_HYDROL_F31_1; 1.
PROSITE; PS00707; GLYCOSYL_HYDROL_F31_2; FALSE_NEG.Hydrolase; Glycosidase; Glycoprotein; Signal.
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N-LINKED (GLC
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"Molecular cloning, sequencing, and expressingly-glucosidase from Mucor javanicus.";
J. Biochem. 119:500-505(1996).
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SEQUENCE FROM N.A., AND PARTIAL SEQUENCE
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MEDLINE=96271012; PubMed=8830045;
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NCBI_TaxID=51122;
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between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
SWISS-PROT entry is copyright. It is produced through a collaboration
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232 INTTV-----APLFFADQFLQLSTSLP--AQHITGLGEHLSPLMLSTDWARITLWRRDT 283
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PROSITE; PS00025; P TREFOIL; 1.
PROSITE; PS00129; GLYCOSYL_HYDROL_F31_1; 1.
PROSITE; PS00707; GLYCOSYL_HYDROL_F31_2; 1.
Hydrolase; Glycosidase; Glycoprotein; Lysosk
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InterPro; IPR000322; Glyco hydro_31.
InterPro; IPR000519; P_treFoil.
Pfam; PF01055; Glyco hydro_31; 1.
Pfam; PF00088; treFoil: 1.
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HSSP; P01359; 2PSP.
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YDAHNLYGLLEAKATHQAVVDITGKRPFILSRSTFVSSGKYTAHWTGDNAAKWEDLAYSI
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MEDILINE=97308536; PubMed=9165762;
MEDILINE=97308536; PubMed=9165762;
Makamura A., Nishimura I., Yokoyama A., Lee D.-G., Hidaka M.,
Masaki H., Kimura A., Chiba S., Uozumi T.;
"Cloring and sequencing of an alpha-glucosidase gene from Aspergillus
iniger and its expression in A. nidulane.";
J. Biotechnol. 53:75-84(1997).
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Eukaryota; Fungi; Ascomycota; Pezizomycotina; Burotiomycetes;
Eurotiales; Trichocomaceae; mitosporic Trichocomaceae; Aspergillus.
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15-SEP-2003 (Rel. 42, Last annotation update)
Alpha-glucosidase precursor (EC 3.2.1.20) (Maltase)
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                                                              -TSPLSSGSSLDDPPYKINNSGDKRPINNKTVPATSIHFGNISEYDAHNLYGLLEAKATH
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MEDLINE=89066802; PubMed=3143729;
Naim H.Y., Sterchi E.E., Lentze M.J.;
Structure, biosynthesis, and glycosylation of human small intestinal
maltase-glucoamylase.;
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"Human small intestinal maltase-glucoamylase cDNA cloning. Homology
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28-FEB-2003 (Rel. 41, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Maltase-glucoamylase, intestinal [Includes: Maltase (EC 3.2.1.20)
(Alpha-glucosidase); Glucoamylase (EC 3.2.1.3) (Glucan 1,4-alpha-glucosidase)].
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Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
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MEDLINE=98112863; PubMed=9446624;
Nichols B.L., Eldering J.A., Avery S.E., Hahn D., Quaroni A.,
Sterchi E.E.;
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Nichols B.L., Eldering J.A., Avery S.E., Hahn D., Quaroni
Sterchi E.E.;
Submitted (DEC-2001) to the EMBL/GenBank/DDBJ databases.
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J. Biol. Chem. 273:3076-3081(1998).
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323; Conservative 157; Mismatches 302; Indels 110;
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                                                                                            -:-CATALTIC ACTIVITY: Hydrolysis of terminal, non-reducing 1,4-
linked D-glucose residues with release of D-glucose.
-:-CATALTIC ACTIVITY: Hydrolysis of terminal 1,4-linked alpha-D-
glucose residues successively from non-reducing ends of the chairs
with release of beta-D-glucose.
-:-SUBGELLULAR LOCATION: Type II membrane protein. Brush border.
-:-TISSUE SPECIFICITY: EXPRESSED IN SMALL INTESTINE, GRANULOCYTE, AND
KINDEY BUT NOT IN SALIVARY GLAND OR PANCREAS.
-:-PTM: N-AND O-GLYCOSYLATED.
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SIGNAL-ANCHOR (TYPE-II MEMBRANE PROTEIN)
(POTENTIAL).
               -:- FUNCTION: MAY SERVE AS AN ALTERNATE PATHWAY FOR STARCH DIGESTION WHEN LUMINAL ALFRA-ANYLASE ACTIVITY IS REDUCED BECAUSE OF INMATURITY OR MALNUTRITION. MAY PLAY A UNIQUE ROLE IN THE DIGESTION OF MALTED DIETARY OLIGOSACCHARIDES USED IN FOOD MANUFACTURING.
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InterPro; IPR000322; Glyco_hydro_31.
InterPro; IPR000519; P_trefoil.
Pfam; PF01058; Glyco_hydro_31; 2.
SMART; SM00018; PD; 2.
SMART; SM00018; PD; 2.
SMART; SM00018; PD; 2.
PROSITE; PS00125; GLYCOSYL HYDROL_F31_1; 2.
PROSITE; PS00025; P_TREFOIL; 1.
Multifunctional enzyme; Transmembrane; Glycoprotein; Hydrolase; Glycosidase; Repeat; Signal-anchor; Sulfation.
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PTM: SULFATED (BY SIMILARITY).

SIMILARITY: BELONGS TO FAMILY 31 OF GLYCOSYL HYDROLASES.

SIMILARITY: Contains 2 P-type (trefoil) domains.
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GO; GO:0005983; P:starch catabolism; TAS
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-!- CATALYTIC ACTIVITY: Hydrolysis of terminal, non-reducing 1,4-linked D-glucose residues with release of D-glucose.
-!- SUBCELBULAR LOCATION: Secreted.
-!- SUBLEILBULAR LOCATION: Secreted.
907 EEPSNV-TVKGNGVPSQTSPTVTY-----DSNLKVAIITDIDLLLGEAY 949
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A., SEQUENCE OF 25-36; 175-194; 375-395 AND 427-451, AND MUTAGENESIS OF ASP-481; GLU-484 AND ASP-647.
MEDLINE=21195240; PubMed=11298744;
MCDLINE=ALMOND A., Shimizu N., Mori H., Kimura A., Chiba S.;
"Carboxyl group of residue Asp647 as possible proton donor in catalytic reaction of alpha-glucosidase from Schizosaccharomyces
                                                                                                                                                                                                                                                                                                                                                     Schizosaccharomyces pombe (Fission yeast).
Eukaryota; Fungi; Ascomycota; Schizosaccharomycetes;
Schizosaccharomycetales; Schizosaccharomycetaceae;
                                                                                                                                                    AGIU SCHPO STANDARD; PRT; 969 AA. 16-00T-2001 (Rel. 40, Last sequence update) 16-00T-2001 (Rel. 40, Last sequence update) 15-SEP-2003 (Rel. 42, Last annotation update) 15-Daylocosidase precursor (EC 3.2.1.20) (Maltase) AGI OR SPAPB24D3.10C.
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EMBL; AL590582; CAC36906.1; -.

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62 GY--QAVNISESQNGVTAYLALLGEPCYAYGTDYPLLFLMVTYEEADRVHISIKDA---- 115
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220 P -> A (IN REF. 1).
507 T -> V (IN REF. 1).
566 D -> N (IN REF. 1).
108686 MW; F3122EZCFA551C25 CRC64;
            GenebB SPombe; SPAPB24D3.10c; -.
InterPro: IPR000322; Glyco_hydro_31.
Pfam; PF01D55; Glyco_hydro_31; 1.
PROSITE; PS00129: GlYCOSYL_HYDROL_F31_1; 1.
PROSITE; PS00107; GLYCOSYL_HYDROL_F31_2; FALSE_NEG.Hydrolase; Glycosidase; Glycoprotein; Signal.
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InterPro; IPR000322; Glyco_hydro_31.
Pfam; PF01055; Glyco_hydro_31; 1.
PROSITE; PS00129; GLYCOSYL_HYDROL_F31_1; 1.
PROSITE; PS00107; GLYCOSYL_HYDROL_F31_2; 1.
Hydrolase; Glycosidase; Polysacchāridē degradation; Glycoprotein;
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    331 NITEIMDVRQNYIDADIPVETFWSDIDYMEKYRDFTVDPVSYSKSDMQTFFSDLVSNHQH 390
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"Identification and cloning of GCA1, a gene that encodes a cell
surface glucoamylase from Candida albicans.";
Med. Mycol. 37:357-366(1999).
-!- CATALYTIC ACTIVITY: Hydrolysis of terminal 1,4-linked alpha-D-
glucose residues successively from non-reducing ends of the chains
with release of beta-D-glucost. ASSOCIATED.
-!- SUBCELLULAR LOCATION: CELL MALL ASSOCIATED.
-!- SIMILARITY: BELONGS TO FAMILY 31 OF GLYCOSYL HYDROLASES.
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                                              YVPIIDAAIYAANPYNHTDDSYYPYYAGVEKDIFLKNPNGSIYIGAVWPGFTAFPDFTNP
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                              YVLILDPGI-----GVDSSYGTYNRGMEADVFIKR-NGEPYLGEVWPGKVYFPDFLNP
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28-FEB-2003 (Rel. 41, Last annotation update)
Glucoamylase 1 precursor (EC 3.2.1.3) (Glucan 1,4-alpha-glucosidase)
GAM1 OR GGA1.
Candida albicans (Yeast).
Bukaryota, Fungi; Ascomycota, Saccharomycotina, Saccharomycetes;
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Calderone R.;
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                                                                                                                                                                           744 YSKELAGVDTQFFVGDALLVTPVLEPGVNHTKGIFPGENAVYYDFYTHKKQKFT----AG 799
                                                                                                                                                                                                 78B
                                                                                                                                                                                                            504 SNASEWKSISEAAAATKTTTTTSSSASTSIDGKNTLAPGKGNINYPPYAINNDQGDHDLA 563
                                                                                                                                                                                                                                                        789 ENLEMGAGGGNRDWTLVKFRCYVTGKSVVLRSEVVNPEYASKMKWSIGKVTFVGFEN 845
                       NKTVPATSIHFGNISEYDAHNLYGLLEAKATHQAVVDI-TGKRPFILSRSTFVSSGKYTA
                                  554 HWTGDNAAKWEDLAYSIPGILNFGLFGIPMVGADICGFSHDTTEELCRRWIQLGAFYPFA
                                                                              RDHSSLGTARQELYLWDSVASSARKVLGLRMRLLPHLYTLMYEAHVSGNPIARPLFFSFP
                                                                                                                        KHVRLDTPADHVNVHVREGSIVAMQGEALTTRDARKTPYQLLVVASRLENISGELFLDDG
                                                                                                                                                      674 ODTKTYEIDSQFLIGKSIMVSPALKQGAVAVDAYFPAGN--WFDLFNY---SFAVGGDSG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WARIANT DISACCHARIDE INTCLERANCE I PRO-1097.
MEDLINE=96189940; PubMed=8609217;
Ouwendijk U., Moolnaar C.B.C., Peters W.J., Hollenberg C.P.,
Gunsel L.A., Fransen J.A.M., Naim H.Y.;
"Congenital sucrase-isomaltase deficiency: identification of a
glutamine to proline substitution that leads to a transport block of
sucrase-isomaltase in a pre-601gi compartment.";
J. Clin. Invest. 97:633-641(1996).
--- FUNCTION: PLAYS AN IMPORTANT ROLE IN THE FINAL STAGE OF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TISSUE=Intestine;
MEDLINE=92359963; PubMed=1353958;
Chantret I., Lacasa M., Chevalier G., Ruf J., Islam I., Mantei N.,
Edwards Y., Swallow D., Rousset M.;
                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                                                                                                         01-JAN-1990 (Rel. 13, Created)
30-MAY-2000 (Rel. 39, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Sucrase-isomaltase, intestinal [Contains: Sucrase (EC 3.2.1.48);
Isomaltase (EC 3.2.1.10)].
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence of the complete cDNA and the 5' structure of the human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            "Isolation of a cDNA probe for a human jejunal brush-border hydrolase, sucrase-isomaltase, and assignment of the gene locus chromosome 3.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Green F., Edwards Y., Hauri H.-P., Povey S., Ho M.W., Pinto M.,
Swallow D.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CARBOHYDRATE DIGESTION. CATALYTIC ACTIVITY: Hydrolysis of sucrose and maltose by alpha-D-glucosidase-type action.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 sucrase-isomaltase gene. Possible homology with a yeast
                                                                                                                                                                                                                                                                                                                      PRT; 1826 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE OF 1-677 FROM N.A.
MEDLINE=88112852; PubMed=2962903;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Biochem. J. 285:915-923(1992)
                                                                                                                                                                                                                                                                                                                      STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gene 57:101-110(1987).
                                                                                                                                                                                                                                                                                                                                                                                                            Homo sapiens (Human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                             NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           glucoamylase
                                                                                                                                                                                                                                                                                                                      SUIS HUMAN
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@ibb-sib.ch).
                                      alpha-amylame, and in isomaltose.
SUBUNIT: THE RESULTING SUCRASE AND ISOMALTASE SUBUNITS STAY
ASSOCIATED WITH ONE ANOTHER IN A COMPLEX BY NON-COVALENT LINKAGES.
SUBCELULAR LOCATION: Type II membrane protein. Brush border.
FTM: THE PRECURSOR IS PROTECLYTICALLY CLEAVED WHEN EXPOSED TO
PANCREALTC PROTEASES IN THE INTESTINAL LUMBN.
PTM: SULFATED (BY SIMILARITY).
DISEASE: Defects in SI are the cause of disaccharide intolerance
CATALYTIC ACTIVITY: Hydrolysis of 1,6-alpha-D-glucosidic linkages
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (TYPE-II MEMBRANE PROTEIN)
                                                                                                                                                                                                                               MISCELLANBOUS: THERE IS A HIGH DEGREE OF HOMOLOGY BETWEEN THE ISOMALTASE AND SUCRASE PORTIONS (41 % OF AMINO ACID IDENTITY) INDICATING THAT THIS PROTEIN IS EVOLVED BY PARTIAL GENE
                      some oligosaccharides produced from starch and glycogen by
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SMART; SM0018; PD: 2.

PROSITE; PS0025; PTREFOLL; 1.

PROSITE; PS00129; GLYCOSYL HYDROL F31 1; 2.

PROSITE; PS00129; GLYCOSYL HYDROL F31 2; 1.

PROSITE; PS00107; GLYCOSYL HYDROL F31 2; 1.

Multifunctional enzyme; Transmembrane; Glycoprotein; Hydrolase; Glycosidase; Repeat; Signal-anchor; Sulfation; Disease mutation.

INIT MBT 0 0 0 SUCRASE-ISOMALTASE, INTESTINAL.
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                                                                                                                                                                                                                                                                                                                    SIMILARITY: BELONGS TO FAMILY 31 OF GLYCOSYL HYDROLASES SIMILARITY: Contains 1 P-type (trefoil) domain.
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N-LINKED (GLCNAC
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Genew; HGNC:10856; SI.
MIM; 222900; .
GO; GO:0005794; C:Golgi apparatus; TAS.
GO; GO:0005794; C:Golgi apparatus; TAS.
InterPro; IPR000322; Glycc hydro 31.
InterPro; IPR000519; P. trefoil.
Pfam; PP01085; Glycc hydro 31; 2.
Pfam; PP01088; trefoil; 2.
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EMBL; M22616; AAA60551.1; ALT_SEQ.
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us-10-043-418-4.rsp

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SEQUENCE FROM N.A.
                                                                                                                                                                 NCBI_TaxID=9986;
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                            SUIS RABIT
P07768;
                                                       01-AUG-1988
                                                                               28-FEB-2003
                                                                   30-MAY-2000
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                  SUIS_RABIT
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                                                                                                                                                                                                       VVGYGYVVR----SVGVDSNRQVLTAKLDLIKPSSVYAPDIKSLNLHVSLETSERLRIR 88
N-LINKED (GLCNAC. ...) (POTENTIAL).
N-LINKED (GLCNAC. ...) (POTENTIAL).
N-LINKED (GLCNAC. ...) (POTENTIAL).
N-LINKED (GLCNAC. ...) (POTENTIAL).
N-LINKED (GLCNAC. ...) (POTENTIAL).
Q -> P (in disaccharide intolerance I;
exhibits intracellular accumulation of mannose-rich SI in the Golgi).
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                                                                                                                                                                                 Gaps
                                                                                                                                                                              90;
                                                                                                                                                     DB 1; Length 1826;
                                                                                                                                                                  Best Local Similarity 38.2%; Pred. No. 1.4e-83;
Matches 301; Conservative 138; Mismatches 258; Indels
                                                                                                                            3F7E4B66FDCF9C8E CRC64;
                                                                                                                                                     Score 1360; DB 1;
Pred. No. 1.4e-83;
                                                                                                     /FTId=VAR_007854.
MISSING (IN REF.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE-83105704; PubMed=715.077;
MEDLINE-83105704; PubMed=715.077;
MEDLINE-83105704; PubMed=715.027;
MEDLINE-83105704; PubMed=715.027;
MEDLINE-83105704; PubMed=715.027;
MEDLINE-83105704; PubMed=715.027;
MEDLINE-83105704; PubMed=715.027;
MIV-terminal sequences of pig intestinal sucrase-isomaltase and pro-
sucrase--isomaltase. Implications for the biosynthesis and membrane
insertion of pro-sucrase--isomaltase.";
CARADATORALE DIGESTION.
CARADATORALYTIC ACTIVITY: Hydrolysis of sucrose and maltose by an
alpha-D-glucosidase-type action.
CATALYTIC ACTIVITY: Hydrolysis of sucrose and maltose by an
alpha-D-glucosidase-type action.
CATALYTIC ACTIVITY: Hydrolysis of 1,6-alpha-D-glucosidic linkages
in some oligosaccharides produced from starch and glycogen by
alpha-amylase, and in isomaltose.
CHOMPLER BY NON-COVALENT LINKAGES.
CHOMPLER LOCATION: Type II membrane protein. Brush border.
CHOMPLER LOCATION: Type II membrane protein. Brush border.
CHOMPLER LOCATION: Type II membrane protein. Brush border.
CHOMPLER LOCATION: Type II membrane protein. Brush border.
CHOMPLER LOCATION: Type II membrane protein. Brush border.
CHOMPLER LOCATION: Type II membrane protein. Brush border.
CHOMPLER LOCATION: Type INTESTINAL LUMEN.
CHOMPLER LOCATION: Type INTESTINAL LUMEN.
CHOMPLER LOCATION: Type INTESTINAL LUMEN.
CHOMPLER LOCATION: Type INTESTINAL LUMEN.
CHOMPLER LOCATION: THE INTESTINAL LUMEN.
CHOMPLER LOCATION: THE SECOND WENCOND BY PARTIAL GENE
CHOMPLER LOCATION: THE PRECEDENT OF THE STATIAL GENE
CHOMPLER LOCATION THE THIS PROTEIN IS EVOLVED BY PARTIAL GENE
                                                                                                                                                                                        Oryctolagus cuniculus (Rabbit).
Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
                                                                                                                     Sucrase-isomaltase, intestinal [Contains: Sucrase (EC 3.2.1.48); Isomaltase (EC 3.2.1.10)].
                                                                                                                                                                                                                                                                                                                                 MEDLINE=86245068; PubMed=3755079;
Hunziker W., Spiless M., Semenza G., Lodish H.F.;
"The sucrase-isomaliase complex: primary structure, membrane-
orientation, and evolution of a stalked, intrinsic brush border
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   InterPro; IPR000322; Glyco hydro_31.
InterPro; IPR000322; Glyco hydro_31.
InterPro; IPR000519; P_trefoil.
Pfam; PF01005; Glyco_hydro_31; 2.
SWART; SM00018; DD; 2.
SWART; SM00018; PD; 2.
PROSITE; PS00125; P_TREFOIL; 1.
PROSITE; PS00170; GLYCOSYL_HYDROL_F31_2; 2.
Multifunctional enzyme; Transmembrane; Glycoprotein; Hydrolase;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SIMILARITY: Contains 1 P-type (trefoil) domain. SIMILARITY: BELONGS TO FAMILY 31 OF GLYCOSYL HYDROLASES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SUCRASE-ISOMALTASE, INTESTINAL
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INIT MET 0 0 0 CHAIN 1 1826 SUCRASE-ISOMALTA
                                                                                                 annotation update)
  1826 AA
                                                                     (Rel. 39, Last sequence update) (Rel. 41, Last annotation updat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRELIMINARY SEQUENCE OF 1-37 AND 1007-1014.
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  STANDARD;
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                                        SIHFGNISEYDAHNLYGLLEAKATHQAVVDI-TGKRPFILSRSTFVSSGKYTAHWTGDNA 560
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489 CNIFHQEVNYDGLWIDMNEVSSFVQGSNKGCNDNTLNYPPY-IPDIVDKL-MYSKTLCMD 546
                                                                                                                                                                                                                  195 AGGGNRDWTLVKFRCYVTGKSVVLRSEVVNPEYASKMKWSIGKVTFVGFENVENVKTYEV 854
                                                                                                                                                                                             621 TARQE--LYLWDS-VASSARKVLGLRMRLLPHLYTLMYEAHVSGNPIARPLFFSFPQDTK 677
                                                                                                                                                                                                                                                                       TYEIDSQFLIGKSIMVSPALKQGAVAVDAYFPAGNWFDLFNYSFAVGGD---SGKHVRLD 734
                                                                         SVQYWG-KQYDVHSLYGYSMAIATERAVERVFPNKRSFILTRSTFAGSGRHAAHWLGDNT
                                                                                                                  561 AKWEDLAYSIPGILNFGLFGIPMVGADICGPSHDTTEELCRRWIQLGAFYPFARDHSSLG
                                                                                                                                        ATWEQWEWSITGMLEFGLFGMPLVGADICGFLAETTEELCRRWWQLGAFYPFSRNHNADG
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Eurotiales; Trichocomaceae; mitosporic Trichocomaceae; Aspergillus.
NCBL_TaxID=5062;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDLINE=9603211; PubMed=7549103;
Minetoki T., Gomi K., Kitamoto K., Kumagai C., Tamura G.;
Minetoki T., Gomi K., Kitamoto K., Kumagai C., Tamura G.;
Minetocide sequence and expression of alpha-glucosidase-encoding
gene (aga) from Aspergilus oryzae..;
Blosci. Blotechnol. Blochem. 59:1516-1521(1995).
-:- FUNCTION: Hydrolyzes malto-oligosaccharides, but has a low
activity toward soluble starch.
-:- CATALYTIC ACTIVITY: Hydrolysis of terminal, non-reducing 1,4-
linked D-glucose residues with release of D-glucose.
-:- INDUCTION: By maltose.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      -!- SIMILARITY: BELONGS TO FAMILY 31 OF GLYCOSYL HYDROLASES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   012558;
15-JUL-1998 (Rel. 36, Created)
15-JUL-1998 (Rel. 36, Last sequence update)
15-SEP-2003 (Rel. 42, Last senotation update)
Alpha-glucosidase precursor (EC 3.2.1.20) (Maltase) (AGL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  886 VTQVTVAENNQSMSTHSNFTYDPSNQVLLIENLNFNLGRNFRVQ 929
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            855 RTSERLRSPRISLIKTVSDNDDPRFLSVEVSKLSLLVGKKFEMR 898
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Pfam; PF01055; Glyco hydro_31; 1.

PROSITE; PS00129; GLYCOSYL_HYDROL_F31_1; 1.

PROSITE; PS00707; GLYCOSYL_HYDROL_F31_2; 1.
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FEBS Lett. 294:11
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                                                                                                                                                                                                                                                                                                                                              28.6%; Score 1357; DB 1; Length 985; ilarity 34.4%; Pred. No. 8.5e-84; Conservative 142; Mismatches 290; Indels 136;
                                                                                               (POTENTIAL)
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Glycosidase; Glycoprotein;
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 Hydrolase;
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-!- FUNCTION: THIS GLUCOAMYLASE HAS A SPECIFICITY TOWARD BOTH
ALPHA-1, 4 AND ALPHA-1, 6 LINKAGES.

-!- CATALYTIC ACTIVITY: Hydrolysis of terminal 1,4-linked alpha-D-
glucose residues successively from non-reducing ends of the chains
with release of beta-D-glucose.

-!- SIMILARITY: BELONGS TO FAMILY 31 OF GLYCOSYL HYDROLASES.
LYTLMYEAHVSGNPIARPLFFSFPQDTKTYEIDSQFLIGKSIMVSPALKQGAVAVDAYFP
                                                                                                                                                                                                                                                      812 GVGHGEVWYDWYSQT-AVDAKPGVNTTISAPLGHIPVFVRGGSILPMQEVALTTRDARKT
                                                                            752 FYTLFHLAHTTGSTVMRALAWEFPNDPSLAAVGTÖFLVGPSVMVIPVLEPQVDTVQGVFP
                                                                                                                                                                          - AGN----WFDLFNYSFAVGGDSGKHVRLDTPADHVNVHVREGSIVAMQGEALTTRDARKT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AMYG_DEBOC STANDARD; PRT; 958 AA.
P22861; 092336;
01-AUG-1991 (Rel. 19, Created)
10-AUG-1991 (Rel. 19, Last sequence update)
15-JUL-1998 (Rel. 36, Last annotation update)
Glucoamylase 1 precursor (BC 3.2.1.3) (Glucan 1,4-alpha-glucosidase)
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STRAIN=ATC 26076;
MEDLINE=91071522;
Dohmen R.J., Strasser A.W.M., Dahlems U.M., Hollenberg C.P.;
Toloning of the Schwanniomyces occidentalis glucoamylase gene (GAMI)
and its expression in Saccharomyces cerevisiae.";
Gene 95:111-121(1990).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PIR; JN0102; JN0102.
InterPro; IPR000322; Glyco hydro_31.
Edm; PF01055; Glyco hydro_31; 1.
PROSITE; PS00129; GLYCOSYL HYDROL F31 1; 1.
PROSITE; PS00107; GLYCOSYL HYDROL F31_2; 1.
Hydrolase; Glycosidase; Polysaccharide degradation; Glycoprotein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Debaryomyces occidentalis (Yeast) (Schwanniomyces occidentalis).
Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
Saccharomycetales; Saccharomycetaceae; Debaryomyces.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SIMILARITY TO OTHER FAMILY 31 MEMBERS.
MEDLINE=92077121; PubMed=1743281;
Naim H.Y., Niermann T., Kleinhans U., Hollenberg C.P.,
Strasser A.W.M.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           POTENTIAL.
GLUCOAMYLASE 1.
BY SIMILARITY.
SER-RICH.
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Schizosaccharomyces.
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                                                                                                                                                                                                       PDIKSLNLHVSLETSERLRIRI --TDSSQQRWEIPETVIPRAGNHSPRRFSTEEDGGNSP
                                                                                                                                                                                                                                                                                                                  244 GNEEAGTTHGVILLNSNGMDVKYEGHRITYNVIGGVIDLYVFAGPSPEMVMNQYTELIGR
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                                                                                                                              Query Match 28.4%; Score 1347; DB 1; Length 958;
Best Local Similarity 34.5%; Pred. No. 3.9e-83;
Matches 326; Conservative 136; Mismatches 320; Indels 164; Gaps
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: Db 593 PPYALDTOTE		DB 653 LLSRSTFVGS	713	Oy 659 VSGNPIARPI	212	DD 833 WYNHS-VINE	176	Db 892 NGFASGSLY1 Qy 831 MKWSIGKVTE	: : Db 937SLANIT	Search completed: Octobe Job time : 18,5417 secs		•								
POTENTIAL. PUTATIVE FAMILY 31 GLUCOSIDASE	GLCNAC) ((GLCNAC) (GLCNAC) (GLCNAC)	(GLCNAC) (GLCNAC) (GLCNAC) ((GLCNAC)	N-LINKED (GLCNAC) (POTENTIAL). N-LINKED (GLCNAC) (POTENTIAL). N-LINKED (GLCNAC) (POTENTIAL). N-LINKED (GLCNAC) (POTENTIAL).	(GLCNAC)	(GLCNAC) (GLCNAC) (GLCNAC)	777	N-LINKEO (GLCNAC) (POTENTIAL). N-LINKED (GLCNAC) (POTENTIAL). N-LINKED (GLCNAC) (POTENTIAL).	-LINKED (GCCNAC) (-LINKED (GLCNAC) (-LINKED (GLCNAC) (-LINKED (GLCNAC) (<pre>\$; Score 1345.5; DB 1; Length 993; \$; Pred. No. 5.2e-83; 151; Mismatches 302; Indels 157; Gaps 24;</pre>	GYVVRSVGVDSNRQVLTAKLDLIKPSS-VYAPDIKSLNLHVSLETSERLRIRITDSSGOR 96 ::	WEIPETVIPRAGNHSPRRFSTEEDGGNSPENNFLADPSSDLVFTLHNTTPFGFSVS 152 :::	RRSSGDILFDTSPDSSDSNTYFIFKDQFLQLSSALPENRSNLYGIGEHTKRSFKLIFGET 212 : : RIADDQVLFDTRGNPLIFEDQYIELTTNMVED-YNVYGL-SGSQQSFRLGNNLT 234	MILMNADIGSENPDVNLYGSHPYMDVRGSKGNEEAGTTHGVLLLNSNGMDVKYEG 268 	HRITYNVIGGVIDLYVFAGPSPEMVMNQYTELIGRPAPMPYMSFGFHQCRYGYKNVSD 326 	LEYVVDGYAKAGIPLEVMMTDIDXMDGYKDFTLDPVNFPEDKMQSFVDTLHKNGQKYVLI 386 	LDPGIGVDSSYGTYNRGMEADVEIKR-NGEPYLGEVWPGKVYFDDFLNPAAT 438 	FWSNEIKOMFQEILPLDGLWIDMNELSNFITSPLSSGSS 476	LDD
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Db 593 PPYALDTDTETHDLAQFGVSPNATMHGNTLRYNLFNTYGYSESKISFEALNSIQPNIRPF 652

Cy 539 ILSRSTFVSSGKYTAHMTGDNAAKWEDLAXSIDGILNFGLFGIPMVGADICGFSHDTTEE 598

Db 653 LLSRSTFVGSGRYAAHMLGDNKSQWSDNVSSISSILTFNLIGIPMVGADVCGYNGNTDEE 712

Cy 599 LCRRWIGGAFPFRAHNSLGSTPQEPRWSASARKVLGLRWRLLPHLYTLAYTEAH 658

Db 713 LCARWALGAFLPFYRAHNSLGSIPQEPRWASVASASRAIEIRYSLLPYWYTLAYTTAYTAGT 772

Cy 659 VSGNPIARPLFFSFPQDTKTYEIDSQFLIGKSIMVSPALKQGAVAVDAYFPAGN---WFD 715

LCARWALGAFPFRAHNSLGSIPQEPRWASVASASRAIEIRYSLLPYWYTLAYTTAGT 773

Cy 659 VSGNPIARPLFFSFPQDTKTYEIDSQFLIGKSIMVSPALKQGAVAVDAYFPAGN---WFD 715

Db 773 VDGTPWVRPLFFFFPRQISLASVDKQFMIGTALLISPALEPNTTYIQGIIPGDNDTIWYD 832

Cy 776 LFNYSFAVGGDSGKHVRLDTPADHVNVHVRGSIVAMQCBALTTRDARKTPYQLLVVASR 775

Db 892 NGFSGSKTVIDGISMYTNSALGYVNIAVRGGNIIPLQOPGYTTYESRNNPYSLLIAMDN 891

Cy 776 LENISGELFLDDGENLRMGAG----GGNRDWTLVKFRCYVTGKSVVLRSEVNNPFYSKITAMDN 891

Cy 776 LENISGELFLDDGSNLRMGAG----GGNRDWTLVKFRCYVTGKSVVLRSEVNNPFYSKITAMDN 891

Cy 776 LENISGELFLDDGSNLRMGAG-----GGNRDWTLVKFRCYVTGKSVVLRSEVNNPFYSK 830

Db 892 NGFASGSLYIDGISMYNSSLSVKLNSNN----TITCVVSG------TWVSSP----
SEATCH COMPLETEE: 27, 2003, 10:20:38

Search completed: October 27, 2003, 10:20:38

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OM protein - protein search, using sw model

Run on:

October 27, 2003, 10:19:13 ; Search time 23.5784 Seconds (without alignments) 3678.964 Million cell updates/sec

4751 1 MSSLHWFPNIFIVVVVFFSL......BVSKLSLLVGKKFEMRLRLT US-10-043-418-4 Title: Perfect score: Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

283308 seqs, 96168682 residues Searched:

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

PIR 76:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:* Database

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Description		alpha-glucosidase	alpha-glucosidase	alpha-qlucosidase	alpha-glucosidase	hypothetical prote	hypothetical prote	•-	alpha-glucosidase	sucrose alpha-qluc	sucrose alpha-qluc	alpha-qluccsidase	probable family 31	glucan 1,4-alpha-g	probable family 31	sucrose alpha-gluc	alpha-glucosidase	hypothetical prote		alpha-glucosidase	hypothetical prote	•	alpha-glucosidase	alpha-glucosidase	probable alpha-glu	17	glucan 1,4-alpha-q	tical pro		_
SUMMARIES	:	T48531	-	JC5463	865057	H96709	T47534	A32609	JC4624	A23945	טאנט	JC4217	T50267	JN0102	T38598	T10799	S19686	T15893	T16693	JC1200	T22575	AH1097	AG1460	AE2402	T07391	AC2472	S46105	T22050	4	4.4
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alpha-glucosidase	H97033	~	169	10.0
alpha-xylosidase	A72394	~	764	10.5
probable glycosyl	AI0968	7	772	10.8
hypothetical 88.1	B65167	N	772	10.8
alpha-xylosidase	D90483	7	731	10.8
hypothetical prote	E86042	N	172	10.9
hypothetical prote	D91195	~	772	10.9
sucrose alpha-gluc	S11386	~	642	12.4
alpha-gincosidase	H90486	ų	0	70.0

ALIGNMENTS

·; Length 902; Indels 100.0%; Score 4751; DB 2; 100.0%; Pred. No. 8.2e-317; ive 0; Mismatches 0; Query Match
Best Local Similarity 100.
Matches 902; Conservative 1 MSSLHWFPNIFIVVVVFFSLRSSQVVLEEEESTVVGYGYVVRSVGVDSNRQVLTAKLDLI

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	PVNFPEDKMQSFVDTLHKNGQKYVLILDPGIGVDSSYGTYNRGMEADVFIKRNGEPYLGE VWFGKVYFPDFLNPAAATFWSNEIKMFQEILPLDGLWIDMNELSNFITSPLSSGSSLDDP	RRWIQLGAFYPFARDHSSLGTARQELYLWDSVASSARKVLGLRWRLLPHLYTLMYEAHVS	FANGGOSGENTALITED TO THE TOTAL TO THE TOTAL TO THE TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOT	ul-2000 lpha-glucosidase frc g2081627 ogy; trefoil homolog Gaps 8; DLIKPS 63	HSLSSL 122 SDSNTY 173

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A;Status: nucleic acid sequence not shown
A;Molecule type: mRMA
A;Residues: 85-115, S',117-121,123-170,'D',172-366,'G',368-529,'H',531-685,'G',687-76<sup>,</sup>
A;Cross-references: EMBL:U22450
                                                                                                                                                                                                                            a gibberellin-inducible alpha
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         C;Superfamily: lysosomal alpha-glucosidase; sucrase/isomaltase homology; trefoil homo:
C;Keywords: glycosidase; hydrolase
F;125-769/Domain: sucrase/isomaltase homology <SIM>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   VWPGKVYFPDFLNPAAATFWSNEIKMFQEILPLDGLWIDMNELSNFIT-SPLSSGSSLDD 479
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               455
                                                                                                 alpha-glucosidase (BC 3.2.1.20) - barley
C;Species: Hordeum vulgare (barley)
C;Date: 20-Jul-1996 & Beoquence_revision 27-Feb-1997 #text_change 22-Jun-1999
C;Accession: S65057; S65058
R;Tibbot, B.K.; Skadsen, R.W.
submitted to the EMBL Data Library, March 1995
A;Description: Molecular cloning and characterization of a gibberellin-induc
A;Reference number: S65057
                                                                                                                                                                                                                                                                                A; Molecule type: mRNA
A;Residues: 1-877 - 471B-
A;Cross-treferences: EMBL:122450; NID:9944900; PIDN:AAB02985.1; PID:9944901
R;Tibbot, B.K.; Skadsen, R.W.
Plant Mol. Biol. 30, 229-441, 1996
A;Title: Molecular cloning and characterization of a gibberellin-inducible,
A;Reference number: S65058; MUID:96178863; PMID:8616248
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            124 SPENNFLADPSSDLVFTLHNTTPFGPSVSRRSSGDILFDTSPDSSDSNTYFIFKDQFLQL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                244 GNEEAGTTHGVLLLNSNGMDVKYEGHRITYNVIGGVIDLYVFAGPSPEMVMNQYTELIGR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      tch 51.6%; Score 2451; DB 2; al Similarity 55.2%; Pred. No. 2e-159; 471; Conservative 136; Mismatches 191;
        AFKLEL
                                                                                                                                                                                                                                                                                                                                                                                                                              A; Accession: S65058
                                                                                                                                                                                                                                                               A;Accession: S65057
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                A; Experimental source: seed C. Comment: This enzyme is a exo-glucohydrolase that catalyzes the hydrolysis of alpha-gl C; Comment: This enzyme is a exo-glucohydrolase; sucrase/isomaltase homology; trefoil homolog C; Superfamily: lysosomal alpha-glucosidase; sucrase/isomaltase homology; trefoil homolog C; Keywords: glycosidase; hydrolase F;149-803/Domain: sucrase/isomaltase homology <SIM>
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                                                                                                                                                                                Gaps
                                                                                                                                                                                25;
                                                                                                                                       57.2%; Score 2719.5; DB 2; Length 913; 57.0%; Pred. No. 9.1e-178;
                                                                                                                                                                                Indels
                                                                                                                                                                                                                                                                                                 VYAPDIKSLNLHVSLETSERLRIRITDSSQQRWEIPETVIPR--
                                                                                                                                                                            219;
A; Residues: 234-261;310-365;507-541;810-840 < MAT2 >
                                                                                                                                   Query Match 57.2%; Score 2719.5; Best Local Similarity 57.0%; Pred. No. 9.1e-Matches 516; Conservative 146; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   KFEMRL 899
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Note: F1612.150
Superfamily: lysosomal alpha-glucosidase; sucrase/isomaltase homology; trefoil homo
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                                                                                                                                             412 RNGEPYLGEVWPGKVYFPDFLNPAATFWSNEIKWFGEILPLDGLWIDMNELSNFITS-- 469
                                                                                                                                                                                                                                                                                                              567
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                                                                                                                                                                                                                                ------SLDDPPYKINNSGDKRPINNKTVPATSIHFGN 507
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                                                            DGYKDFTLDPVNFPEDKMQSFVDTLHKNGQKYVLILDPGIGVDSSYGTYNRGMEADVFIK
                                                                                                                                                                       453 TIPEGKOCPSGEGPGWVCCLDCKNITKTRWDDPPYKINATGVVAPVGFKTIATSATHYNG
                                                                                                                                                                                                                                                                                                              ISEYDAHNLYGLLEAKATHQAVVDITGKRPFILSRSTFVSSGKYTAHWTGDNAAKWEDLA
                                                                                                                                                                                                                                                                                                                                                                                               568 YSIPGILNFGLFGIPMYGADICGFSHDTTBELCRRWIQLGAFYPFARDHSSLGTARQELY
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     263; Indels 106;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Conservative 144; Mismatches
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                                                                                                                                                                                                                                                                       888
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                                                                                                                              SGELFLDDGENLRMGAGGGNRDWTLVKFRCYVTGK--SVVLRSEVVNPEYASKMKWSIGK 837
                                                                                                                                                                                                                   || || || || || || || SGYLFLDDGDSPEYGR----RSDWSMVRFNYKIPNNKGAIKVKSEVVHNSYAQSRTLVISK 812
                                                                                                                                                                                                                                                                                                              862
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        113 RRFSTEEDGGNSPENNFLADPSSDLVFTLHNTTPFGFSVSRRSSGDILFDTSPDSSDSNT 172
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        173 YFIFKDQFLQLSSALPENRSNLYGIGEHTK-RSFRLIPGETWTLWNADIGSENPDVNLYG 231
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            292 MYMNQYTELIGRPAPMPYWSFGFHQCRYGYKNVSDLEYVVDGYAKAGIPLEVMWTDIDYM 351
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                                                                                                                                                                                                                                                                                                   VVLMGHRSPAAPKKLTVHVNSAE------VEASSSAGTRYQNAGGLGGVAHIGGLS
                     SGNPIARPLFFSFPQDTKTYEIDSQFLIGKSIMVSPALKQGAVAVDAYFPAGNWFDLFNY
                                           VTFVGFENVENVK--TYEVRTSERLRSPRISLIKTVSDNDDPRFLS-----VEVSKLS
                                                                                                      SFAVGGDSGKHVRLDTPADHVNVHVREGSIVAMQGEALTTRDARKTPYQLLVVASRLENI
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44.6%; Score 2120.5; DB 2; Length
Best Local Similarity 44.8%; Pred. No. 9e-137;
Matches 422; Conservative 166; Mismatches 277; Indels
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A;Gene: F24J5.20
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A; Molecule type: DNA
A; Residues: 1-552 cMAR>
A; Residues: 1-552 cMAR>
A; Residues: 1-552 cMAR>
A; Note: order of exons in Figure 2 is incorrect
B; Martiniuk, F.; Mehler, M.; Tzall, S.; Meredith, G.; Hirschhorn, R.
DNA Cell Biol. 9, 85-94, 1990
A; Title: Sequence of the cDNA and S'-flanking region for human acid alpha-glucosidase, s with previous cDNA and amino acid sequences.
A; Reference number: A32609; MUID:90262651; PMID:2111708
A; Accession: A32609
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A;Status: not compared with conceptual translation
A;Nolecule type: mRNA
A;Nolecule type: mRNA
A;Residues: 1-90,'N', 92-129 <MA3>
R;Hoefsloot, L.H.; Hoogeveen-Westerveld, M.; Kroos, M.A.; van Beeumen, J.; Reuser, A.;
EMBO J. 7, 1697-1704, 1988
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C; Superfamily: lysosomal alpha-glucosidase; sucrase/isomaltase homology; trefoil homo)
C; Keywords: glycoprotein; glycosidase; hydrolase; lysosomal storage disease; lysosome;
F; 22-130/Domain: trefoil homology <TRF>
F; 208-867/Domain: trefoil homology <TRF>
F; 208-867/Domain: sucrase/isomaltase homology <SIM>
F; 20-105, 120-105, 120-105, 120-105, 120-105, 120-105, 120-105, 120-105, 120-105, 120-105, 120-105, 120-105, 120-105, 120-105, 120-105, 120-105, 120-105, 120-105, 120-105, 120-105, 120-105, 120-105, 120-105, 120-105, 120-105, 120-105, 120-105, 120-105, 120-105, 120-105, 120-105, 120-105, 120-105, 120-105, 120-105, 120-105, 120-105, 120-105, 120-105, 120-105, 120-105, 120-105, 120-105, 120-105, 120-105, 120-105, 120-105, 120-105, 120-105, 120-105, 120-105, 120-105, 120-105, 120-105, 120-105, 120-105, 120-105, 120-105, 120-105, 120-105, 120-105, 120-105, 120-105, 120-105, 120-105, 120-105, 120-105, 120-105, 120-105, 120-105, 120-105, 120-105, 120-105, 120-105, 120-105, 120-105, 120-105, 120-105, 120-105, 120-105, 120-105, 120-105, 120-105, 120-105, 120-105, 120-105, 120-105, 120-105, 120-105, 120-105, 120-105, 120-105, 120-105, 120-105, 120-105, 120-105, 120-105, 120-105, 120-105, 120-105, 120-105, 120-105, 120-105, 120-105, 120-105, 120-105, 120-105, 120-105, 120-105, 120-105, 120-105, 120-105, 120-105, 120-105, 120-105, 120-105, 120-105, 120-105, 120-105, 120-105, 120-105, 120-105, 120-105, 120-105, 120-105, 120-105, 120-105, 120-105, 120-105, 120-105, 120-105, 120-105, 120-105, 120-105, 120-105, 120-105, 120-105, 120-105, 120-105, 120-105, 120-105, 120-105, 120-105, 120-105, 120-105, 120-105, 120-105, 120-105, 120-105, 120-105, 120-105, 120-105, 120-105, 120-105, 120-105, 120-105, 120-105, 120-105, 120-105, 120-105, 120-105, 120-105, 120-105, 120-105, 120-105, 120-105, 120-105, 120-105, 120-105, 120-105, 120-105, 120-105, 120-105, 120-105, 120-105, 120-105, 120-105, 120-105, 120-105, 120-105, 120-105, 120-105, 120-105, 120-105, 
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A;Molecule type: mRNA
A;Residues: 631-644, "W,646-680 «RES>
A;Residues: 631-644, "W,646-680 «RES>
A;Cross-references: GB:S/6893; NID:9912786; PIDN:AAB33842.1; PID:9912787
A;Note: homozygous mutation of Asp-645 to His causes an infantile form of Pompe's dise; R;Fuller, M.; van der Ploeg, A.; Reuser, A.J.J.; Anson, D.S.; Hopwood, J.J.
Eur. J. Blochem. 234, 903-909, 1995
A;Title: Isolation and characterisation of a recombinant, precursor form of lysosomal A;Reference number: S63526; MUID:96163476; PMID:8575451
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   R;Martiniuk, F; Bodkin, M.; Tzall, S.; Hirschhorn, R.
Am. J. Hum. Genet. 47, 440-445, 1990
A;Title: Identification of the base-pair substitution responsible for a human acid alg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A; Molecule type: protein
A; Residues 70-99;123-126, VLL',130-145;204-215;230-249;332-345;349-370;394-401,'R',46
A; Residues 70-99;123-126, VLL',130-145;204-215;230-249;332-345;349-370;394-401,'R',46
R; Lin, C.Y.; Shieh, J.J.
Biochem. Biophys. Res. Commun. 208, 886-893, 1995
A; Title: Identification of a de novo point mutation resulting in infantile form of Pon A; Reference number: 152309; MUID:95209708; PMID:7695647
A; Accession: 152309; MUID:95209708; PMID:7695647
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A;Residues: 1-126,'VLL',130-198,'R',200-222,'H',224-371,'L',373-401,'R',403-412,'TSRS7
A;Cross-references: EMBL:Y00839
A;Accession: S18847
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A,Residues: 68-74,'X',76-79,'X',81 <FUL>
C,Comment: In common with other lysosomal enzymes, posttranslational processing incluce processing at both amino and carboxyl ends.
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A;Introns: 182/3; 231/2; 286/3; 319/1; 359/1; 398/3; 442/3; 479/3; 517/3; 546/1; 585/;
A;Note: GAA 1, GAA 2, and GAA 4 are common alleles in the normal population
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A; Cross-references: GB:M34424; NID:g182907; PIDN:AAA52506.1; PID:g182908
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A;Reference number: A35698; MJID:90365036; PMID:2203258 A;Contents: partial sequence of GAA 2 allelic form
                compared with conceptual translation
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A; Residues: 1-952 < MA2>
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C;Date: 21-May-1990 #sequence revision 05-Apr-1995 #text change 18-Jun-1999
C;Accession: A40577; A32609; A35698; S00831; S18847; I52309; S63526
B;Martiniuk, F.; Bodkin, M.; Tzall, S.; Hirschhorn, R.
A;Title: Isolation and partial characterization of the structural gene for human acid A;Reference number: A40577; MUD:91229698; PMID:1674202
LNLHVSLETSERLRIRITDSSQQRWEIPETVIPR-----AGNHSPRRFSTEEDGGNSPE 126
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                                                  NNFLADPSSDLVFTLHNTTPFGFSVSRRSSGDILFDTSPDSSDSNTYFIFKDQFLQLSSA
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                               Gaps
Query Match 31.9%; Score 1515.5; DB 1; Length 952; Best Local Similarity 38.1%; Pred. No. 2.4e-95; Matches 336; Conservative 137; Mismatches 302; Indels 107;
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alpha-glucosidase (EC 3.2.1.20) - Rhizomucor circinelloides f. circinelloides C.Species: Rhizomucor circinelloides f. circinelloides C.bate: 10-May-1996 #sequence_revision 19-Jul-1996 #text_change 20-Jun-2000 C.Accession: JG4624; PC4149
.R.Sugimoto, M.; Suzuki, Y.

688 VSNDVQTLVGSDILLSPVLDEGKTSVKAQFPGGQWYDWYTHELTVDNKSNKKVKTVTLDA 747

PADHVNVHVREGSIVAMQGEALTTRDARKTPYQLLVVASRLENISGELFLDDGENLRMGA 795

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736

A; Title: Molecular cloning, sequencing, and expression of a cDNA encoding alpha-gluco A; Reference number: JC4624; MUID:96271012; PMID:8830045
A; Recession: JC4624
A; Molecule type: mRNA
A; Residues: 1-864 < 8001.
A; Residues: 1-864 < 8001.
A; Residues: 1-864 < 8001.
A; Residues: 203-214; 492-495; 612-623; 715-731; 742-751; 769-778 < 8002.
A; Residues: 203-214; 492-495; 612-623; 715-731; 742-751; 769-778 < 8002.
A; Residues: 203-214; 492-495; 612-623; 715-731; 742-751; 769-778 < 8002.
A; Residues: 203-214; 492-495; 612-623; 715-731; 742-751; 769-778 < 8002.
A; Residues: 203-214; 492-495; 612-623; 715-731; 742-751; 769-778 < 8002.
A; Residues: 203-214; 492-495; 612-623; 715-731; 742-751; 769-778 < 8002.
A; Residues: 203-214; 492-495; 612-623; 715-731; 742-751; 769-778 < 8002.
A; Note: the source is designated as Mucor javanicus IF04570
C; Comment: This encryme is an exo-carbohydrase, and catalyzes the splitting of an alph.
C; Superfamily: 1; Stosomal alpha-glucosidase; sucrase/isomaltase homology; trefoil homo C; Reywords: glycoprotein; glycoprotein; glycoprotein; glycoprotein; glycoprotein; elementates homology < SIM>
F; 122-805; Domain: sucrase/isomaltase homology < SIM>
F; 130/Active site: Asp #status predicted 66 YAPDIKSLNLHVSLETSERLRIRITDSSQQRWEIPETVIPRAGNHSPRRFSTEEDGGNSP 125 Gaps 93; 864; Length 31.6%; Score 1500.5; DB 2; 38.8%; Pred. No. 2.2e-94; Biochem, 119, 500-505, 1996

241 300 LIGRPAPMPYWSFGFHQCRYGYKNVSDLEYVVDGYAKAGIPLEVWWTDIDYMDGYKDFTL 359 210 LIGKPWMPSHWMLGWHHCRYGYPNIDKVETVKRKYKEANIPLQTVWVDIDYMEETKDFTF 329 DPVNFPEDKMQSFVDTLHKNGQKYVLILDPGIGVDSSYGTYNRGMEADVFIKR-NGEPYL 418 GEVWPGKVYPPDFLNPAAATFWSNEIKMFQEILPLDGLWIDMNELSNFITSPLSSG---- 474 ----SSLDDPP----YKINNSGDKRPINNKTVP 499 450 GNQPYRWTYTEEEQAANHTRWEKELKAMGNPPGEERNLLYPKYAINNGAGN--LSEFTVA 507 618 619 LGTARQELYLWDSVASSARKVLGLRMRLLPHLYTLMYEAHVSGNPIARPLFFSFPQDTKT 678 679 YEIDSQFLIGKSIMVSPALKQGAVAVDAYFPAGNWFDLFNYSFAVGGDSGKHVR---LDT 735 217 -----GKAHGALLMNAHGMDVITTEGRITYKVIGGILDFYFFAPKSGKPNDLSIAYTD 269 NHSFWPYLKNSIANILNFQMFGVSYSGADVCGFNSDTTEELCTRWMEIGAFYPFARNHNN 627 SALPENRSNLYGIGEHTKRSFRLIPGETMTLWNADIGSENPD----VNLYGSHPFYMDVRG SKGNEEAGTTHGVLLLNSNGMDVKYEGHRITYNVIGGVIDLYVFAGPS--PEMVMQYTE ATSIHFGNISEYDAHNLYGLLEAKATHQAVVDITGK-RPFILSRSTFVSSGKYTAHWTGD NAAKWEDLAYSIPGILNFGLFGIPMVGADICGFSHDTTEELCRRWIQLGAFYPFARDHSS E-NNFLADPSSDLVFTLHNTTPFGFSVSRRSSGDILFDTSPDSSDSNTYFIFKDQFLQLS Best Local Similarity 38.8%; Pred. No. 2.2e-94; Matches 307; Conservative 140; Mismatches 252; Indels FGKTIKDITVDVEYETEERLHVKISDKAKKQYLVPDSPL 330 200 559 568 1 126 360 628 185 242 419 475 ò CC ç q ò q ò g ò g ò S ò q ò a ठे 셤 ò g ò 5 ò

QY 212 TMTLWNADJGSENPDVNLYGSHPFYMDVRGSKGNEEAGTTHGVLLLNSNGMDVKYEGHRI 271 Eb 257 TWPIFTRDQHTDDNNNNLYGHQTFFMCIEDTTGKSFGVFLMNSNAMEIFLQPTPI 311 QY 272 -TYNVIGGVIDLYVFAGPSPEMVNQYTELIGRPAPMPYWSFGFHQCRYGYKNVSDLEYV 330 QY 1	Db 312 VTÝKVÍGGILDFÝIFLGDTPEGVVOGYGÉLÍGRÞÁMPAÝMÁSLGFQLSRMNÝNSLDVVKEV 371 GY 331 VDGYAKAGIPLEVMMTDIDYMEGYKDFTLDPVNFPEDKOMGSFVOTLHKNGGKYVLILDPG 390	OY 444 IXMFORILPLDGLWIDMNELSNFITSPLSSGSSLDDPPYXINNSGDKRPINNKTVPAT 501 :	OY 561 AKWEDLAYSIPGILAFGLFGIPMVGADICGFSHDTTEELCRRWIQLGAFYPFAEDHSSLG 620 : : :	Oy 678 TYEIDSQFLIGKSIMVSPALKQGAVAUDAYFPAGNWFDLFNYSFAVGGDSGKHVRLD 734 1	2y 795 AGGGNRDWTLVKFRCYVTGKSVVLRSEVVNPEYASKGKWSIGKVTFVGFENVENVKTYEV 854	RESULT 10 UUHJ UUHJ BUCTOSE alpha-glucosidase (EC 3.2.1.48) / oligo-1,6-glucosidase (EC 3.2.1.10) [validat sucrose alpha-glucosidase (EC 3.2.1.10) [validat N;Alternate names: limit dextrinase; small intestinal sucrase/isomaltase (SI) C.Species: Homo sapiens (man) C.Species: Homo sapiens (man) C.Date: 19-Nov-1988 #sequence_tevision 24-May-1996 #text_change 08-Dec-2000 C;Accession: S36082; AZ7326; S24329; A61136 R.Lacasa, M. R.Lacasa, M. R.Lacasa, M. R.Macheren umber: S36082	A,Accession: S36082 A,Accession: MAA A,Rolecule type: mRNA A,Rolecule type: mRNA A,Rolecule type: mRLA A,Residues: 1-1827 <lac> A,Cross-references: EMBL:X63597; NID:g36644; PIDN:CAA45140.1; PID:g36645 R,Green, F: Edwards, Y.; Hauri, H.P.; Povey, S.; Ho, M.W.; Pinto, M.; Swallow, D. R,Green, T. 101-110, 1987 A,itle: Isolation of a cDNA probe for a human jejunal brush-border hydrolase, sucrase A,Recession: A27326; MUD:88112852; PMID:2962903 A,Rocession: A27326 A,Rolecule type: mRNA A,Residues: 1-61, X', 663-678 <gre> A,Rolecule type: mRNA A,Residues: 1-61, X', 663-678 (GRE> A,Cross-references: GB.M.22616 R,Chantret, I: Lacasa, M.; Chevalier, G.; Ruf, J.; Islam, I.; Mantei, N.; Edwards, Y. Biochem. J. 285, 915-923, 1992</gre></lac>
Db 748 PLTHIPIHIRGGAIIPTKTPKYTVGETFATPYNLVIALDKKGQASGRLYIDDGESLEVKS 807 Qy 796 GGGNRDWT 803 :: : Db 808 SSGYHFHLQEWS 819	RESULT 9 A23945 sucrose alpha-glucosidase (EC 3.2.1.48) / oligo-1,6-glucosidase (EC 3.2.1.10) - rabbit NyAlternate names: small intestinal sucrase/isomaltase (SI) C;Species: Oryctolagus cuniculus (domestic rabbit) C;Date: 03-Mar-1994 #sequence_revision 03-Mar-1994 #text_change 24-May-1996 C;Accession: A23945; B25987; A29163 R;Hunziker, W.; Spiess, M.; Semenza, G.; Lodish, H.F. Cell 46, 227-234, 1986	A;Title: The sucrase-isomaltase complex: primary structure, membrane-orientation, and ev A;Reference number: A23945; MJD:86245068; PMID:3755079 A;Accession: A23945 A;Accession: A23945 A;Molecule type: mRNA A;Residues: 1-1827 <hun> R;Sjoestroem, H.; Noren, O.; Christiansen, L.A.; Wacker, H.; Spiess, M.; Bigler-Meier, EFBS Lett. 148, 321-325, 1982 A;Title: N-terminal sequences of pig intestinal sucrase-isomaltase and pro-survase-isomal</hun>	A; Reference number: A25987; MUID: 83105704; PMID: 7152027 A; Accession: B25987 A; Molecule type: protein A; Molecule type: protein A; Residues: 2-32, 'XXX', 36-38; 1008, 'N', 1010-1014, 'E' <532> R; Frank, G.; Brunner, J.; Jauser, H.; Wacker, H.; Semenza, G.; Zuber, H. FEBS Lett. 96, 183-188, 1978 A; Title: The hydrophobic anchor of small-intestinal sucrase-isomaltase. N-terminal seque A; Reference number: A29163: MIID: 79086207: PMID: 729784	A;Accession: A29163 A;Molecule type: protein A;Residues: 2, 'VNA',6-32, 'XXX',36-38 <fra> A;Residues: 2, 'VNA',6-32, 'XXX',36-38 <fra> C;Comment: Carbohydrate analysis of the mature enzyme complex indicates both N- and O-liac;Complex: the two product chains remain associated after cleavage C;Complex: the two product chains remain associated after cleavage C;Function: cISM- A;Description: oligo-1,6-glucosidase catalyzes the hydrolysis of 1,6-alpha-D-glucosidic A;Pathway: carbohydrate digestion</fra></fra>	C;Function: <suc> A;Description: sucrose alpha-glucosidase catalyzes the hydrolysis of the 1,2-alpha-D-glu A;Pethway: carbohydrate digestion C;Superfamily: sucrase/isomaltase; sucrase/isomaltase homology; trefoil homology C;Reywords: carbohydrate digestion; duplication; glycoprotein; glycosidase; hydrolase; m F;2-1607/Product: oligo-1,6-glucosidase (isomaltase chain) #status experimental <iso> F;3-3-109/Pomain: membrane associated #status predicted <imm> F;3-1607/Eroduct: oligo-1,6-glucosidase (isomaltase chain) F;3-109/Domain: trefoil homology <irfi></irfi></imm></iso></suc>	F;189-843/Domain: sucrase/isomaltase homology <sim> F;931-977/Domain: trefoil homology <trz> F;008-1827/Product: sucrose alpha-glucosidase (sucrase chain) #status experimental <sug <sim2="" domain:="" f;1062-1734="" homology="" isomaltase="" sucrase=""> F;12/Binding sites: carbohydrate (Thr) (covalent) #status experimental F;99,45,85,859,866,904,1235,1303,1325,1344,1364,1403,1535,1532,1748,1763,1799/Binding F;1007-1008/Cleavage site: Arg-Ile (trypsin) #status predicted Cuery Match Sites Arg-Ile (trypsin) #status predicted Similarity 35.3%; Pred. No. 2.9-84;</sug></trz></sim>	: Conservative 17: VVCYGYVVRSVGVDSNRQVI

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alpha-glucosidase (EC 3.2.1.20) - Aspergillus oryzae

C.Species: Aspergillus oryzae

C.Species: Aspergillus oryzae

C.Species: Apergillus oryzae

C.Species: Apergillus oryzae

C.Species: Apergillus oryzae

C.Species: Apergillus oryzae

R.Minetoki, T.; Gomi, K.; Kitamoto, K.; Kumagai, C.; Tamura, G.

Biosci. Biotechnol. Biochem. S9, 1516-1521, 1995

A.Title: Nucleotide sequence and expression of alpha-glucosidase-encoding gene (agdA)

A.Reference number: JC4217; MJID: 96032211; PMID: 7549103

A.Residues: L-985 cMIN

A.Residues: 1-985 cMIN

A.Residues: 1-985 cMIN

A.Cross-references: DDBJ: D45179; NID: g1054564; PIDN: BAA08125.1; PID: g1054565

C.Comment: This enzyme catalyzes the liberation of alpha-glucose from the non-reducing portant enzyme in the food industry as the isomalto-oligosaccharides.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A;Gene: agdA
A;Gene: agdA
A;Introns: 234(2; 371/2; 428/2
C;Superfamily: Schwarniomyces glucan 1,4-alpha-glucosidase GAM1; sucrase/isomaltase
C;Keywords: glycoprotein; glycosidase; hydrolase
F;152-898/Domain: sucrase/isomaltase homology <SIM>
F;152-898/Domain: sucrase/isomaltase homology <SIM>
F;126,145,255,349,424,508,536,539,602,624,661,835,881,929,957/Binding site: carbohyd
                                                                                  247 EAGTTHGVLLLNSNGMDVKYEGHRITYNVIGGVIDLYVFAGPSPEMVMNQY-TELIGRPA 305
                                               NKTVPATSI-HFGNISEYDAHNLYGLLEAKATHQAVVDI-TGKRPFILSRSTFVSSGKYT 552
                                                                                                                                                                                                                                                                                                                            SRNHNSDGYEHQDPAFFGQNSLLVKSSRQYLTIRYTLLPFLYTLFYKAHVFGETVARPVL 718
                                                                                                                                                                                                                                                                                                                                                                                       670 FSFPQDTKTYEIDSQFLIGKSIMVSPALKQGAVAVDAYFPAGNWFDLFNYSFAVGGDSG- 728
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     -----KHVRLDTPADHVNVHVREGSIVAMQGEALTTRDARKTPYQLLVVASRLENISGE 782
                                                                                                                                                               AHWIGDNAAKWEDLAYSIPGILNFGLFGIPMVGADICGFSHDTTEELCRRWIQLGAFYPF
                                                                                                                                                                                                                     AHWLGDNTASWEQMEWSITGMLEFSLFGIPLVGADICGFVAETTEELCRRWMQLGAFYPF
                                                                                                                                                                                                                                                                       ARDHSSLGTARQELYLWDS---VASSARKVLGLRMRLLPHLYTLMYEAHVSGNPIARPLF
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    161 PSFNFXVIRKATGDVLFNT-----KGSTLVYENQFIEFVTLLPE-EYNLYGLGERMNQ-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  31 ESTVVGYGYVVRSVGVDSNRQVLTAKLDLI-KPSSVYAPDIKSLNLHVSLETSERLRIRI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 290; Indels 136;
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larity 34.4%; Pred. No. 1.8e-84;
Conservative 142; Mismatches 290; Indels 13
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298; Conserv
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Matches 29
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C; Superfamily: sucrase/isomaltase isucrase/isomaltase homology; trefoil homology
C; Keywords: carbohydrate digestion; duplication; glycoprotein; glycosidase; hydrolase; m
F; 2-1007/Product: oligo-1,6-glucosidase (isomaltase chain) #status experimental «XATI»
F; 13-32/Domain: membrane associated #status predicted «TMM»
F; 42-60/Region: serine/threonine-rich
F; 519-109/Domain: trefoil homology «TRF»
F; 189-840/Domain: sucrase/isomantase homology «SIM»
F; 190-8-137/Product: sucrose alpha-glucosidase (sucrase chain) #status experimental «MAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     F;1062-1734/Domain: sucrase/isomaltase homology <SIM2>
*12/Dinding site: carbohydrate (Ser) (covalent) #status absent
F;99,437,455,825,904,926,1235,1303,1340,1354,1403,1535,1572,1675,1748,1763,18:5/Bind
F;1007-1008/Cleavage site: Arg-Ile (trypsin) #status predicted
                                                                                                                                                                                                                                               inte
              structure of the human sucrase-isomalt
                                                                                                                                                                                                                                                                                                                                                                                                                                                              A,Map position: 3425.2-3426.2
C;Complex: the two product chains remain associated after cleavage
C;Punction: <1SN-
A;Description: Oilyo-1,6-glucosidase catalyzes the hydrolysis of 1,6-alpha-D-glucosidic
A;Pathway: carbohydrate digestion
                                                                                                                                                                                                               Gastroenterology 101, 618-625, 1991
A;Title: Expression of sucrase-isomaltase and dipeptidylpeptidase IV in human small
A;Reference number: A61136; MUID:91317403; PMID:1677636
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              147
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            252 DLSWKTWPIFTRDQLPGDNNNNLYGHQTFFMCI-----EDTSGKSFGVFLMNSNAMEIFI 306
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                                                                                                                                                                                    L.; Rigal, A.; Bonicel, J.; Maroux, S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             34 VVGYGYVVR----SVGVDSNRQVLTAKLDLIKPSSVYAPDIKSLNLHVSLETSERLRIR
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                                                                                                                                                                                                                                                                                              A,Accession: A61136
A,Molecule type: protein
A,Residues: 2-14,'F',16-20;1008-1015,'E',1017-1021,'TX',1024
A;Reference number: S24329; MUD:92359963; PMID:1353958
A;Accession: S24329
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DB 1;
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Pred. No. 3.
                                                                                                                                                                                                                                                                                                                                                                                                                                            A;Cross-references: GDB:120377; OMIM:222900
                                                                                                                         A;Residues: 1-661,'F',663-931 <CHA>
A;Cross-references: EMBL:X63597
R;Gorvel, J.P.; Ferrero, A.; Chambraud,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   28.6%;
38.2%;
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Best Local Similarity
Matches 301; Conserv
                                                                                                    Molecule type: mRNA
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A;Gene: GDB:SI
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Glucan 1,4-alpha-glucosidase (EC 3.2.1.3) GAM1 precursor - yeast (Schwanniomyces occiding a cid maltase; glucoamylase c; Species: Schwanniomyces occidentalis c; Species: Schwanniomyces occidentalis c; Date: 10-Mar-1994 #sequence_revision 05-Apr-1995 #text_change 18-Jun-1999 c; Accession: JN0102 F; Dahlems, R.Johnen, R.J.; Strasser, A.W.M.; Dahlems, U.M.; Hollenberg, C.P. A; Strasser, A.W.M.; Dahlems, U.M.; Hollenberg, C.P. A; Title: Cloning of the Schwanniomyces occidentalis glucoamylase gene (GAM1) and its A; Reference number: JN0102; MUID:91071592; PMID:1979298
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             250 YLEHRYTPSENLNSDGQPSYTSSTHGVLALTANGMEVLLRPNYLQYRIIGGIVDLYIYVG 309
                                                                                                                                                                                                              310 GTKNPKDTVSQFVQSVGTPAMQQHWTFGFHICRWGYKNVFDLVEVKENFKNFEIPVDTFW 369
                                                                                                                                                                                                                                                              TDIDYMDGYKDFTLDPVNFPEDKMQSFVDTLHKNGQKYVLILDPGIGV-----DSSYG 398
                                                                                                                                                                                                                                                                                    466
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    -----ITSPLSSGS-----SLDDPPYKINNSGDKRPINNKTVP 499
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         500 ATSIHFGNISEYDAHNLYGLLEAKATHQAVVDI-TGKRPFILSRSTFVSSGKYTAHWTGD 558
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LGTARQELYLWDSVASSARKVLGLRMRLLPHLYTLMYBAHVSGNPIARPLFFSPPQDTKT 678
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           YEIDSOFLIGKSIMVSPALKQGAVAVDAYFPAGN---WFDLFNYSFAVGGDSGKHVRLDT 735
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PADHVNVHVREGSIVAMQGEALTTRDARKTPYQLLVVASRLENISGELFLDDGENLRMGA 795
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      145 WDAPLYHFQPQFGDRTYNFSF---NSQPFEFWVTRVSDGEVLFOTRGHK-----LIFED 195
                                           OFLOLSSALPENRSNLYGIGEHTKRSFRLIPGETMTLWNADIGSENP---DVNLYGSHPF
                                                                  236 YMDVR-----GSKGNEE-AGTTHGVLLLNSNGMDVKYEGHRITYNVIGGVIDLYVFAG
                                                                                                                                                                                       --PSPEMVMNQYTELIGRPAPMPYWSFGFHOCRYGYKNVSDLBYVVDGYAKAGIPLEVMW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           790 ANADRQFMVGSALLVTPVLEPNVDYVRGVFPGDNSTIMYDWYDHK-VIYRQHNENITLSA
                                                                                                                                                                                                                                                                                                                                      399 TYNRGMEADVFIKR-NGEPYLGEVWPGKVYFPDFLNPAAATFWSNEIKMFQEI-----
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A; Molecule type: mRNA
A; Residues: 1-958 < DOH>
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A,Cross-references: EMBL:AL133522; PIDN:CAB63549.1; GSFDB:GN0066; SPDB:SPAC922.32cA;Experimental source: strain 972h(-); cosmid c922
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Superfamily: Schwanniomyces glucan 1,4-alpha-glucosidase GAM1; sucrase/isomaltase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          probable family 31 glucosidase (imported) - fission yeast (Schizosaccharomyces) C;Species: Schizosaccharomyces pombe C;Species: Schizosaccharomyces pombe C;Date: O9-1000 #sequence_revision 09-Jun-2000 #text_change 21-Jul-2000 C;Accession: T50267
R;Hunt, C.; Aves, S.; McDougall, R.C.; Rajandream, M.A.; Barrell, B.G. R;Hunt, C.; Aves, S.; McDougall, R.C.; Rajandream, M.A.; Barrell, B.G. A;Reference number: Z25031
A;Reference number: Z25031
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                                                                                                                                392 YEEGEKFLANKLHAGGRRWVPIVDGALYIPNPENASDAYETYDRGAKDDVFIKNPDGSLY1 451
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 272 YVSYSHGVFLRNAHGQEILLRDQKLIWRTLGGSVDLTFYSGPTQAEVTKQYQLSTVGLPA 331
                                     PMPYWSFGFHQCRYGYKOVSDLEYVVDGYAKAGIPLEVMWTDIDYMDGYKDFTLDPVNFP
                                                                    MOQYNTLGFHQCRWGYNNWSEFEDVLANFERFEIPLEYLWADIDYMHGYRNFDNDQHRFS
                                                                                                            EDKMOSFVDTLHKNGQKYVLILDPGI-----GVDSSYGTYNRGMEADVFIKR-NGEPYL
                                                                                                                                                                                                                    452 GAVWPGYTVYPDWHHPKASDFWANELVTWWNKLHYDGVWYDMAEVSSFCVGSCGTGNLSM
                                                                                                                                                                                                                                                                                              NPAHPPFALPGEPGNVYDYPEGFNITNATEAASASAGAASQSAAASSTTTSAPYLRTTP
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                                                                                                                                                                                      GEVWPGKVYFPDFLNPAAATFWSNEIKMFQEILPLDGLWIDMNELSNFI-----
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Matches 303; Conservative 151; Mismatches 282;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             28.4%; Score 1350; DB 2; 33.4%; Pred. No. 5.5e-84;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gene: SPAC1039.11c; SPDB:SPAC922.02c
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Db 843 AESRQNPFGLIVALDNDGKAQGSLYLDDGESLVVDSSLLVSFSVSDN 889 Qy 820 SEVVNPEYASKWKWSIGKVTFVGFENVENVKTYEVRT 856 :	C;Date: 20-Oct-2000 #sequence_revision 20-Oct-2000 #text_change 20-Oct-2000 C;Accession: T3858; S65559; T38911 R;Pearson, D.; Churcher, C.M.; Barrell, B.G.; Rajandream, M.A.; Walsh, S.V. submitted to the EMBL Data Library, November 1995 A;Reference number: Z21801 A;Reference number: D18598 A;Molecule type: DNA A;Residues: 1-385 < PEA>	A;Cross_references: EMBL:267961; PIDN:CAA91887.1; GSPDB:GN00066; SPDB:SPAC30D11.01c A;Experimental source: strain 972h-; cosmid c30D11 R;Pearson, D.; Churcher, C.M. submitted to the EMBL Data Library, November 1995 A;Reference number: S62559 A;Accession: S62559 A;Accession: S62559 A;Accession: S62559 A;Accession: S62559 A;Reference number: S62559	. Walsh, S.V.	A.TOSS-TETEZENEES: EMBL:Z69,728; FIDN:CAM935/1.1; GSPUB:GNU0U005; SPUB:BFACSOF8.01 A.Experimental source: strain 972h-; cosmid C56F8 C;Genetics: A.Gene: SPOB:SPAC30D11.01c; SPDB:SPAC56F8.01 A.Map position: 1L C;Superfamily: Schwanniomyces glucan 1,4-alpha-glucosidase GAM1; sucrase/isomaltase h. F;165-384/Domain: sucrase/isomaltase homology (fragment) <sim></sim>	Query Match 28.3%; Score 1345.5; DB 2; Length 993; Best Local Similarity 33.6%; Pred. No. 1.1e-83; Matches 308; Conservative 151; Mismatches 302; Indels 157; Gaps 24; Qy 38 GYVVRSVGVDSNRQVLTAKLDLIKPSS-VYAPDIKSLNLHVSLETSERLRIRITDSSQQR 96	Qy 97 WEIPETVIPRAGNHSPRRFSTEEDGGNSPENNFLADPSSDLVFTLHNTTPFGFSVS 152 :::	CY 213 MTLWNADIGSENPOYNLYGSHPFYMDVRGSKGNEEAGTTHGYLLLNBNGMDVKYEG 268 235 KTFW-ATGYGUSPEANWYGSHPFYMDVRGSKGNEEAGTTHGYLLLNBNGMDVKYEG 268 CA 269 HRITTWYLGGVLDLYYPGPSPENVANOYTELIGRPAPMPYWSFGFHQCRYGYKUVSD 326 Db 293 TYIKYRMIGGIIDLEVYSGSTVSPKYTIQQYVQSIGTPTMQPYWSLGFQWSRWGYKTLSD 352 CO 327 LEYVVDGYAKAGIPLEVWMTDIDYMDGYKDFTLDPVNFPEDKMQSFVDTLHKUNGQKYULI 386 Db 327 LEYVVDGYAKAGIPLEVWMTDIDYMBGFKTLDPVNFPEDKMQSFVDTLHKUNGQKYULI 386 CO 327 LEYVVDGYAKAGIPLEVWMTDIDYMBGFKTFFTVNSTAFPPNOTLDFFRSLDESHQHYVPV 412 CO 337 LDPGIGVDSSYGTYNRGMEADVFIKR-NGEPYLGEVWPGKYYFDDFLNPAAAT 438 CO 387 LDPGIGVDSSYGTYNRGMEADVFIKR-NGEPYLGEVWPGKYYFDDFLNPAAAT 438 413 LDPAIYAANPHKSADRTYYPYYSGFEDNIFIKNPNGSATVGMAMFGFVVYPDFTNPAVLO 472
nces: GB:M50207; GB:M34666; NID:g169845; FIDN:AAA33923.1; FID:g169846 Schwanniomyces glucan 1,4-alpha-glucosidase GAMI; sucrase/isomaltase hom signal sequence #status predicted <sig> ct: glucan 1,4-alpha-glucosidase #status predicted <mat> in: sucrase/isomaltase homology <sim> 3,416,513,580,602,813,907/Binding site: carbohydrate (Asn) (covalent) #stite: Asp #status predicted</sim></mat></sig>	Query Match 28.4%; Score 1347; DB 1; Length 958; Best Local Similarity 34.5%; Pred. No. 8.3e-84; Matches 326; Conservative 136; Mismatches 320; Indels 164; Gaps 28; Qy 8 PNIFIVVVPFSLRSSQVVLEEEESTVVGYGYVVRSVGVDSNRQVLTAKLDLIKPSSVYA 67	68 PDIKSLNIAVSLETSERLRIRITDSSQQRWEIPETVIPRAGNHSPRRFSTEEDGGGNSP 125	OY 186 ALPENSOLYGIGEHTKRSFRIIPOETWILWNADIGSENDOWLYGSHPPYMDVRGSK 243	OY 304 PAPMPYWSFGFHOCRYCYKONOSDLEYVVDGYAKAGIPLEVXWJDIDYMDGYKDFTLDPVN 363	416 PYLGEVWPGKVYFPDFLNPAAATFWSNEIKWFOEILPLDGIWIDWNELSNFI		OY 587 DICGFSHDTTEELCRRWIQLGAFYPFARDHSSLGTARQELYLWDSVASSARKVLGLRRWL 646

182

227 282 286 337 346 397 459

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                                                                                                                                                183 -- PHOFVKEETG-----IPAADTLYDVQVSENPFSIKVIRKSNNKVLCDTSVGP-
                                                                                                                                                                                                            DSNTYFIFKDQFLQLSSALPENRSNLYGIGEHTKRSFRL-IPGETMTLMNADIGSENPDV
Search completed: October 27, 2003, 10:22:15 Job time: 28.5784 secs
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R;Chandrasena, G; Osterholm, D.E.; Sunitha, I.; Henning, S.J.
Gene 150, 355-360, 1994

A;Title: Cloning and sequencing of a full-length rat sucrase-isomaltase-encoding cDNA, A;Reference number: Z17155; MUID:95121929; PMID:7821806
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C,Species: Rattus norvegicus (Norway rat)
C,Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 21-Jul-2000
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A;Molecule type: mRNA
A;Residues: 1-1841 <CHA>
A;Cross-references: EMBL:L25926; NID:g414818; PIDN:AAA65097.1; PID:g773669
A;Experimental source: strain Sprague-Dawley, intestine
                                  --ITSPLSSGSS
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                                  FWSNEI - - - - - - - - - KMFQEILPLDGLWIDMNELSNF
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1393.955 Million cell updates/sec
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1 MSSLHWFPNIFIVVVVFFSL......EVSKLSLLVGKKFEMRLRLT 902
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| cgn2_6/ptodata/1/pubpaa/USO6_PUBCOMB.ppp: +
| cgn2_6/ptodata/1/pubpaa/USO6_PUBCOMB.ppp: +
| cgn2_6/ptodata/1/pubpaa/USO7_NEW_PUB.ppp: +
| cgn2_6/ptodata/1/pubpaa/USO7_NEW_PUB.ppp: +
| cgn2_6/ptodata/1/pubpaa/USO8_PUBCOMB.ppp: +
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| cgn2_6/ptodata/1/pubpaa/USO8_PUBCOMB.ppp: +
| cgn2_6/ptodata/1/pubpaa/USO9_PUBCOMB.ppp: +
| cgn2_6/ptodata/1/pubpaa/USO0_PUBCOMB.ppp: +
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GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
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Maximum Match 100%
Listing first 45 summaries
                                                                                                                                                      OM protein - protein search, using sw model
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Gapop 10.0 , Gapext 0.5
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Maximum DB 9
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ALIGNMENTS

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KPSSVYAPDIKSLNLHVSLETSERLRIRITDSSQQRWEIPETVIPRAGNHSPRRFSTEED 120
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                                                                           APPLICANT: Muslin, Elizabeth H.
APPLICANT: Muslin, Elizabeth H.
APPLICANT: Muslin, Elizabeth H.
APPLICANT: Muslin, Elizabeth H.
APPLICANT: Muslin, Elizabeth H.
TITLE REPERENCE: 960296, 97486
FILE REPERENCE: 960296, 97486
CURRENT APPLICATION NUMBER: US/10/043,418
CURRENT FILING DATE: 2002-06-25
FRIOR FILING DATE: 2001-01-10
NUMBER OF SEQ ID NOS: 7
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 4
LENGTH: 902
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100.0%; Pred. No. 0;
tive 0; Mismatches
               Sequence 4, Application US/10043418; Publication No. US20020184662A1; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Best Local Similarity 100.
Matches 902; Conservative
                                                                                                                                                                                                                                                                                                                                                              ; TYPE: PRT
; ORGANISM: Arabidopsis
US-10-043-418-4
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243 PFYMDVRSS---PVAGSTHGVLLLNSNGMDVEYTGNRITYKVIGGIIDLYFFAGPSPGQV 299
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                                                                                                                                                    GKPYLGSVWPGPVYFPDFLKRSALTFWTDEIKRFLNLLDVDGLWIDMNEISNFISSPPIP 479
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                                                                                                  174 FIFKDOFLOLSSALPENRSNLYGIGEHTKRSFRLIPGETMTLWNADIGSENPDVNLYGSH
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                                                                                 9 PNIFIVVVVFFSLR---SSOVVLBEEESTVVGYGYVVRSVGVDS-NRQVLTAKLDLIKPS
                                                                                                                                     SVYAPDIKSLNLHVSLETSERLRIRITDSSQQRWEIPETVIPRAGNHSP------RRFST
                                                                                                                                                                                          118 EEDGGNSPENN----FLADPSSDLVFTLANTTPFGFSVSRRSSGDILFDTSPDSSDSNTY
                                                          Gaps
                                 DB 14; Length 903;
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                             Guery Match 59.6%; Score 2830.5; DB 14; Length Best Local Similarity 59.6%; Pred. No. 8.7e-255; Matches 540; Conservative 138; Mismatches 205; Indels
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               LQLSSALPENRSNLYGIGEHTKRSFRLIPGETMTLKNADIGSENPOVNLYGSHPFYMDVR
                                                                                                                                                                           PYKINNSGDKRPINNKTVPATSIHFGNISBYDAHNLYGLLEAKATHQAVVDITGKRPFIL
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Publication No. US20020184662A1
GENERAL INFORMATION:
APPLICANT: HOHSON, Cynthia A.
APPLICANT: Muslin, Elizabeth H.
APPLICANT: Clark, Suzanne E.
ITILE OF INVENTION: Modified barley alpha-glucosidase
FILE REPERENCE: 960296.97486
CURRENT FILING DATE: 2002-06-25
PRIOR APPLICATION NUMBER: 60,260,787
PRIOR PILING DATE: 2001-01-10
NUMBER: PATENTING DATE: 2001-01-10
SOFTWARE: Patentin Ver. 2.1
SEQ ID NOS: 7
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ORGANISM: Spinach
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APPLICANT: Henson, Cynthia A.
APPLICANT: Huslin, Elizabeth H.
APPLICANT: Clark, Suzame E.
TITLE OF INVENTION: Modified barley alpha-glucosidase
FILE REFERENCE: 960296.97486
CURRENT PILING DATE: 2002-06-25
PRIOR APPLICATION NUMBER: 60/260,787
PRIOR APPLICATION NUMBER: 60/260,787
PRIOR APPLICATION NUMBER: 2001-010
NUMBER FILING DATE: 2001-010
SOFFWARE: PATENTIN VET. 2.1
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Best Local Similarity 55.2%; Pred. No. 2.4e-219;
Matches 471; Conservative 136; Mismatches 191;
                                                                                                                                                                                                                                                                                                                                                       Sequence 1, Application US/10043418
Publication No. US20020184662A1
GENERAL INFORMATION:
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                                                         APPLICANT: Henson, Cynthia A.
APPLICANT: Henson, Cynthia A.
APPLICANT: Huslin, Elizabeth H.
APPLICANT: Clark, Suzanne E.
TITLE COF INVENTION: Modified barley alpha-glucosidase
FILE REFRENCE: 960296.97486
CURRENT APPLICATION NUMBER: US/10/043,418
CURRENT FILING DATE: 2002-06-25
PRIOR APPLICATION NUMBER: 60/260,787
PRIOR PILING DATE: 2001-01.10
NUMBER: PATENTING DATE: 2001-01.10
SOFTWARE: PATENTIN VET. 2.1
Sequence 2, Application US/10043418
Publication No. US20020184662A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                TYPE: PRT
CORGANISM: Sugar beet
US-10-043-418-2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 707;
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PRIOR FILING DATE: 2001-03-08
PRIOR APPLICATION NUMBER: 60/277,826
PRIOR FILING DATE: 2001-03-22
PRIOR APPLICATION NUMBER: 60/279,840
PRIOR FILING DATE: 2001-03-29
PRIOR FILING DATE: 2001-03-29
PRIOR FLING DATE: 2001-04-11
PRIOR PLING DATE: 2001-04-11
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PRIOR PLING DATE: 2001-07-31
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                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: PRT
ORGANISM: Artificial Sequence
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                                                      CRRWIQLGAFYPFARDHSSLGTARQELYLWDSVASSARKVLGLRMRLLPHLYTLMYEAHV
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                                 LSRSTFVSSGKYTAHWTGDNAAKWEDLAYSIPGILNFGLFGIPWVGADICGFSHDTTEEL
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APPLICANT: Smithson, Glennda
TITLE OF INVENTION: Proteins and Nucleic Acids Encoding Same
FILE REFERENCE: 21402-228
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PRIOR APPLICATION NUMBER: 60/257,495
PRIOR PRILING DATE: 2000-12-21
PRIOR FILING DATE: 2000-12-21
PRIOR FILING DATE: 2000-12-20
PRIOR FLING DATE: 2000-12-20
PRIOR FLILING DATE: 2001-02-20
PRIOR PRILING DATE: 2001-02-20
PRIOR PRILING DATE: 2001-02-20
PRIOR APPLICATION NUMBER: 60/269,940
PRIOR APPLICATION NUMBER: 60/274,192
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Publication No. US20030170630A1
GENERAL INFORMATION:
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Grosse, William M
Lepley, Denise M
Burgess, Catherine E
Shimkets, Richard A
Grosse, William M
Szekeres, Edward S
Vernet, Corine A.M.
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APPLICANT: Tchernev, Velizar T
APPLICANT: Liu, Xiaohong
APPLICANT: Spytek, Kimberly A
APPLICANT: Zerhusen, Bryan D
APPLICANT: Patturajan, Meera
APPLICANT: Grosse, William M
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Boldog, Ferenc L
Gorman, Linda
Gangolli, Esha A
Fernandes, Elma R
Rieger, Daniel K
Edinger, Shiomit R
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LVVGEEFELKVAMS 876
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Sciore, Paul
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613 ARDHSSLGTARQELYLWDS---VASSARKVLGLRMRLLPHLYTLMYEAHVSGNPIARPLF 669
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T: Millet, Isabelle
T: Sciore, Paul
T: Ellerman, Karen
T: MacDougall, John R
T: Smithson, Glennda
T: Smithson, Glennda
T: WWENTION: Proteins and Nucleic Acids Encoding Same
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CURRENT FILING DATE: 2001-12-21
PRIOR APPLICATION NUMBER: 60/257,495
PRIOR FILING DATE: 2000-12-21
PRIOR FILING DATE: 2000-12-20
PRIOR FILING DATE: 2000-12-20
PRIOR APPLICATION NUMBER: 60/269,940
PRIOR APPLICATION NUMBER: 60/209,940
PRIOR PILING DATE: 2001-03-08
PRIOR PELING DATE: 2001-03-08
PRIOR APPLICATION NUMBER: 60/274,192
PRIOR APPLICATION NUMBER: 60/279,840
PRIOR PILING DATE: 2001-03-29
PRIOR PILING DATE: 2001-03-29
PRIOR PLING DATE: 2001-03-29
PRIOR APPLICATION NUMBER: 60/293,656
PRIOR APPLICATION NUMBER: 60/283,656
PRIOR APPLICATION NUMBER: 60/283,656
PRIOR APPLICATION NUMBER: 60/283,656
PRIOR APPLICATION NUMBER: 60/309,247
PRIOR FILING DATE: 2001-04-13
PRIOR PELING DATE: 2001-04-13
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PRIOR FILING DATE: 2001-04-13
PRIOR FILING DATE: 2001-04-13
                                                                                                                                                                                                                                                                                                                                                                       Sequence 44, Application US/10032189; Publication No. US20030170630A1; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Burgess, Catherine E
Shimkets, Richard A
Grosse, William M
Szekeres, Edward S
Vernet, Corine A.M.
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APPLICANT: Tchernev, Velizar T
APPLICANT: Liu, Xiaohong
APPLICANT: Spytek, Kimberly A
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Boldog, Ferenc L
Gorman, Linda
Gangolli, Esha A
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Grosse, William M
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Rieger, Daniel K
Edinger, Shlomit F
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                                                                                                                                                                                                                                   783 LFLDDGE 789
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US-10-032-189-44
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APPLICANT: Park, Jason
APPLICANT: Park, Jason
APPLICANT: Park, Jason
APPLICANT: Schulz, Stephanie
TITLE OF INVENTION: Compositions And Methods For Identifying And Targeting Cancer (
TITLE OF INVENTION: Alimentary Canal Origin
FILE REFERENCE: TJU2413
CURRENT FILING DATE: 2001-03-27
PRIOR APPLICATION NUMBER: 60/192,229
PRIOR FILING DATE: 2000-03-27
NUMBER OF SEQ ID NOS: 2
SOFTWARE: Patentin version 3.0
SEQ ID NO 2
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                845
                                         ITDSSQQRWEIPETVIPRAGNHSPRRFSTEEDGGNSPENNFLADPSSDLVFTLH-NTTPF
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                788 GENLRMGAGGGNRDWTLVKFRCYVTGKSVVLRSEVVNPEYASKMKWSIGKVTFVGFEN
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Best Local Similarity 38.2%; Pred. No. 6.8e-117;
Matches 301; Conservative 138; Mismatches 258;
                                                                                                                                                  Sequence 2, Application US/09819247
Patent No. US20010036635A1
GENERAL INFORMATION:
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US-09-819-247-2
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US-09-819-247-2
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Sequence 40, Application US/10032189
Publication No. US20030170630A1
GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Alsobrook II, John P
APPLICANT: Tchernev, Velizar T
APPLICANT: Liu, Xiaohong
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Vernet, Corine A.M.
                                                  886 KLSLLVGKKFEMRL 899
                                                                                                               898 KLSLNIATDWEVRI 911
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Ferenc L
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Gorman,
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18.5%; Score 877.5; DB 12; Length 912;
Best Local Similarity 27.7%; Pred. No. 2.5e-72;
Matches 253; Conservative 152; Mismatches 326; Indels 183;
PRIOR APPLICATION NUMBER: 60/313,331
PRIOR FILING DATE: 2001-08-17
NUMBER OF SEQ ID NOS: 260
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 44
                                                                                                                                                                                                                    TYPE: PRT
ORGANISM: Homo sapiens
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APPLICANT: Gorman, Linda
APPLICANT: Gorman, Linda
APPLICANT: Gangolli, Esha A
APPLICANT: Rieger, Daniel R
APPLICANT: Edinger, Shlonit R
APPLICANT: Gunther, Erik
APPLICANT: Gunther, Erik
APPLICANT: Sciore, Paul
APPLICANT: Sciore, Paul
APPLICANT: MacDougall, John R
APPLICANT: Smithson, Glennda
TITLE OF INVENTION: Proceins and Nucleic Acids Encoding Same
FILE REFERENCE: 21402-228
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PRICR APPLICATION NUMBER: 60/257,495
PRICR FILING DATE: 2000-12-21
PRICR APPLICATION NUMBER: 60/257,495
PRICR APPLICATION NUMBER: 60/259,171
PRICR FILING DATE: 2000-12-20
PRICR FILING DATE: 2001-02-20
PRICR FILING DATE: 2001-03-20
PRICR FILING DATE: 2001-03-20
PRICR FILING DATE: 2001-03-20
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PRICR PILING DATE: 2001-08-17
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                                                                                           144 T-TPFGFS-----VSRRSSGDILF-------DTSPDSSDSNTYFIFK 177
                                                                                                                                               D------QFLQLSSALPEN-----RSNLYGIGEHTKRSFRLI---PGETMTLW 216
                                                                                                                                                                                                                                                                                                        FGFHQCRYGYKNVSDLEYVVDGYAKAGIPLEVMWTDIDYMDGYKDFTLDPVNFPEDXXQS 371
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                                                                                                                                                                                                                 83 RLKINEETPLKPRFEVPDVLTSKPS--TVRLISCSGDTGSL----ILADGKGDL--KCHI
                                                                                                                                                                                                                                                    -----GGVIDLYVFAGPSPEMVMNOYTELIGRPAPMPYWS
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                                         84 RLRIRITDSSQQRWEIPETVIPRAGNHSPRRFSTEEDGGNSPENNFLADPSSDLVFTLHN
                                                                                                                                                                                                 NADI-GSENPD-VNLYGSHPFYMDVRGSKGNEEAGTTHGVLLLNSNGMDVKYEGH-RITY
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               Matches 256; Conservative 152; Migmatches 322; Indels 187; Gaps
 27.9%; Pred. No. 3.1e-72;
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Best Local Similarity
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Sequence 120, Application US/10032189 Publication No. US20030170630A1 GENERAL INFORMATION:

RESULT 9 US-10-032-189-120

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103 VIPRAGNHSPRRFSTEEDGGNSPENNFLADPSSDLVFTLHNTTPFGFSVSRRSSGDLLFD 162
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APPLICANT: Mactobogall, Oshn K
APPLICANT: Smitthson, Glenada
ITILE OF INVENTION: Proteins and Nucleic Acids Encoding Same
ITILE OF INVENTION: Proteins and Nucleic Acids Encoding Same
ITILE OF INVENTION: Proteins and Nucleic Acids Encoding Same
CURRENT APPLICATION WURBER: US/10/032,189
CURRENT FILING DATE: 2001-12-21
PRIOR PLING DATE: 2000-12-21
PRIOR APPLICATION WURBER: 60/269,940
PRIOR APPLICATION WURBER: 60/269,940
PRIOR APPLICATION WURBER: 60/269,940
PRIOR PLING DATE: 2001-03-08
PRIOR PLING DATE: 2001-03-08
PRIOR PLING DATE: 2001-03-29
PRIOR PLING DATE: 2001-03-29
PRIOR APPLICATION WURBER: 60/279,840
PRIOR PLING DATE: 2001-04-11
PRIOR PLING DATE: 2001-04-11
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PRIOR PLING DATE: 2001-04-13
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                                                                                                                                                                                                                     Burgess, Catherine E
Shimkets, Richard A
Grosse, William M
Tchernev, Velizar T
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Fernandes, Elma R
Rieger, Daniel K
Edinger, Shlomit R
Gunther, Brik
Millet, Isabelle
Sciore, Paul
                                                    Liu, Xiaohong
Spytek, Kimberly A
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                                                                                                                                                                                                                                                                                                         Szekeres, Edward S
Vernet, Corine A.M
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Grosse, William M
Lepley, Denise M
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Ferenc L
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MacDougall, Johr
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178 D------QFLQLSSALPEN-----RSNLYGIGEHTKRSFRLI----PGETWTLW 216
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                                                                                                                                                                                                        APPLICANT: Ellerman, Karen
APPLICANT: Ellerman, Karen
APPLICANT: MacDougall, John R
APPLICANT: Smithson, Glennda
TITLE OF INVENTION: Proteins and Nucleic Acids Encoding Same
FILE REFERENCE: 21402-228
CURRENT FILING DATE: 2001-12-21
PRIOR APPLICATION NUMBER: 60/257, 495
PRIOR APPLICATION NUMBER: 60/259, 171
PRIOR APPLICATION NUMBER: 60/259, 171
PRIOR PILING DATE: 2000-12-20
PRIOR PLING DATE: 2000-12-20
PRIOR PLING DATE: 2000-02-20
PRIOR FILING DATE: 2001-03-20
PRIOR PLING DATE: 2001-03-20
PRIOR PLING DATE: 2001-03-22
PRIOR APPLICATION NUMBER: 60/277, 826
PRIOR PLING DATE: 2001-03-22
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                            Gorman, Linda
Gangolli, Esha A
Fernandes, Elma R
Rieger, Daniel K
Edinger, Shlomit R
Gunther, Erik
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Sciore, Paul
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SOFTWARE: PatentIn Ver. 2.1
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TYPE: PRT
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APPLICANT:
APPLICANT:
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TSPDSSDSNTYFIFKDQFLQLSSALPENRSNLYGIGEHTKRSFRL---IPGETMTLWAD 219
                                                                                              ---FYMDVRGS----KGNEEAGTTHGVLL--L 257
                                                                                                                                                                                                                                                                                                             NPAAATFWSNEIKM--FQEILPLDGLWIDMNELSNPITSPLSSGSSLDDPPYKINNSGDK 490
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                                             251 TFKTHSDSKPY---GPMSVGLDFSLP-GMEHVYGIPEHAD-NLRLKVTEGGEPYRLYNLD 305
                                                                                                                                                                                                                                365 QGSGETPOTDVRWMSET-----GIIDVFLLLGPSISDVFRQYASLTGTQALPPLFSLG 417
                                                                                                                                                                                                                                                                              FHQCRYGYKNVSDLEYVVDGYAKAGIPLEVMWTDIDYMDGYKDFTLDPVNFPEDKMQSFV 373
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                                                                                                                                    306 VFOYELYNP-MALYGSVPVLLAHNPHRDLGIFWLNAAETWVDISSNTAGKTLFGKMOYL
                                                                                                                                                                                    258 NSNG----MDVKYEGHRITYNVIGGVIDLYVFAGPSPEMVMNQYTELIGRPAPMPYWSFG
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Publication No. US20030170630A1
GENERAL INFORMATION:
APPLICANT: Alsobrook II, John P
APPLICANT: Tchernev, Velizar T
APPLICANT: Liu, Xiaohong
APPLICANT: Liu, Xiaohong
APPLICANT: Spyrek, Kimberly A
APPLICANT: Serhusen, Bryan D
APPLICANT: Gerhusen, Bryan D
APPLICANT: Gerhusen, Bryan D
APPLICANT: Lepley, Denise M
APPLICANT: Burgess, Catherine E
APPLICANT: Shimkets, Richard A
APPLICANT: Shimkets, Richard A
APPLICANT: Grosse, William M
APPLICANT: Grosse, William M
                                                                                           IGS---ENPDVNLYGSHP----
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Vernet, Corine A.M.
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                                                                                               489 DKRPINNKTVPATSIHFGNISEYDAHNLYGLLEAKATHQAVVDIT-GK-RPFILSRSTFV 546
                                                                                                                                                                                              GAFYPFARDHSSLGTARQELYLW-DSVASSARKVLGLRMRLLPHLYTLMYEAHVSGNPIA 665
                                                                                                                                                                                                                                                              LFLDDGENLRMGAGGGNRDWTLVKFRCYVTGKSVVLR----SEVVNPEYASK-----MK 832
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                                                                                                                                                                                                                                             666 RPLFFSFPQDTKTYEIDSQFLIGKSIMVSPALKQGAVAVDAYFPAGN--WFDLFNYSFAV 723
              FLNPAAATFWSN--EIKMFQEILPLDGLWIDMNELSNFITSPLSSGSSLDDPPYKINNSG
                                                                                                              547 SSGKYTAHWIGDNAAKWEDLAYSIPGILNFGLFGIPMVGADICGFSHDTTEELCRRWIQL
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                                                                      FINDKVREWYSSLFAFPVYQGSTDILFLWNDMNEPSVF----
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Publication No. US20030170630A1
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Shimkets, Richard A
Grosse, William M
Szekeres, Edward S
Vernet, Corine A.M.
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E--KLSLNIATDWEVRI 913
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APPLICANT: Alsobrook II, John P
APPLICANT: Tchernev, Velizar T
APPLICANT: Liu, Xiaohong
APPLICANT: Spytek, Kimberly A
APPLICANT: Zerhusen, Bryan D
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Gunther, Erik
Millet, Isabelle
Sciore, Paul
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Gorman, Linda
Gangolli, Esha A
Fernandes, Elma R
Rieger, Daniel K
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MacDougall, John R
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Grosse, William M
Lepley, Denise M
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Ferenc L
Linda
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TITLE OF INVENTION: Proteins and Nucleic Acids Encoding Same FILE REFERENCE: 21402-228
CURRENT APPLICATION NUMBER: US/10/032,189
CURRENT FILING DATE: 2001-12-21
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                                                                                                                                                                          PRIOR APPLICATION NUMBER: 60/257,495
PRIOR FILING DATE: 2000-12-1
PRIOR FILING DATE: 2000-12-21
PRIOR FILING DATE: 2000-12-20
PRIOR FILING DATE: 2000-12-20
PRIOR FILING DATE: 2001-02-20
PRIOR PELING DATE: 2010-02-20
PRIOR PILING DATE: 2011-02-20
PRIOR FILING DATE: 2001-03-08
PRIOR FILING DATE: 2001-03-08
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PRIOR FILING DATE: 2001-03-08
PRIOR PILING DATE: 2001-03-22
PRIOR PLING DATE: 2001-03-29
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PRIOR PORTAME: PARENTE AND PARENTE PARENTE PARENTE PARENTE PARENTE PARENTE PARENTE PARENTE PARENTE PARENTE PARENTE PARENTE PARENTE PARENTE PARENTE PARENTE PARENTE PARENTE PARENTE PARENTE PARENTE PARENTE PARENTE PARENTE PARENTE PARENTE PARENTE PARENTE PARENTE PARENTE PARENTE PARENTE PARENTE PARENTE PARENTE PARENTE PARENTE PARENTE PARENTE PARENTE PARENTE PARENTE PARENTE PARENTE PARENTE PARENTE PARENTE PARENTE PARENTE PARENTE PARENTE PARENTE PARENTE PARENTE PARENTE PARENTE PARENTE PARENTE PARENTE PARENTE PARENTE PARENTE PARENTE PARENTE PARENTE PARENTE PARENTE PARENTE PARENTE PARENTE PARENTE PARENTE
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                                                                                                                                           ENT FILING DATE: 2001-12-21

R APPLICATION NUMBER: 60/257,495

R FILING DATE: 2000-12-21

R FILING DATE: 2000-12-20

R FILING DATE: 2000-12-20

R FILING DATE: 2001-12-20

R FILING DATE: 2001-02-20

R APPLICATION NUMBER: 60/27,192

R FILING DATE: 2001-03-08

R FILING DATE: 2001-03-08

R FILING DATE: 2001-03-08

R FILING DATE: 2001-03-08

R FILING DATE: 2001-03-22

R APPLICATION NUMBER: 60/277,826

R APPLICATION NUMBER: 60/277,826
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ORGANISM: Homo sapiens
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Best Local Similarity
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455 RLASKRRKLVAIVDPHIKVDSGYRVHEELRNLGLYVKTRDGSDYEGWCWPGSAGYPDFTN 514
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      52 VLTA---KLDLIKPSSVYAPDIKSLNLHVSLETSERLRIRITDSSQQRWE----IPETVI 104
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               105 PRAGNHSPRRFSTEEDGGNSPENNFLADPSS-DLVFTLHNTTPFGFSVSRRSSGDILFDT 163
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            164 SPDSSDSNTYFIFKDQFLQLSSALPENRSNLYGIGEHTKRSFRL---IPGETMTLWNADI 220
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   221 GS---ENPDVNLYGSHP-----FYMDVRGS----KGNEEAGTTHGVLL--LN 258
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         234 ----SDSKPY---GPMSVGLDFSLP-GMEHVYGIPEHAD-NLRLKVTEGGEPYRLYNLDV 284
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                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
18.1%; Score 862; DB 12; Length 944;
Best Local Similarity 30.2%; Pred. No. 7.4e-71;
Matches 254; Conservative 127; Mismatches 315; Indels 146;
PRIOR APPLICATION NUMBER: 60/279,840
PRIOR FILING DATE: 2001-03-29
PRIOR FILING DATE: 2001-04-11
PRIOR APPLICATION NUMBER: 60/283,656
PRIOR APPLICATION NUMBER: 60/283,656
PRIOR FILING DATE: 2001-04-13
PRIOR FILING DATE: 2001-04-13
PRIOR FILING DATE: 2001-07-31
PRIOR FILING DATE: 2001-08-17
PRIOR FILING DATE: 2001-08-17
PRIOR FILING DATE: 2001-08-17
PRIOR FILING DATE: 2001-08-17
NUMBER OF SEQ ID NOS: 260
SOFTWARE: PATENTIN NUMBER: 60/313,331
NUMBER OF SEQ ID NOS: 260
SOFTWARE: PATENTIN NUMBER: 60/313,331
SOFTWARE: PATENTIN VET: 2.1
                                                                                                                                                                                                                                                                                                                                     ; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-032-189-122
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        ----TMLKDAQHYGGWEHRDVHNIYGLYVHMATADGLRQRSGGMERPFVLARAFFAGSQ 609
                                                                                                                                                                                                             669 FFSFPQDTKTYEIDSQFLIGKSIMVSPALKQGAVAVDAYFPAGN--WFDLFNYSFAVGGD 726
                                                                                                                                                                                                                                                                                              SGKH-----VRLDTPADHVNVHVREGSIVA%QGEALTTRDARK-TPYQLLVVASRLENIS 780
                                                                                                                                                                                                                                                                                                                               --KHHGPQTLYLPVTLSSIPVFQRGGTIVPRWMRVRRSSECMKDDPITLFVALSPQGTAQ 840
                                                                                                                                                                                                                                                                                                                                                                              GELFLDDGENLRMGAGGGNRDWTLVKFRCYVTGKSVVLRSEVVNPEYASKMKWSIGKVTF 840
                                                                                                                                                                                                                                                                                                                                                                                                     550 KYTAHWIGDNAAKWEDLAYSIPGILNFGLFGIPMVGADICGFSHDTTEELCRRWIQLGAF
                                                                                     609 RFGAVATGDNIAEWDHLKISIPMCLSLGLVGLSFCGADVGGFFKNPEPELLVRAYQMGAY
                                                                                                                                610 YPFARDHSSLGTARQELYLWDSVASS-ARKVLGLRMRLLPHLYTLMYEAHVSGNPIARPL
                                                                                                                                                     Isabelle

Jre, Paul

Eilerman, Karen

AcCANT: MacDougall, John R

JCANT: Smibhson, Glennda

ITLE CNIVENTION: Proteins and Nucleic Acids Encoding Same
FILE REFERENCE: 21402-228

CURRENT FILING DATE: 2001-12-21
PRIOR FILING DATE: 2001-12-21
PRIOR FILING DATE: 2000-12-20
PRIOR FILING DATE: 2000-12-20
PRIOR FILING DATE: 2000-12-20
PRIOR FILING DATE: 2001-07
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PRIOR APPLICATION NUMBER: 60/27
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, Sequence 122, Application US/10032189
, Publication No. US20030170630A1
, GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Patturajan, Meera
Grosse, William M
Lepley, Denise M
Burgess, Catherine E
Shimkers, Richard A
Grosse, William M
Szekeres, Edward S
Vernet, Corine A.M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Casman, Stacie J
Boldog, Ferenc L
Gorman, Linda
Gangolli, Esha A
Fernandes, Elma R
Rieger, Daniel K
Edinger, Shlomit R
Gunther, Erik
Millet, Isabelle
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APPLICANT: Tchernev, Velizar T
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Spytek, Kimberly A
Zerhusen, Bryan D
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52 VLTA---KLDLIKPSSVYAPDIKSLNLH--VSLETSBRLRIRITDSSO----ORWEIPET 102
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                                                                                                                                                                                                                                                                                                                                                                                          263 ------PTS------VGLDFSLP-GMEHVYGIPEHAD-SLRLKVTE 294
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    209 PGETMTLWNADIGS---ENPDVNLYGS-----HPFYMDVR------GSKGNEEA 248
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      295 GGEPYRLYNLDVFQYELNNP-MALYGSVPVLLAHSFHRDLGIFWLNAAETWVDISSNTAG 353
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             249 GTTHGVLL--LNSNG----MDVKYEGHRITYNVIGGVIDLYVFAGPSPEMVMNQYTELIG 302
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  303 RPAPMPYWSFGFHQCRYGYKNVSDLEYVVDGYAKAGIPLEVMWTDIDYMDGYKDFTLDPV 362
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    407 IQALPPLFSLGYHQSRWNYRDEADVLEVDQGFDDHNMPCDVIWLDIEHADGKRYFTWDPT 466
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            354 KILFGKMLDYLQGSGETPQTDIRWMSE-----SGIIDVFLMLGPSVFDVFRQYASLTG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                             152 SRRSSGDILFDTSPDSSDSNTYFIFKDQFLQLSSALPENRSNLYGIGEHTKRSFRL---I
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                                                                                                                                        Query Match 17.9%; Score 851.5; DB 12; Length 966; Best Local Similarity 30.2%; Pred. No. 7.3e-70; Matches 242; Conservative 116; Mismatches 301; Indels 141; Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         769 LLVVASRLENISGELFLDDG 788
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                                                          ORGANISM: Mus musculus
                                                                                      US-10-032-189-121
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           LENGTH: 966
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APPLICANT: MacDougall, John R
APPLICANT: Smithson, Glendah
TITLE OF INVENTION: Proteins and Nucleic Acids Encoding Same
FILE REFERENCE: 21402-228
CURRENT APPLICATION NUMBER: US/10/032,189
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PRIOR APPLICATION NUMBER: 60/257,495
PRIOR FILING DATE: 2000-12-21
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Publication No. US20030170630A1
PAPPLICANT: Alsobrook II, John P
APPLICANT: Trehernev, Velizar T
APPLICANT: Liu, Xiachong
APPLICANT: Liu, Xiachong
APPLICANT: Spytek, Kimberly A
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Shimkets, Richard A
Grosse, William M
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Fernandes, Elma R
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Vernet, Corine A.M
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Grosse, William M
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Millet, Isabelle
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Boldog, Ferenc L
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                                                                                                    280 İYGIPQHAE-SHQLKATTGDGDAYRLYNLDVYGYQIYDKMGIYGSVPYLL-----AHKL 331
                                                                                                                                                      249 GTTHGVLLLNSNGMDVKYEGHRITYNVIG-------GVIDLYV 284
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Grosse, William M
Lepley, Denise M
Burgess, Catherine E
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Szekeres, Edward S
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APPLICANT: Tchernew, Velizar T
APPLICANT: Liu, Xiaohong
APPLICANT: Spytek, Kimberly A
APPLICANT: Zerhusen, Bryan D
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Gorman, Linda
Gangolli, Esha A
Fernandes, Elma R
Rieger, Daniel K
Edinger, Shlomit R
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Matches 241; Conservative 130; Mismatches 330; Indels 121; Gaps
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APPLICANT: MacDougall, John R
APPLICANT: Smithson, Glennda
TITLE OF INVENTION: Proteins and Nucleic Acids Encoding Same
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CURRENT APPLICATION NUMBER: 05/10/032,189
CURRENT FILING DATE: 2001-12-1
PRIOR PLILNG DATE: 2001-12-21
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PRIOR FLILNG DATE: 2000-12-20
PRIOR FLILNG DATE: 2000-12-20
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PRIOR APPLICATION NUMBER: 60/283,656
PRIOR FLILNG DATE: 2001-04-11
PRIOR APPLICATION NUMBER: 60/309,247
PRIOR FLILNG DATE: 2001-07-31
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PRIOR PELING DATE: 2001-08-17
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Vernet, Corine A.M
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Boldog, Ferenc L
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APPLICANT: Gunther, Erik
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APPLICANT: Ellerran, Karen
APPLICANT: Ellerran, Karen
APPLICANT: Marchangall, John R
APPLICANT: Smithson, Glennda
TITLE OF INVENTION: Proteins and Nucleic Acids Encoding Same
FILE REFERENCE: 2140-228
CURRENT FILING DATE: 2000-12-21
FRIOR APPLICATION NUMBER: 60/257,495
FRIOR APPLICATION NUMBER: 60/258,171
FRIOR APPLICATION NUMBER: 60/258,171
FRIOR APPLICATION NUMBER: 60/259,840
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FRIOR FILING DATE: 2001-03-19
FRIOR FILING DATE: 2001-04-13
FRIOR APPLICATION NUMBER: 60/28,656
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FRIOR FILING DATE: 2001-04-13
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              GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
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US-09-55-6877-180
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Sequence 4, Application US/08430925A

Patent No. 5763252

GENERAL INPORMATION:

APPLICANT: Skadesn, Ronald W

APPLICANT: Tibbot, Brian K

TITLE OF INVENTION:

CORRESPONDENCE ADDRESS:

ADDRESSE: Quarles & Brady

STREET: Madison

STREET: Jouth Pinckney Street

CITY: Madison

STREET: US

COUNTRX: US

ZIP: 53703

COMPUTER READALE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/430,925A

FILING DATE:

CLASSIFICATION NUMBER: 27,386

RECISTRATION NUMBER: 27,386

REFERENCE/DOCKET NUMBER: 37,386

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                   US-09-135-166-10
US-08-942-046-10
US-08-945-265-2
US-09-447-533-2
PCT-US95-05512-2
US-08-206-791-5
PCT-US95-10661A-5
US-08-39-828C-37
US-09-397-885-3
US-09-397-885-5
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US-08-769-969-362-5
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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APPLICANT: Allen, Stephen M.
TILE OF INVENTION: Plant Alpha-Glucosidase II Homologs
FILE REFERENCE: BB1273 US NA
CURRENT APPLICATION NUMBER: US/09/437,054A
CURRENT FILING DATE: 2001-05-14
PRIOR PILING DATE: 2001-05-14
PRIOR FILING DATE: 1998-No. 6316698ember-10
NUMBER OF SEQ ID NOS: 19
SOFTWARE MICROSOFT Office 97
SEQ ID NO 8
LENGTH: 914
TYPE: PRT
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                                                                                                                                                                   53 LTAKLDLIKPSSVYAPDIKSLNLHVSLETSERLRIRITDS-----SQQRWEIPETVI---
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                                                                                                                               Gaps
                                                                                                                            119;
                                                                              Length 914;
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Patent No. 6316698
GENERAL INNEWATION:
APPLICANT: Allen, Stephen M.
APPLICANT: Kinney, Anthony J.
TITLE OF INVENTION: Plant Alpha-Glucosidase II Homologs
FILE REFERENCE: BB1273 US NA
                                                                           DB 4;
                                                                         Query Match
18.1%; Score 858.5; DB 4;
Best Local Similarity 30.1%; Pred. No. 1.6e-72;
Matches 244; Conservative 133; Mismatches 315;
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; ORGANISM: Glycine max US-09-437-054A-8
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; Sequence 2, Application US/09376343; Patent No. 6506592
                                                                                                                                                                                                                               TYPE: PRT ORGANISM: Sulfolobus solfataricus
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                                                          GENERAL INFORMATION:
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US-08-897-843A-1
                  US-09-376-343-2
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                                                                                                                                                                                                                                                                                           -----PENNFLADPSSDLVFTL------HNTTPFGFSVSRRSSGD---ILFDTSPD 166
                                                                                                                                                                                                                                                                                                                     126 LWLTRVKEEQIDGVSSFSSVFYLSDGYEGVLRHDP----FEVFARESGSGKRVL----- 175
                                                                                                                                                                                                                                                                                                                                                   SSDSNTYFIF-----YGIGEHTK 202
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                                                                                                                                                                                                                                                                                                                                                                                                                               71 KSLNLHVSLETSERLRIRITDSS-----QQRWEIPETVIPRAGNHSPRRFSTEEDGGNS-
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          CURRENT FILING DATE: 2001-05-14
PRIOR APPLICATION NUMBER: 60/107,909
PRIOR FILING DATE: 1998-No. 6316698ember-10
NUMBER OF SEQ ID NOS: 19
SEQ ID NO 17
LENGTH: 919
CURRENT APPLICATION NUMBER: US/09/437,054A
                                                                                                                 TYPE: PRT
ORGANISM: Solanum tuberosum
                                                                                                                                   ; ORGANISM: SOLUS-09-437-054A-17
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                                                         Use
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APPLICANT: Blum, Paul H.
TITLE OF INVENTION: Hyperthermophilic Alpha-Glucosidase Gene and Its I FILE REFERENCE: N1231-200
CURRENT APPLICATION NUMBER: US/09/376,343
CURRENT FILING DATE: 1999-08-18
EARLIER APPLICATION NUMBER: 60/096,860
EARLIER FILING DATE: 1998-08-18
NUMBER: OF SEQ ID NOS: 4
SOFTWARE: Patentin Ver. 2.0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Matches 182; Conservative 127; Mismatches 260; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DNAEITSSSNEIKFSREIYVSKLIITSEKPVSKIIVDDSKEIQV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               15.0%; Score 713.5; DB 4; 28.3%; Pred. No. 7e-59;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ; Sequence 1, Application US/08897843A; Patent No. 6514493
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491 RPINNKTVPATSIHFGNISEYDAHNLYGLLEAKATHQAVVDITG--KRPFILSRSTFVSS 548
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEE: Knobbe, Martens, Olson & Bear
: 620 Newport Center Drive 16th Floor
Newport Beach
                                                                                                                                                                                                                                                                                                                                                                                                                         760 RDARK-TPYQLLVVASRLENISGELFLDDG 788
                                                                                                                                                                                                                                                                                                                                                                                                                                                                814 SDCMKDDPITLFVALSPQGTAQGELFLDDG 843
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME: Altman, Daniel E
REGISTRATION NUMBER: 34,115
REFERENCE/DOCKET NUMBER: DYOU6.001APC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICATION NUMBER: US/08/633,770A FILING DATE: U1JY 8, 1996
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/EP94/03398
FILING DATE: OCT-15-1994
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                        720 SFAVGGDS-----GKHVR-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 2, Application US/08633770A
Patent No. 5908760
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELECOMMUNICATION INFORMATION: TELEPHONE: 714-760-0404
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 1070 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELEFAX: 714-760-9502
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              , MOLECULE TYPE: protein US-08-633-770A-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NUMBER OF SEQUENCES: 1:
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ZIP: 92660
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskett
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      amino acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         280 FQYELINIP-MALYGSVPVLLAHSPHRDLGIFWLNAAETWVDISSNTAGKTLFGGMLDYLQ 338
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DTLHKNGQKYVLILDPGIGVDSSYGTYNRGMEADVFIK-RNGEPYLGEVWPGKVYFPDFL 432
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          -PTS-----VGLDFSLP-GMEHVYGIPEHAD-SLRLKVTEGGEPYRLYNLDV 279
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 221 GS---ENPDVNLYGS-----HPFYMDVR------GSKGNEEAGTTHGVLL--LN 258
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SNG----MDVKYEGHRITYNVIGGVIDLYVFAGPSPEMVMNQYTELIGRPAPMPYWSFGF 314
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         339 GSGETPQTDIRWMSE-----SGIIDVFLMLGPSVFDVFRQYASLTGTQALPPLFSLGY 391
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  HOCRYGYKNVSDLEYVVDGYAKAGIPLEVMWTDIDYMDGYKDFTLDPVNFPED-KMOSFV 373
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DSKRRN---VVAIVDPHIKVDSGYRVHEELRNHGLYVKTRDGSDYEGWCWPGSASYPDFT 508
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NPAAATFWSNEIKM--FQEILPLDGLWIDMNELSNFITSPLSSGSSLDDPPYKINNSGDK 490
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NPRMRALWSNMFSFDNYEGSAPNLYVWNDMNEPSVF-----NGPEV-----549
                 APPLICANT: Deleo, Albert B.; Loftus, Douglas; Appella, Ettore
TITLE OF INVENTION: CDNA CLONE FOR MURINE TUMOR
TITLE OF INVENTION: REJECTION ANTIGEN GPI10 AND TUMOR PEPTIDE VACCINE
NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:
ADDRESSEE: Diane R. Meyers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               52 VLTA----KLOLIKPSSVYAPDIKSLNLHVSLETSERLRIRITDSSQQRWEIPETVIPRAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       192 NGAQPE-ATPGDGDKPEETQEKAEKDEPGAWEETFKTHSDSKPYG-------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              109 NHSPRRFSTEEDGGNSPENNFLADPSS----DLVFTLH-NTTPFGFSVSRRSSGDILFDT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ZIP: 15219

ZIP: 15219

CMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: BM PC compatible
COPEDATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/897,843A
                                                                                       AUNKESSEE: Liane R. Meyers
STREET: 600 Grant Street, 42nd Floor
CITY: Pittsburgh
STATE: PA
                                                                                                                                                                                                                                                                                                                                                                                                                     CLASSIFICATION: 424
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  : 938 amino acids
amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ANTI-SENSE: NO
FRAGMENT TYPE: N-terminal
ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ORGANISM: Mus musculus
DEVELOPMENTAL STAGE: Br
TISSUE TYPE: Embryo
CELL LINE: NIH 3T3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TOPOLOGY: linear
GENERAL INFORMATION
                                                                                                                                                                                                            USA
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                                                                                                                                                                                                          COUNTRY:
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Best Local S:
Matches 221
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APPLICANT: Bojsen, Kirsten
APPLICANT: Yu, Shukun
APPLICANT: Kragh, Karsten
APPLICANT: Christensen, Tove
APPLICANT: Marcuseen, Jan
TITLE OF INVENTION: ALPHA-1,4-GLUCAN LYASE FROM A FUNGUS, ITS
TITLE OF INVENTION: ALPHA-1,00 GENE CLONING AND EXPRESSION IN MICROCRGANISMS
550 -----TMLKDAVHYGGWEHRDIHNIYGLYVHWATADGLIQRSGGIERPFVLSRAFFSGS 603
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                609 FYPFARDHSSLGTARQELYLWDSVASSARKVLGLRMRLLPHLY---TLMY-----EAHV 659
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 664 YGPFFRAHATWTLGGESMAVSVSIPRCNPRC-----LVPAIFFAALLVYPLLSSSQGRV 717
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SGNPIARPLFFSFPQDTKTYEIDSQFLIGKSIMVSPALKQGAVAVDAYFPAGNWFDLFNY 719
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ---LDTPADHVNVHVREGSIVAMQGEALTT 759
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        756 -- AHGGRSICLAKKRCGMTFRAIRSIMGPRPCICPVTLSSIPVFOGGGTIVPRWMRVRRS 813
                                                                                                                                                                                                                                                                                                                                      549 GKYTAHWIGDNAAKWEDLAYSIPGILNFGLFGIPMVGADICGFSHDTTEELCRRWIQLGA
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78 SLETSERLRIRITD-----SSQQRWEIPETVIPRAGNHSPRRFSTEEDGGNSPENNFL 130
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            327 IVRLYTGLVGRSKIKPRYILGAHQACYGYQQESDLYSVVQQYRDCKFPLDGIHVDVDVQD 386
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 -----PYLG 419
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  131 ADPSSDLVFTLHNTTPFGFSVSRRSSGDILFDTSPDSSDSN---TYFIFKDQFLQLSSAL 187
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 214 KPGHGEYVGWGEMGGIQFMKEP-TFMNYFNFDNMQYQQVYAQGALDSREP---LYHSDPF 269
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  YMDVRGSKGNEEAGTTHGVLLLNSNGMDVKYEGHRITYNVIG---GVIDLYVFAGPSPEM 292
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                270 YLDV---NSNPEHKNITATFIDNYSQIAIDFGKTNSGYIKLGTRYGGIDCYGISADTVPE 326
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GFRTFTTNPHTFPNPK--EMFTNLRNNGIKCSTNITPVISINNREGGYSTLLEGVDKKYF 444
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SGSSLDDPPYKINNSGDKRPINNKTVPATSIHFGNISEYDAHNL--YGL--LEAKATHQA 528
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                                                                                                                                                                                                SOFTWARE: Patentin Release #1.0, Version #1.25 (EPO) CURRENT APPLICATION DATA:
APPLICATION DATE: US/08/633,770A
FILING DATE: Unly 8, 1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 10.1%; Score 479.5; DB 2; Best Local Similarity 22.4%; Pred. No. 3.5e-36; Matches 200; Conservative 111; Mismatches 307;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FILING DATE: July 8, 1996
CLASSIFTCATION: 435
PRIOR APPLICATION DATA:
APPLICATION NURBER: PCT/EP94/03398
FILING DATE: OCT-15-1994
ATTORNEY/AGENT INFORMATION:
NAME: Altman, Daniel E
REGISTRATION NUMBER: 34,115
RESERENCE/DOCKET NUMBER: DYOUG.001APC
TELEDPHONE: 714-760-0404
                                                                                                                                                    COMPUTER: IBM Compatible OPERATING SYSTEM: DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE CHARACTERISTICS:
LENGTH: 1066 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELEFAX: 714-760-9502
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MOLECULE TYPE: protein US-08-633-770A-1
                                                                                                      COMPUTER READABLE FORM:
MEDIUM TYPE: Diskett
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      amino acid
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                                                        U.S.A.
                                                     COUNTRY: U
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APPLICANT: Bojsen, Kirsten
APPLICANT: W. Shukun
APPLICANT: Wrash, Karsten
APPLICANT: Warcusen, Tove
APPLICANT: Christensen, Tove
APPLICANT: Marcusen, Jan
TITLE OF INVENTION: ALFRA-1,4-GLUCAN LYASE FROM A FUNGUS, ITS
TITLE OF INVENTION: PURIFICATION GENE CLONING AND EXPRESSION IN MICROORGANISMS
CORRESPONDENCE ADDRESS:
ADDRESSEE: Knobbe, Martens, Olson & Bear
                                                     33;
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                                                                                                    130 LADPSSDLVFTLHNTTPFGPSVSRRSSGDILFDTSPDSSDSN---TYFIFKDQFLQLSSA
                                                                                                                                ---IGSENPDVNLYGSHP
                                                                                                                                                                                                                                                 213 IKPGHGEYVGWGEMGGIEFMKEP-TFMNYFNFDNMQYQQVYAQGALDSREP---LYHSDP
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                                                        Gaps
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                                                     Indels 209;
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  10.4%; Score 494.5; DB 2; Length 1070; 23.8%; Pred. No. 1.3e-37;
                                                Matches 184; Conservative 108; Mismatches 273;
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620 Newport Center Drive 16th Floor
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                         Similarity
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Query Match
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                                                                                               666 GGFEPYRDANGVEEKYCSPELLIRWYTGSFLLPWLRNHYVKKDRKWFÇEPYSYPKHLETH
                                                                                                                                                                                                                  KTYE----IDSQFLIGKSIMVSPALKQGAVAV---DAYFPA-GNWF------
                                                                                                                                     SSIGTARQELYLWDSVASSARKVLGLRMRLLPHLYTLMYEAHVSGNPIARPLFFSFPQDT
                                                                                                                                                                                                                                                                                             -----DLFNYSFAVGGDSGKHVRLDTPADH-----VNVHVREGSIVAMQGEALTT
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TITLE OF INVENTION: ALPHA-1,4-GLUCAN LYASE FROM
TITLE OF INVENTION: A FUNGUS INFECTED ALGAE, ITS PURIFICATION
TOMBER OF SEQUENCES: 25
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              E: Knobbe, Martens, Olson & Bear
620 Newport Center Drive 16th Floor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   REFERENCE/DOCKET NUMBER: DYOUT.001APC
TELECOMMUNICATION INFORMATION:
TELEPHONE: 714-760-0404
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER: IBM COMPATIBLE
OPERATING SYSTEM: DOS
SOFTWARE: FastEC Version 1.5
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/633,768A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 2, Application US/08633768A
Patent No. 6013504
GENERAL INFORMATION:
APPLICANT: YU, GHUKUN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRIOR APPLICATION DATA:
APPLICATION NAMBER: 9321301.5
FILING DATE: 15-OCT-1993
ATTORNEY AGENT INPORMATION:
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BOJSEN, KIRSTEN
KRAGH, KARSTEN
BOJKO, MAJA
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                                                          589 CGF----SHDTTEELC
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REGISTRATION NUMBER: 3
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7 MOLECULE TYPE: protein
US-08-633-768A-2
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MEDIUM TYPE: Diskett
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                                                                                                                                                                                                                                             220 IGSEN------PDVNLYGSHPFY-----MDVRGSKGNEEAGTTHGVLL-----L 257
                                                                                                                                                                                                                                                                      355 NTGGTSWNCGEENLAY--MGAQCGPFDQHFVYGDGDGLEDVVQAFSLLQGKEFENQVLNK 412
                                                                                                                                                                                                                                                                                                                                                                                                          RPAPMPYWSFGFHQCRYGY-----KUVSDLEYVVDGYAKAGIPLEVMWTDIDY 350
                                                                                                                                                                                                                                                                                                                                                                                                                                 ---- GQKYVL 385
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         532 NOTLREKGLYTKNDSLTNTNFGTTNDG------PSDAYIGHLDYGGGGNCDALFPDW 582
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     432 LNPAAATFW-SNEIKMFQEILPLDGLWIDMNELSNFITSPLSSGSSLDD-PPYKINNSGD 489
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  490 KRPINNK-----TVPATSIHFGNISE---YDAHNLYGLLEAKATHQ----AVVDITG 534
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  535 K--RPFILSRSTFVSSGKYTAHWTGDNAAKWEDLAYSIPGILNFGLFGIPMVGADICGFS 592
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   333 AILPTRYTLDGSNKSMNTY-TDKDPLVFEVFPLGNNRADGMCYLDDGGITTDAEDHGKFS 991
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  114 RFSTEEDGGNSPENNFLADPSSDLVFTLHNTTPFGFSVSRRSSG----DILFDTSPDSSD
                                                                                                                                                            170 SNTYFIFKDQFLQLSSALPENRSNLYGIGE-----HTKRSFRLI--PGETMTLWNAD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         696 ALKQGAVAVDAYFPA-----GNWFDLFNYSFAVGGDSGKHVR-LDTPADHVNVHVREG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      789 ----ENLRMGAGGGNRDWTLVKFRC----YVTGKSVVLRSEVVNPEYASKMKWSIG 836
                                            Gaps
Ouery Match
7.7%; Score 366; DB 3; Length 1091;
Best Local Similarity 22.2%; Pred. No. 2.6e-25;
Matches 199; Conservative 133; Mismatches 330; Indels 234;
                                                                                                                                                                                                                                                                                                                         258 NSNGMDVKYEGHRITYNVIG---GVIDL-YVFA-GPSPEMYMNQYTELIG-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          748 SIVAMO----GEALTIRDARKTPYQLLVVASRLENISGELFLDDG----
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GENERAL INFORMATION:
APPLICANT: YU, SHUKUN APPLICANT: BOJSEN, KIRSTEN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RESULT 9
US-08-633-768A-1
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527 QTLRERQLYTKNDSLTGT-DFGMTDD----GPSDAYIGHLDYGGGVECDALFPDWGRPDV 581
                                                    437 ATFWSNEIKMPQEILPLDGLWIDMNELSNFITSPLSSGSSLDDPPYKINNSGDKRPINN- 495
                                                                                                                                                                         627 PNADDPSNGQYNWKTYHPQVLVTDMRYENHGREPMVTQRNIH-AYTLCES-TRKEGIVEN 684
                                                                                                                                                                                                                                                              685 ADTLIKERRSYIISRGGYIGNQHFGGMWVGDNSTISNYIGMMIANNINAMSCLPLVGSD 744
                                                                                                                                                                                                                                                                                                                                                         685 FLI----GKSIMVSPALKQGAVAVDAYFPA-----GNWFDLFNYSFAV-GGDSGKHVR 732
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    915 YPVPQSESPIFVREGALLPTRYTLNGENKSLNTYTDEDPLVFEVFPLGN--NRADGMCYL 972
                                                                                                                                                                                                                                    533 TG-----KRPFILSRSTFVSSGKYTAHWTGDNAAKWEDLAYSIPGILNFGLFGIPMVGAD 587
                                                                                                                                                                                                                                                                                                                            588 ICGF-SHDT-----TEELCRRWIQLGAFYPFARDH-----SSLGTARQELYLWDSV 632
                                                                                                                                                                                                                                                                                                                                                                                                                       633 ASSARKVLGLRMRLLPHLYTLMYEAHVSGNPIARPLFFSFPQDTKTYBIDS------Q 684
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       733 LDTPADHVNVHVREGSIV----AMQGE--ALTT-RDARKTPYQLLVVASRLENISGELFL 785
                                                                                496 -----KT----VPATSIHFGN----ISEYDAHNLYGLLEAKATHQAVVDI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TITLE OF INVENTION: ALPHA-1,4-GLUCAN LYASE AND
TITLE OF INVENTION: ITS USE IN THE PRODUCTION OF 1,5-ANHYDROFRUC
TITLE OF INVENTION: TOSE
NUMBER OF SEQUENCES: S.
CORRESPONDENCE ADDRESS:
ADDRESSEE: Knobbe, Marten ()
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620 Newport Center Drive 16th Floor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: Windows
SOFTMARE: FastSEQ for Windows Version 2.0b
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/275,608
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRIOR APPLICATION:
PRIOR APPLICATION DATA:
PAPLICATION NUMBER: PCT/EP95/02172
PILING DATE: 06-JUN-1995
FILING DATE: 15-APR-1997
APPLICATION NUMBER: PCT/EP94/03397
FILING DATE: 15-CCT-1994
ATTORNEY/AGENT INFORMATION:
NAME: Aleman, Daniel E
REGISTRATION NUMBER: 34,115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 3, Application US/09275608
Patent No. 6541237
GENERAL INFORMATION:
APPLICANT: YU, Shukun
APPLICANT: JSEN, Kirsten
APPLICANT: MARCUSSEN, Jan
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COUNTRY: U.S.A.
ZIP: 92660
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskett
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                175 IFKDQ-FLQLSSALPENRSN-----LYGIGE-HTKRSFRLI---PGETMTLWNAD--- 219
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          175 DPGMTFTSEGFLTFETKDLSVIIYGN--FKTRVTRKSDGKVIMENDEVGTASSGNKCRGL 232
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                     APPLICANT: BOJKO, MAJA
APPLICANT: NIELSEN, JOHN
APPLICANT: NIELSEN, JOHN
TITLE OF INVENTION: ALPHA-1,4-GLUCAN LYASE FROM
TITLE OF INVENTION: A FUNGUS INFECTED ALGAE, ITS PURIFICATION
NUMBER OF SEQUENCES: 25
CORRESPONDENCE ADDRESS:
ADDRESSEE: Knobbe, Martens, Olson & Bear
STREET: 620 Newport Center Drive 16th Floor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Indels 215;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             7.5%; Score 357.5; DB 3; Length 1088; llarity 23.4%; Pred. No. 1.7e-24; Conservative 119; Mismatches 312; Indels 215;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                254 VLLLNSNGMDVKYEGHRITYNVIGGVIDLYVF-AGPSPEMVMNQYTELIG---
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APPLICATION NUMBER: US/08/633,768A
FILING DATE: US/08/633,768A
FILING DATE: US-07-UL-1996
CLASSTFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 9321301.5
FILING DATE: 15-07-1993
ATTORNEY/AGENT INFORMATION:
NAME: Altmar, Daniel E
REGISTRATION NUMBER: 34,115
REGISTRATION NUMBER: 34,115
REGISTRATION NUMBER: DYOUT.001APC
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                              COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM COMPALIBLE
OPPERATING SYSTEM: DOS
SOFTWARE: FastSEQ Version 1.5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   INFORMATION FOR SEQ ID NO: 1:
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LENGTH: 1088 amino acids
KRAGH, KARSTEN
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TELEFAX: 714-760-9502
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Best Local Similarity
Matches 197; Conserv
                                                                                                                                                                                                                                                     STATE: CA
COUNTRY: U.S.A.
ZIP: 92660
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DYOU9.001C1

REFERENCE/DOCKET NUMBER:

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259 ------SNGMDVKYEGHRITYNVIGGVIDLYVF-AGPSPEMVMQYTELIG-- 302
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ITS USE IN THE PRODUCTION OF 1,5-ANHYDROFRUC
TOSE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                7.0%; Score 333.5; DB 4; Length 570; 23.8%; Pred. No. 1e-22; ive 84; Mismatches 193; Indels 171;
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620 Newport Center Drive 16th Floor
                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
COMPUTER: IBM COMPATIBLE
SOFTWARE: FastSEQ for Windows Version 2.0b
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CLASSIFICATION:

PRIOR APPLICATION DATA:

APPLICATION NUMBER: PCT/EP95/02172

RILING DATE: 06-JUN-1995

APPLICATION NUMBER: 08/836,156

FILING DATE: 15-APR-1997

APPLICATION NUMBER: PCT/EP94/03397

FILING DATE: 15-OCT-1994

ATTORNEY/AEBAT INFORMATION:

NAME: Altenan, Daniel E

REGISTRATION NUMBER: 34,115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/275,608
                                                                     Sequence 4, Application US/09275608; Patent No. 6541237; Patent No. GSTAZA7 APPLICANT: VU, Shukun APPLICANT: VU, Shukun
                                                                                                                                                      APPLICANT: JSEN, Kirsten
APPLICANT: MARCUSSEN, Jan
TITLE OF INVENTION: ALPHA-1
TITLE OF INVENTION: ITS USE
TITLE OF INVENTION: TOSE
NUMBER OF SEQUENCES: 21
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         23.8%;
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amino acid
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Matches 140; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELEFAX: 714-760-9502
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                                                                                                                                                                                                                                                                                                                                                             Newport Beach
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                                                                                                                                                                                                                                                                                                                 ADDRESSEE:
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                                                                                                                                                                                                                                                                                                                                                                                                       COUNTRY:
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                                                                                                                                                                                                                                                                                                                                                             CITY:
STATE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              463 VDVDMQDDLRVFTTKPEYMSANMVGEGGDPNNRSVFEWAHDRG----LVCQTNVTCFLRN 518
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             |:| |: | : : | : : | : : | : DNSGKPYEVNQTLREKQLYTKNDSLNNTDFGTTSDGPGDAYIGHLDYGGGVECDAIFPDW 578
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           529 VVDITG----KRPFILSRSTFVSSGKYTAHWIGDNAAKWEDLAYSIPGILNFGLFGIPMV 584
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               |:|| ||:
|SDIGGFTQYNDAGDPTPEDLMVRFVQAGCLLPWFRNHYDRWIESKKHGKKYQELYMYPG 807
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           632 VASSARKVLGLRMRLLPHLYTLMYEAHVSGNPI--ARPLFFSFPQDTKTYEI-DSQFLI- 687
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 124 SPENNFLADPSSDLVFTLHNTTPPGFSVSR--RSSGDILF--DTSPDSSDSNTY--FIFK 177
                                                                                                                                                                                                                                                                                                                                                                                                                    181 SPE-GFLSFETKDL-----NVIIYGNCKMRVTKKDGYLVMENDECNSQSDGNKCRGLMYV 234
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ----KRSFRLIPGETM 213
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DRL--YGNAIASVQTNFHKDTSRNEKFYGAGEVNCRYEEQGKAPTYVLERS-----GLAM 287
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TLWNAD-IGSENPDV--NLYGSHPFY-------MDVRGSKGN-------EE 247
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TNYNYDNLNYNOPDVVPPGYPDHPNYYIPMYYAAPWLVVQGCAGTSKQYSYGWFMDNVSQ 347
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SYMNIGDIAWNGGQENLAYMGAQ-----YGPFDQHFVYGDGDGLEDVVKAFSFLQGKEFE 402
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      -----RPAPMPYWSFGFHQCRYGY------KOVSDLEYVVDGYAKAGIPLEVMW 345
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TDIDYMDGYKDFTLDPVNFPEDKM------QSFVDTLHKNGQKYVLILDPGIGV----393
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    633 --NEND--PSNGRYNWKSYHPQVLVTDMRYGAEYGREPMVSQRNIH-AYTLCESTRREGI 687
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                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                       Query Match
7.5%; Score 356.5; DB 4; Length 1092;
Best Local Similarity 22.7%; Pred. No. 2.1e-24;
Matches 183; Conservative 116; Mismatches 278; Indels 229;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ---GKSIMVSPALKQGAVAVDAYFPA-GNWF----
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TELECOMMUNICATION INFORMATION TELEPHONE: 714-760-0404
                                                                                   INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 1092 amino acids
TYPE: amino acid
STRANDEDNESS: single
                                              TELEFAX: 714-760-9502
                                                                                                                                                                                                    TOPOLOGY: linear MOLECULE TYPE: protein
                                                                                                                                                                                                linear
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702 VAVDAYFPAGN-WFDLFNYSFAVGGDSGKHVRLDTPADHVNVHVREGSIVAMQGEALTTR 760
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493 INNKTVPATSIHFGNISEYDAHNLYGLLEAKATHQAVVDITGK--RPFILSRSTFVSSGK 550
                                                                                                                                                265
                                                                                                                                                                                                                                                                                                                               326 FLDYPNIPEAYTDLVKXFYLMGDNFLVAPIYQNTAADEKGNDVRNGIYLPDKQQVWIDYY 385
                                                                                                                                                                                                 610 YPFARDHSSLGTARQELYLWDSVASSARKVLG-LRMRLLPHLYTLMYEAHVSGNPIARPL 668
                                                                                                                                                                                                                                                                                              669 FPSFPQDTKTYE--IDSQFLIGKSIMVSPALKQGA-----VAVDAYFPAGN--WFDLF 717
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                                                                                                                              551 YTAHWTGD-NAAKWEDLAYSIPGILNFGLFGIPWVGADICGFSHDTTEELCRRWIQLGAF
                                                                                                                                                                                                                                | | : | | : : | | : : | | 266 TPIQLNMDGWGANPKTPFSFDQQTTAINRAYNKQKTMLMPYNYTASAQSVFDGKPMVRGL
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29.9%; Pred. No. 1.4e-09;
ive 23; Mismatches 71; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Allen, Stephen M.
APPLICANT: Kinney, Anthony J.
TITLE OF INVENTION: Plant Apha-Glucosidase II Homologs
FILE REFERENCE: BB1273 US NA
CURRENT FILING DATE: 2001-05-14
CURRENT PLLING DATE: 1998-NO. 6316698ember-10
RRIOR PILING DATE: 1998-NO. 6316698ember-10
NUMBER OF SEQ ID NOS: 19
SOFTWARE: Microsoft Office 97
SEQ ID NO 10
                                                                                                                                                                                                                                                                                                                                                                                                                                            US-09-437-054A-10; Sequence 10, Application US/09437054A; Patent No. 6316698
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ORGANISM: Triticum aestivum
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les 52; Conservative
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UNSURE
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UNSURE
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UNSURE
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UNSURE
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US-09-437-054A-10
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                                              GLVCQTNVTCFLKNEKNPY--EVNQSLREKQLYTKSDSLDNIDFGTTPDGPSDAYIGHLD 275
                                                                                                                              276 YGGGVECDALFPDWGRPDVAQWWGDNYKKLFS--IGLDFVWQDM------TVPAMMPHR 326
                                                                                                                                                                                                                             NLYGLLEAKATHQAVVDITG----KRPFILSRSTFVSSGKYTAHWTGDNAAKWEDLAYSI 570
                                                                                                                                                                                                                                                                                                                                                                                             PGILNFGLFGIPMVGADICGFS-HD----TTEELCRRWIQLGAFYPFARDH-----SS 618
---WPGKVY---- 427
                                                                                                                                                                                                 LDDPPYKINNSG-----ISEYDAH 514
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                                                                                               -----FPDFLNPAAATFW-SNEIKMFQEILPLDGLWIDMNELSNFITSPLSSGSS
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CURRENT FILING DATE: 2000-08-08
NUMBER OF ESO ID NOS: 422
SOFTWARE: FastESQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Glenn, Matthew
APPLICANT: Havukkala, Ilkka J.
APPLICANT: Bloksberg, Leonard, N.
APPLICANT: Bloksberg, Leonard, N.
APPLICANT: Dekker, James
APPLICANT: Christensson, Anna C.
APPLICANT: Christensson, Anna C.
APPLICANT: Glensson, Anna C.
APPLICANT: Glensson, Anna C.
APPLICANT: Reid, Julian R.
APPLICANT: Reid, Julian R.
APPLICANT: Coolbear, Timothy
TITLE OF INVENTION: Polymucleotides, mail
TITLE OF INVENTION: them and methods For
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 331, Application US/09634238
Patent No. 6544772
GENERAL INFORMATION:
APPLICANT: Glenn, Matthew
GM----EADVFIKRNGEPYLGEV-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ORGANISM: Lactobacillus rhamnosus
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Best Local Similarity 21.2*
Matches 102; Conservative
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COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch, 1.4Mb storage COMPUTER: HP VECTEA 486/33
OPERATING SYSTEM: MSDOS VERSION 6.2
SOFTWARE: ASCII Text
CARRENT APPLICATION DATA:
FILING DATE:
FILING DATE:
                                                                                                                                                                                                        ADDRESSEE: Human Genome Sciences, STREET: 9410 Key West Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        REFERENCE/DOCKET NUMBER: PB369P2
TELECOMMUNICATION INFORMATION:
TELEPHONE: (301) 309-8504
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      36,373
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NAME: A. Anders Brookes
REGISTRATION NUMBER: 36,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELEFAX: (301) 309-8512
INFORMATION FOR SEQ ID NO: 5
SEQUENCE CHARACTERISTICS.
LENGTH: 1416 amino acide
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PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
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                                                                                                                                                                                       CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                  STREET: 9410 Key CITY: Rockville STATE: Maryland COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: amino acid
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TITLE OF INVENTION: ANTISENSE INTRON INHIBITION OF STARCH BRANCHING ENZYME
TITLE OF INVENTION: EXPRESSION
FILL REPERENCE: 078837,0112
CURRENT APPLICATION NUMBER: US/09/367,895
CURRENT FILING DATE: 1999-12-08
PRIOR APPLICATION NUMBER: PCT/IB98/00270
PRIOR FILING DATE: 1998-0.2-23
PRIOR APPLICATION NUMBER: GB/970663.6
PRIOR APPLICATION NUMBER: GB/9706060.2
PRIOR APPLICATION NUMBER: GB/9706060.2
PRIOR APPLICATION NUMBER: GB/9706060.2
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PRIOR APPLICATION NUMBER: GB/9706060.2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           401 NRGMEADVFIKRNGEPYLGEVWPGKVYFPDFLNPAAATFWSNEIKMFQEILPLDGLWIDM 460
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         381 ESYFHA-----GERGYHKLWDSRLF--NYANWEVLRFLLSNLRWWLEEVNFDGFRFD- 430
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2.8%; Score 131.5; DB 4; Length 906;
Best Local Similarity 20.0%; Pred. No. 0.0047;
Matches 141; Conservative 85; Mismatches 259; Indels 221;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              837 KVTFVGFENVEN -- VKTYEVRTSERLRSPRISLIKTV----SDND 875
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US-09-367-895-41
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RESULT 15

Sequence 404, Application US/09071035
Patent No. 6448043
GENERAL INFORMATION:
APPLICATE GILH. Choi
TITLE OF INVENTION: Enterococcus faecalis Polynucleotides and Polypeptides
NUMBER OF SEQUENCES: 496 74 NLHVSLETSERLRIRITDSSQQRWEIPETVIPRAGNHSPRRFSTEED--GGNSPENNFLA 131 294 TPGKD------YTLSDNSLGRIAV-TVPNMNQQKAYSLSINRTIYLESASDYN- 339 214 -----TLWNADIGSE-----GSKGN 245 510 VNPLNAETAWGNYDQNGAYSSRTTVSVMGSKEKPIQNLEIKVKHPNYLSLRATKEIYFYY 569 570 KLGTDYTVTPTS----DGSVIKFTTPITNEIQIPIGFNYVPDSLPKDKSIPVDTIPITMS 625 132 DPSSDLVFTLHNTTPFGFSVSRRSSGDILFDTSPDSSDSNTYFIFKDQFLQLSSALPENR 191 340 -YLYSQQYPTTKIGSISLKSTTGTKQTTDFTAKTSQTSKVİADREMRSMSYİSFQSKGKY 398 399 YVTIYGTLTETKVGQQIVLESTNGQEIRNPKFTAYG~-PLYENVKLEDYFDIKTEGGKLT 456 246 EEAGTTHGVLLLNSNGMDVKYEGHRITYNVIGGVIDLYVFAGPSP--EMVMNQYTELIGR 303 Matches 196; Conservative 129; Mismatches 351; Indels 412; 2.7%; Score 126; DB 4; Length 1416; 18.0%; Pred. No. 0.036; 304 PAPM-----PYWSFGFHQCRYGY-----KOVSDLEYVVDG---336 KAGIPLEVMWTDIDYMDGYK-----ò

369MQSFVDTLHKNGQKYVL	389 - PGIGVDSSYGTY-NRGMEADVFIKRNGEPYLGEVWPGKVYFPDFLNPAAATFWSNEIKM 446	7 FQEILPLDGLWIDMNELSNFITSPLSSGSSLDDPPYKINNSGD	490	6 LYGLLEAKATHQAVVDITGKRPFILSRSTF-VSSGKYTAHWIGDNAAKWE 564	5 DLAYSIPGILNFGLFGIPMYGADICGFSHDTTEELCRRWIGLGGFYPFARDHSSLGTARQ 624 1		9 YEIDSQFLIGKSIMVSPALKQGAVAVDAYFPAGNWFDLFNYSFAVGGDSGKHVRLDTFAD 736 : :	9 HVNVHVREGSIVAMQGEALTTRDARKTPYQLLVVASRLENISGELFL 785	6 DDGENLRMGAGGGNRDWTLVKFRCYYTGKSVVLRSEVVNPEYASKMKWS 834 1:	SOUND SOUND SOUND SOUND SOUND SOUND SOUND SOUND SOUND SOUND SOUND SOUND SOUND SOUND SOUND SOUND SOUND SOUND SOUND SOUND SOUND SOUND SOUND SOUND SOUND SOUND SOUND SOUND SOUND SOUND SOUND SOUND SOUND SOUND SOUND SOUND SOUND SOUND SOUND SOUND SOUND SOUND SOUND SOUND SOUND SOUND SOUND SOUND SOUND SOUND SOUND SOUND SOUND SOUND SOUND SOUND SOUND SOUND SOUND SOUND SOUND SOUND SOUND SOUND SOUND SOUND SOUND SOUND SOUND SOUND SOUND SOUND SOUND SOUND SOUND SOUND SOUND SOUND SOUND SOUND SOUND SOUND SOUND SOUND SOUND SOUND SOUND SOUND SOUND SOUND SOUND SOUND SOUND SOUND SOUND SOUND SOUND SOUND SOUND SOUND SOUND SOUND SOUND SOUND SOUND SOUND SOUND SOUND SOUND SOUND SOUND SOUND SOUND SOUND SOUND SOUND SOUND SOUND SOUND SOUND SOUND SOUND SOUND SOUND SOUND SOUND SOUND SOUND SOUND SOUND SOUND SOUND SOUND SOUND SOUND SOUND SOUND SOUND SOUND SOUND SOUND SOUND SOUND SOUND SOUND SOUND SOUND SOUND SOUND SOUND SOUND SOUND SOUND SOUND SOUND SOUND SOUND SOUND SOUND SOUND SOUND SOUND SOUND SOUND SOUND SOUND SOUND SOUND SOUND SOUND SOUND SOUND SOUND SOUND SOUND SOUND SOUND SOUND SOUND SOUND SOUND SOUND SOUND SOUND SOUND SOUND SOUND SOUND SOUND SOUND SOUND SOUND SOUND SOUND SOUND SOUND SOUND SOUND SOUND SOUND SOUND SOUND SOUND SOUND SOUND SOUND SOUND SOUND SOUND SOUND SOUND SOUND SOUND SOUND SOUND SOUND SOUND SOUND SOUND SOUND SOUND SOUND SOUND SOUND SOUND SOUND SOUND SOUND SOUND SOUND SOUND SOUND SOUND SOUND SOUND SOUND SOUND SOUND SOUND SOUND SOUND SOUND SOUND SOUND SOUND SOUND SOUND SOUND SOUND SOUND SOUND SOUND SOUND SOUND SOUND SOUN	9 LLVGKKFE 896 : :: 4 IYVGDSWK 1181	
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Search completed: October 27, 2003, 10:26:53 Job time: 22.3042 secs

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ABG69611 ABG69612 ABB50119 AAM80202

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Listeria monocytog Human protein SEQ Human protein SEQ

Carbohydrate-assoc Soybean alpha-gluc Human Novila prote Potato alpha-gluco S. tuberosum alpha Breast and ovarian Drosophila melanog Drosophila melanog S. solfataricus ma Plasmid pNOV4833 m MalA fusion protei

> ABG69610 AAW18580 AAG66099

ABB67421 ABB69429 ABP96604

AAB58849

Alpha-1-6-glucanas Alpha-glucosidase Human MDDT SEQ ID M.vulgaris alpha-1

AAB42826 AAR04869 AAM00087 ABP51380

AAR72712 AAW88256 AAU23490

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ABP96615 ABP96625

ABP96616

Human ORFX ORF2590

Alpha-1,4-glucan l Morchella vulgaris

Novel human enzyme

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                                                                                                                                       FPNIFIVVVVFFSLRSSQVVLEEBESTVVGYGYVVRSVGVDSNRQVLTAKLDLIKPSSVY
                                                                                                                                                          -----SESGEVVGYGYRVVRAKVDSSSNTLTAFLKLINASSLY
                                                                                                                   Gaps
                                                                                                                  36;
                                                                                             57.0%; Score 2706; DB 23; Length 901;
larity 58.2%; Pred. No. 2.5e-220;
Conservative 120; Mismatches 222; Indels 36
            relates to a recombinant vector containing
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The present sequence represents an alpha-glucosidase isolated from buckwheat (Fagopyrum esculentum Moeench). The alpha-glucosidase gene can be used for the preparation of alpha-glucosidase derived from
                                                                                                                                                                                                                                                                                                                                            Buckwheat; alpha-glucosidase; enzyme; Fagopyrum esculentum Moeench;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 901;
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58.2%; Pred. No. 2.5e-220;
ive 120; Mismatches 222;
                                                                                                                                                                                                                                                                                                Buckwheat alpha-glucosidase protein SEQ ID NO:1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Location/Qualifiers
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                                                                                                                                      901
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/label= signal
32..901
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                                                                                                                                   ABB09151 standard; Protein;
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Matches 527; Conservative
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                                                                                        The invention relates to a recombinant vector containing alpha-glucosidase gene derived from buckwheat. A transformant containing the recombinant vector can be used for preparing alpha-glucosidase by culturing the transformant and isolating alpha-glucosidase from the culture. This sequence represents a buckwheat alpha-glucosidase protein.
                                                                                                                                                                                                                                                                                                     IKSLNLHVSLETSERLRIRITDSSQQRWEIPETVIPRAGN---HSPRRFSTEEDGGNSPE
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                                                                                                                                                                                                                      Length 901
              and
                               transformant useful for preparation of alpha-glucosidase
                                                                                                                                                                                                                                                     Indels
                gene,
              recombinant vector containing alpha-glucosidase
                                                                                                                                                                                                                    56.9%; Score 2703; DB 23;
58.6%; Pred. No. 4.5e-220;
iive 119; Mismatches 228;
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                                                             Claim 2; Page 8-9; 18pp; Japanese
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             RPAPMPYWSFGFHQCRYGYKNVSDLEYVVDGYAKAGIPLEVMWTDIDYMDGYKDFTLDPV
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                                                                          NFPEDKMQSFVDTLHKNGQKYVLILDPGIGVD-SSYGTYNRGMEADVFIKRNGEPYLGEV
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186 SLPADRSNLYGIGEHTKPTFRLARNQTLTLWNADIASYNVDLNLYGSHPFYLDVRA----
                         EEAGTTHGVLLLNSNGMDVKYEGHRITYNVIGGVIDLYVFAGPSPEMVMNQYTELIGRPA
                                                                                                                                     EDKWQSFVDTLHKNGQKYVLILDPGIGVD-SSYGTYNRGMEADVFIKRNGEPYLGEVWPG
                                                                                                                                                  361 LDKMQRFVNKLHKNGQKYVAILDPGININTTTYGTFQRAMKADIFIKRQGEPYQGEVWPG
                                                                                                                                                                                         KVYFPDFLNPAAATFWSNEIKMFQEILPLDGLWIDMNELSNFITSPLSSGSSLDDPPYKI
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                                                                                                                                                                                                                                                                                                                                                                        Alpha-glucosidase, barley, starch grain hydrolysis, alpha-amylase, glucoamylase, industry, germplasm, hydrolytic enzyme.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 | ALPENRSNLYGIGEHTKRSFRLIPGET#TLWNADIGSENPDVNLYGSHPFYMDVRGSKGN 245
          VGFENVENVKTYEVRISERLRSPRISLIKTVSDNDDPRFLSVEVSKLSLLVGKKFEMRLR 900
                           69
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  70 IKSLNLHVSLETSERLRIRITDSSQORWEIPETVIPRAGN---HSPRRFSTEEDGGNSPE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NNFLADPSSDLVFTLHNTTPFGFSVSRRSSGDILFDT-SPDSSDSNTYFIFKDQFLQLSS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               10 IFIVVVFFSLRSSQVVLEEEESTVVGYGYVVRSVGVDSNRQVLTAKLDLIKPSSVYAPD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The present sequence represents an alpha-glucosidase isolated from buckwheat (Fagopyrum esculentum Moeench). The alpha-glucosidase gene can be used for the preparation of alpha-glucosidase derived from
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                        Buckwheat; alpha-glucosidase; enzyme; Fagopyrum esculentum Moeench;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      26;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 901;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        tch 36.9%; Score 2703; DB 23; Length al Similarity 58.6%; Pred. No. 4.5e-220; 529; Conservative 119; Mismatches 228; Indels
                                                                                                                                                                                                                                             protein SEQ ID NO:2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           gene
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/label= signal
32..901
/label= alpha_glucosidase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A buckwheat-derived alpha-glucosidase
                                                                                                                                                                                                                                                                                                                                           Location/Qualifiers
                                                                                                                                                              ABB09152 standard; Protein; 901 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (NISO ) NIPPON SHOKUHIN KAKO
                                                                                                                                                                                                                                              Buckwheat alpha-glucosidase
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                                                                                                                                                                                                                   (first entry)
                                                                                                                                                                                                                                                                                                                Fagopyrum esculentum.
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IT 899
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(WISC) WISCONSIN ALUMNI RES Skadsen RW, Tibbot BK; WPI; 1998-347329/30 N-PSDB; AAV11736 DNA ઠે

This sequence represents a novel barley alpha-glucosidase protein. Recombinant alpha-glucosidase can be used to increase the rate of starch grain hydrolysis when used together with alpha-amylase or can supplement glucoamylase in industrial starch hydrolysis systems. Useful DNA sequence characteristics from this enzyme can be identified which can be used as hybridisation probes for identifying germplasm with high levels of efficient hydrolytic enzymes. encoding barley alpha-glucosidase protein - useful for producing ombinant protein to increase rate of starch grain hydrolysis when Claim 1; Col 21-26; 19pp; English. used with alpha amylase

877 AA; Sequence

13; 123 Gaps 26; Length 877; Indels Matches 471; Conservative 136; Mismatches 191; 51.6%; Score 2451; DB 19; 55.2%; Pred. No. 1.1e-198; Best Local Similarity Query Match

69 DIKSLNLHVSLETSERLRIRITDSSQQRWEIPETVIPRAG-----NHSPRRFSTEEDGGN SPENNFLADPSSDLVFTLHNTTPFGFSVSRRSSGDILFDTSPDSSDSNTYFIFKDQFLQL DVQRLAVYASLETDSRLRVRITDADHPRWEVPQDIIPRPAPGDVLHDAPPASSAPLQG--59 124 g ò

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PPYKINNSGDKRPINNKTVPATSIHFGNISEYDAHNLYGLLEAKATHQAVVDITGKRPFI 480

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455 539 515 599 575 629 635 719 695

PPYRINNDGTGRPINNKTVRPLAVHYGGVTEYEEHNLFGLLEARATGRGVLRDTGRRPFV LSRSTFVSSGKYTAHWTGDNAAKWEDLAYSIPGILNFGLFGIPMVGADICGFSHDTTEEL 456 516 540

CGRWIQLGAFYPFSRDHSAIFTVRRELYLWPSVAASGRKALGLRYOLLPYFYTLMYEAHM SGNPIARPLFFSFPQDTKTYEIDSQFLIGKSIMVSPALKQGAVAVDAYFPAGNWFDLFNY 099

CRRWIQLGAFYPFARDHSSLGTARQELYLWDSVASSARKVLGLRMRLLPHLYTLMYEAHV

900

g ò 720 SFAVGGDSGKHVRLDTPADHVNVHVREGSIVAMQGEALTTRDARKTPYQLLVVASRLENI 779

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837 862 SGELFLDDGENLRMGAGGGNRDWTLVKFRCYVTGK--SVVLRSEVVNPEYASKMKWSIGK 813 VVLMGHRSPAAPKKLTVHVNSAE------VEASSSAGTRYQNAGGLGGVAHIGGLS SGYLFLDDGDSPEYGR - - - RSDWSMVRFNYKIPNNKGAIKVKSEVVHNSYAQSRTLVISK VIFVGFENVENVK--TYEVRISERLRSPRISLIKTVSDNDDPRPLS------VEVSKLS LLVGKKFEMRLRLT 902 |:||::||::| LVVGEEFELKVAMS 876 969 780 95 838 883 863 à g à a 8 g

Potato alpha-glucosidase protein fragment Ä AAY51670 standard; Protein; 682 (first entry) 01-JUN-2000 AAY51670; RESULT 6

Alpha-glucosidase; potato; transgenic plant; starch; branching; amylose; amylogectin; granule size; sidechain; food; packaging; hydrolysis; paper; pulp; adhesive; soil stabilization; wetting agent; plant protection; fertilizer.

DE19836097-A1. 03-FEB-2000

Solanum tuberosum

98DE-1036097, 98DE-1036097 31-JUL-1998; 31-JJL-1998; (AGRE) HOECHST-SCHERING AGREVO GMBH.

Frobberg C;

2000-225174/20. N-PSDB; AAZ89108

New nucleic acid encoding potato alpha-glucosidase, used to produce transgenic plants that contain modified starch

Claim la; Page 5; 22pp; German.

This invention describes a novel potato alpha-glucosidase (I). (I) is used to produce transgenic plants (or plant or bacterial cells) that produce starch with modified degrees of branching, amylose/amylopectin ratio, phosphate content, starch granule size and/or sidechain structure, and thus altered physical and chemical properties. This starch is used for all usual applications, particularly in preparation of foods, packaging materials and disposable articles, but also for Mydrolysis to glucose (for manufacture in adhesives; for treating textiles; for soil stabilization; as wetting agent in plant protection and fertilizer compositions as binding agent in plant protection and fertilizer compositions as binding materials, leather and in casting; as flocculant for soil or coal slurries; and in polymers, as simple filler or reactive component, e.g. in polyweethane foams. Modified starch produced using plants that contain (I) are easily hydrolyzed, reducing the requirement for expensive enzymes. This sequence represents the potato alpha-glucosidase protein described in the method of the invention

682 AA Sequence

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Nagata T,
                                 (UYNI-) UNIV NIHON SCHOOL JURIDICAL PERSON
                                                                                                                                            Claim 2; Page 1154-1158; 2690pp; English
                                                    Takahashi Y,
18-MAY-2001; 2001WO-JP04192
                 18-MAY-2000; 2000JP-0145977
                                                    Asai S,
                                                                      WPI; 2002-034733/04.
N-PSDB; ABI99468.
                                                                                                                                                                                                                                                                                                      953 AA;
                                                    Ishikawa K,
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                                                      I D L Y V F A G P S P E M Y M N Q Y T E L I G R P A P M P Y W S G F F H Q C R Y G Y K V V D G Y A K A G I
                                                                                         PLEVMMTDIDYMDGYKDFTLDPVNFPEDKKQSFVDTLHKNGQKYVLILDPGIGVDSSYGT
                                                                                                                           PLEVMMIDIDYMOGFKDFTLDPVNFFLERVIFFLRKLHONDOKYVLIVDFGISINNTYDT
                                                                                                                                                                                         MNELSNF1TSPLSSGSSLDDPPYKINNSGDKRPINNKTVPATSIHFGNISEYDAHNLYGL
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                          Gaps
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                         11;
       DB 21; Length 682;
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     Query Match 49.5%; Score 2350.5; DB 21; Lengt Best Local Similarity 63.5%; Pred. No. 2.5e-190; Matches 432; Conservative 104; Mismatches 133; Indels
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The present invention describes a method for examining ischaemic conditions, comprising measuring the expression levels of particular genes (I) in a test sample or determining the expression profile of a gene group in the sample comprising genes selected from (I). The method is useful for examining the ischaemic condition (e.g. compressive ischaemia, occlusive ischaemia or vasospastic ischaemia) by measuring expression levels of particular genes (ABI992102 to ABI99212, encoding the protein sequences in ABBS7020 to ABBS7374) or by determining the expression profile of agene group comprising these genes. The expression levels or expression profiles produced by these genes are used as an indicator when screening for ischaemic condition-improving drugs or therapeutics for ischaemic diseases. ABI99913 and ABI99914 represent PCR primers for a mouse ischaemic condition related sequence, which are used in the exemplification of the present invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               137 RLENLSSTESGYTATLTRISP-TFFPKDVLTLQLEVLMETDSRLHFKIXDPASKRYEVPL 195
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                453 LDGLWIDMNELSNFITSPLSS--GSSLDDPPYKINNSGDKRPINNKTVPATSIHFGNISE 510
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Examining the ischemic condition (e.g. occlusive ischemia) by measuring expression levels of particular genes defined in the specification or by determining the expression profile of a gene group comprising these
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                                                                                                                                    LDTPADHVNVHVREGSIVAMQGEALTTRDARKTPYQLLVVASRLENISGELFLDDGENLR 792
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Acremonium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The present sequence represents a sugar transferase protein of Acremoni sp. $4G13. The protein preferably catalyses the glucose transfer of an alpha-1 right arrow 3 bond or the glucose transfer of an alpha-1 right arrow 3 and an alpha-1 right arrow bond to a sugar receptor by reacting with a substrate selected from starch and its decomposition
YNLHNLYGLTEAIASSRALVKTRGTRPFVISRSTFSGHGRYAGHWTEDVRTSWEHLAYSV
                              SVASSA-RKVLGLRMRLLPHLYTLMYEAHVSGNPIARPLFFSFPQDTKTYEIDSQFLIGK
                                                                    ETAQQAMRKAFALRYALLPYLYTLFHRAHVRGDTVARPLFLEFREDPSTWSVDRQLLWGP
                                                                                                SIMVSPALKQGAVAVDAYFPAGNWFDL------FNYSFAVGGDSGKHVR
                                                                                                            MGAGGGNRDWTLVKFRCYVTGKSVVLRSEVVNPBYASKMKWSIGKVTFVGFENV-ENVKT
                    PGILNFGLFGIPMVGADICGFSHDTTEELCRRWIQLGAFYPFARDHSSLGTARQELYLWD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         New sugar transferase gene and enzyme - useful for catalysing the transfer of an alpha-1 right arrow 3 bond to a sugar receptor for
                                                                                                                                                                                                                            YEVRTSERLRSPRISLIKTVSDNDDPRFLSVEVSKLSLLVGKKFEM 897
                                                                                                                                                                                                                                                                                                                                                             Acremonium sp. 84G13, glucose transfer; sugar transferase
                                                                                                                                                                                                                                                                                                                                           An enzyme with sugar transferase activity.
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                                                                                                                                                                                                                                                                                   AAW88044 standard; Protein; 922
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            saccharide preparation
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Query Match
30.0%; Score 1424; DB 20; Length 922;
Best Local Similarity 35.9%; Pred. No. 2.1e-111;
Matches 317; Conservative 129; Mismatches 285; Indels 152;

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240 EYNTLGGVLDFYFFVGDSPSRAVEBYGEIAGRPPMQPYWGLGFHQCKYGYQDAFMVABVV 299
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   360 AYVES-GTLDRGLDDDVFLLRSNGSVWLGVVWPGVTVFPDWFAENITQYWNNEFALFFDA 418
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     479 TECEDGETAGSSKRDGSPGQPGLVTRQPGFSRPRHPFHRRQEYEGDQKGLPGRDLLYPEY 538
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                                                                                                                                                                                                                                                                                                                                                                                                                           332 DGYAKAGIPLBUMWTDIDYMDGYKDFTLDPVNFPEDKMQSFVDTLHKNGQKYVLILDPGI 391
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    96
GYVVRSVGVDSNRQVLTAKLDLI-KPSSVYAPDIKSLNLHVSLETSERLRITDSSQQR
                          WEIPETVIPRAGNHSPRRFSTEEDGGNSPENNFLADPSSDLVFTLHNTTPFGFSVSRRSS
                                                                                                                                                                     GDILFDTSPDSSDSNTYFIFKDQFLQLSSALPENRSNLYGIGEHTKRSFRLIPGETMTLW
                                                                                                                                                                                                             134 DEVLFDTSAAS-----IVFESQYLRLRTSIPTD-PYLYGLGAHNDPMRLESVGYIRTFW
                                                                                                                                                                                                                                                                                                                                         TYNVIGGVIDLYVFAGPSPEMMMNOYTELIGRPAPMPYWSFGFHQCRYGYKNVSDLEYVV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          593 HDTTEELCRRWIQLGAFYPFARDHSSLGTARQELYLWDSVASSARKVLGLRMRLLPHLYT
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                                                                                                       GADICGFSHDTTEELCRRWIQLGAFYPFARDHSSLGTARQELYLWDSVASSARKVLGLRM 644
                                                                                                                                                                                                                                                               29 EEESTVVGYGYVVRSVGVDSNRQVLTAKLDLI-KPSSVYAPDIKSLNLHVSLETSERLRI 87
                                    QAVVDITG--KRPFILSRSTFVSSGKYTAHWTGDNAAKWEDLAYSIPGILNFGLFGIPMV
                                                                                                                                                                        RLLPHLYTLMYEAHVSGNPIARPLFFSFPQDTKTYEIDSQFLIGKSIMVSPALKQGAVAV
                                                                                                                                                                                            DAYFP-AGN---WFDLFNYSFAVGGDSGKHVRLDTPADHVNVHVREGSIVAMQGEALTTR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DNA encoding truncated variants of Aspergillus glucosyltransferase is claimed. Deletion from the N- or C-terminal reduces GTase activity of the protein. Specifically, glucoamylase with reduced GTase activity can be prepared. The full-length GTase structural gene was isolated as a 4.3kb SphI fragment from chromosomal DNA of A.niger #499.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 30.0%; Score 1423; DB 14; Length 985; Best Local Similarity 35.4%; Pred. No. 2.8e-111; Matches 308; Conservative 145; Mismatches 278; Indels 140;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Glucoamylase prepn. with reduced glucosyl-transferase activity using microorganism transformed using plasmids including DNA fragments having deletion of N-end or C-end of Aspergillus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GTase; glucoamylase; GAase; recombinant production; truncated;
N-terminal deletion; C-terminal deletion.
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EARQTPWALLAALGSNGTASGQLYLDDGESI 896
                                                                                                                                                                                                                                                                                                                DARKTPYQLLVVASRLENISGELFLDDGENL
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N-PSDB; AAQ50982.
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                                                                                                                                                                                                                                                                                                                                                                                              Glycosyltransferase was prepared from a culture of A. niger containing recombinant DNA encoding GTase (AAQ50468). GTase can bobtained effectively using this method and in larger quantities. The probes (AAQ50466-67) were used to detect transformants containing the GTase gene.
                                                                                                                                                                                                                                                                                                            1. of glucosyl:transferase - using glucosyl:transferase gene
recombinant DNA of Aspergillus niger
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Conservative 145; Mismatches 278;
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transformation; expression.
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                                Aspergillus niger
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New recombinant glucoamylase from Endomyces fibuliger, useful for
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                             Saccharomycopsis fibuligera
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  114 OILPTHVDSTNASWYFLSENLVPR--------PKASLNASVSQSDLFVSW
                                                                                                                                                                 HNTTPFGFSVSRRSSGDILFDTSPDSSDSNTYFIFKDQFLQLSSALPENRSNLYGIGEHT
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                                                                      RI----TDSSQQRWE-IPETVIPRAGNHSPRRFSTEEDGGNSPENNFLADPS-SDLVFTL
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EARQTPWALLAALGSNGTASGQLYLDDGESI 896
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The present sequence represents Endomyces fibuliger (also called Saccharomycopsis fibuligera) glucoamylase GLA2. The invention describes the recombinant GLA2 enzyme, which is useful for hydrolysing carbohydrate-containing materials, especially materials containing rice carbohydrates. The glucoamylase is used to produce glucose and alcohol from starch containing materials. GLA2 is useful for hydrolysing carbohydrate containing materials e.g. mixtures of a source of proteins and a source of carbohydrates, especially a mixture of leguminous plant or of a cooked oleaginous plant and of a cooked or roasted cereal source e.g. a mixture of soya or cooked beans and of cooked or roasted wheat or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   38 GYVVRSVGVDSNRQVLTAKLDLIKPSSVYAPDIKSLNLHVSLETSERLRIRI-----TDSS
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Endomyces fibuliger; glucoamylase; GLA2; hydrolysis; carbohydrate; glucose; alcohol; starch; leguminous plant; cooked; oleaginous plant; roasted; cereal; soya; wheat; rice.

Endomyces fibuliger glucoamylase GLA2 protein.

(first entry)

28-JAN-2000

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                                                                                                    DHSSLGTARQELYLWDSVASSARKVLGLRMRLLPHLYTLMYEAHVSGNPIARPLFFSFPQ 674
                                                                                                                                    DIKTYEIDSOFLIGKSIMVSPALKOGAVAVDAYFP-AGN-----WFDLFNYSFAVGGDS 727
                                                                                                                                                                                                                   D2H; hPEPT1; human; GI tract receptor; sucrose-isomaltase complex; intestinal peptide-associated transporter; hypertension; diabetes; osteoporosis; haemophilia; anaemia; cancer; migraine; angina pectoris; therapeutic agent delivery; therapy; probe.
                                                                            EYASFTSSLAAASPTSDEDSSVSSTSASIDSLNTLAPGKGNINYPPYAINNDQGDHDLAT
                                           HAVSPNATHQDGTLEYDVHNLYGYLETNATFEALLEIQPNKRPFIISRSSFAGSGRQTGH
                                                                                                                                                   NRNVSTVDTQFFVGDALVVTPVLEQGVDTVKGTFPGSGNEEVYYDWYTHEKQNFT----D
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                                 KTVPATSIHFGNISEYDAHNLYGLLEAKATHQAVVDI-TGKRPFILSRSTFVSSGKYTAH
                                                                                                                                                                      GKHVRLDTPADHVNVHVREGSIVAMQGEALTTRDARKTPYQLLVVASRLENISGELFLDD
                                                                   WIGDNAAKWEDLAYSIPGILNFGLFGIPMVGADICGFSHDTTEELCRRWIQLGAFYPFAR
                                                                                                                                                                                                                                                                                                                                                                     Gastro-intestinal transport receptor; binding protein; hSI; HPT1;
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Patterson CA,
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----ITSPLSSGSSLDD
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Omahony DJ,
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New proteins that bind specifically to receptors in the gastro-intestinal tract and related nucleic acid - chimaeras and antibodies, used to deliver therapeutic or diagnostic agents to, or through, the gastrointestinal tract, e.g. insulin or leuprolide

Disclosure; Fig 3; 294pp; English

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peptide-associated transporter (HPTI), hPEPTI, D2H and human sucrose-isomaltase complex (hSI). (I) provide active transport of therapeutic agents through human and animal GI tissue (into the blood) for in vivo delivery, particularly for treatment or prevention of hypertension, diabetes, osteoporosis, haemophila, anaemia, cancer, migraine, or angian pectoris. Specifically they are used to deliver insulin or leuprolide, but many other guitable therapeutic agents are disclosed, including genes or inhibitory nucleic acid, imaging agents and antension. (I) may also provide targeting to the GI tract. Other uses of (I) are: (i) to determine the level of specified receptors in a sample (ii) a binding assay); and (iii) to screen for molecules that bind (I). Immunogenic analogues or derivatives of (I) are used to raise antibodies and in immunoassays. The antibodies are used to locate, detect and measure (I), e.g. for imaging, monitoring treatment, tissue analysis etc., also for peptide purification and immobilisation.
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This sequence is the human hSI protein. The invention relates to purified proteins (1) that bind specifically to at least one of tgastro-intestinal (GI) tract receptors human intestinal
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    cancer ceils or primary and/or metastatic stomach or oesophageal cancer cells by testing cells; in extraintestinal tissues and/or body fluids for expression of SI (sucrase isomaltase). CDX1 or CDX2 (transcription factors). Expression of these markers indicates possible presence of the specified cancer cells. The method is used to diagnose (or monitor) metastatic colorectal cancer or primary and/or metastatic stomach or oesophageal cancer cells, also to confirm identification of such cells. These cancers can be treated by administration of an SI ligand and (optionally conjugated) sytostatic agent or radioimaged by administering a conjugate of the SI ligand and detectable agent. The present sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          782
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ITDSSQQRWEIPETVIPRAGNHSPRRFSTEEDGGNSPENNFLADPSSDLVFTLH-NTTPF 147
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             useful
or CDX2
                                                             VVGYGYVVR----SVGVDSNRQVLTAKLDLIKPSSVYAPDIKSLNLHVSLETSERLRIR
                           -----KHVRLDTPADHVNVHVREGSIVAMQGEALTTRDARKTPYQLLVVASRLENISGE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human, sucrase isomaltase, SI, stomach cancer, colorectal cancer, oesophageal cancer, cytostatic, metastasis, CDXI, CDX2, tumour.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             In vitro screening for specific gastrointestinal cancer cells, for diagnosis, by detecting expression of the markers SI, CDX1
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al Similarity 38.2%; Pred. No. 1.7e-105;
301; Conservative 138; Mismatches 258; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Disclosure; Page 114-119; 119pp; English
                                                                                                                                                                                                                                                                                                                                                           AAU09028 standard; Protein; 1827 AA
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|TDPNNRRYEVPHQYV-----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human sucrase isomaltase, SI
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N-PSDB; AAS14674.
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Best Local Similarity
Matches 301; Conserv
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28.6%; Score 1357; DB 18; Length 985;
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                                                                                                                                                                                                             The invention relates to isolated polynucleotide (I) and polypeptide (II) sequences. (I) is useful as hybridisation probes, polymerase chain reaction (PCR) primers, oligomers, and for chromosome and gene mapping, and in recombinant production of (II). The polynucleotides are also used in diagnostics as expressed sequence tags for for identifying expressed genes. (I) is useful in gene therapy techniques to restore normal activity of (II) or to treat disease states involving (II). (II) is useful for generating antibodies against it, detecting or quantitating a polypeptide in tissue, as molecular weight markers and as a food supplement. (II) and its binding partners are useful in medical imaging of sites expressing (II). (I) and (II) are useful in medical imaging of sites expressing (II). (I) and (II) are useful in medical disorders involving aberrant protein expression or biological activity. The polypeptide and polynucleotide sequences have applications in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits to assess biodiversity and canno acid sequences. Agglonolo Agglosial represent novel human amino acid sequences of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      207
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           326 DLEYVVDGYAKAGIPLEVMWTDIDYMDGYKDFTLDPVNFPEDKMQSFVDTLHKNGQKYVL 385
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      127 ILDPAISIGRRANGTTYATYERGNTQHVWINESDGSTPIIGEVWPGLTVYPDFTWPNCID 486
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     139 FWSNEIKMFQEILPLDGLWIDMNELSNFITSPLS--SGSSLDDPPYKINNSGD--KRPIN 494
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Note: The sequence data for this patent did not appear in the printed specification, but was obtained in electronic format directly from WIPO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             34 VVGYGYVVR----SVGVDSNRQVLTAKLDLIKPSSVYAPDIKSLNLHVSLETSERLRIR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GFSVSRRSSGDILFDTSPDSSDSNTYFIFKDQFLQLSSALPENRSNLYGIGEHTKRSFRL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  202 SIQVIRKSNGKTLFDTSIGP-----LVYSDQYLQISARLPSD--YIYGIGEQVHKRFRH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EGHRI-TYNVIGGVIDLYVFAGPSPEMVMNQYTELIGRPAPMPYWSFGFHQCRYGYKNVS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       386 ILDPGIGV-----DSSYGTYNRGMEADVFIKRN--GEPYLGEVWPGKVYFPDFLNPAAAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ITDSSQQRWEIPETVIPRAGNHSPRRFSTEEDGGNSPENNFLADPSSDLVFTLH-NTTPF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                      New isolated polynucleotide and encoded polypeptides, useful in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits and to assess
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              90;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 1829;
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28.6%; Score 1360; DB 22; Lengtn JBest Local Similarity 38.2%; Pred. No. 1.7e-105;
Matches 301; Conservative 138; Mismatches 258; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                      Claim 20; SEQ ID No 45353; 103pp; English.
                              Tang YT;
                             Drmanac RT, Liu C,
                                                             WPI: 2001-639362/73
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1829 AA;
(HYSE-) HYSEQ INC
                                                                            N-PSDB; AAS79181
                                                                                                                                                         biodiversity
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613 ARDHSSLGTARQELYLWDS---VASSARKVLGLRMRLLPHLYTLMYEAHVSGNPIARPLF 669
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             -----KHVRLDTPADHVNVHVREGSIVAMQGEALTTRDARKTPYQLLVVASRLENISGE 782
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                                                                                                                                                           AHWTGDNAAKWEDLAYSIPGILNFGLFGIPMVGADICGFSHDTTEELCRRWIQLGAFYPF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FSFPQDTKTYBIDSQFLIGKSIMVSPALKQGAVAVDAYFPAGNWFDLFNYSFAVGGDSG-
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Fungus; fungal; enhancer element; promoter; recombinant protein.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         the present sequence is encoded by the agdA gene
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Aspergillus oryzae alpha-glucosidase.
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-AGN---WFDLFNYSFAVGGDSGKHVRLDTPADHVAVHVREGSIVAMQGEALTIRDARKT 765
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Best Local Similarity 34.4%; Pred. No. 1.1e-105;
Matches 298; Conservative 142; Mismatches 290; Indels 136; Gaps
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GenCore . Copyright (c) 1993 OM nucleic - nucleic search, using sw	2003, 10	Title: US-10-043-418-5 Perfect score: 29 Sequence: 1 cggtgaagttgacaggatccaaggtgaag	Scoring table: IDENTITY NUC Gapop 10.0 , Gapext :	Searched: 22781392 seqs, 12152	Total number of hits satisfying chose	Minimum DB seq length: 0 Maximum DB seq length: 200000000	Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 sur	Database : EST:*	1: 2:	3: em_estin:* 4: em_estmu:*					13: 9D_est4:* 14: 9D_est5:* 15: em_estfun:*					em gss_rod		8 g	Pred. No. is the number of results score greater than or equal to the and is derived by analysis of the	•	Result Ouery No. Score Match Length DB ID	538 12 628 13 468 14 749 28

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                                                                          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. I (bases I to 901). I NIH-MCC http://mgc.nci.nih.gov/.
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CDNA Library Arrayed by: The ILM A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be found through the ILM A.G.E. Consortium/LLNL at:
http://image.llnl.gov.m column: 14
High quality sequence stop: 713.
Location/Qualifiers
1. 900
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Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ATCC
                                                                                                                                                                                                                                                                                                                                                                             /organism="Homo sapiens"
                                                                                                                                                                     Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ATCC
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              BUB59266.1 GI:24044258
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                                               Homo sapiens (human)
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BU159643
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              VERSION
KEYWORDS
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/lab host="hilloB (phage resistant)"
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CoCI; cDNA made by Oilgo-dT priming. Directionally
cloned into BcoRI/KhoI sites using the following S
adaptor: GGCAGGGG(G). Library constructed by Ling Hong
in the laboratory of Gerald M. Rubin (University of
California, Berkeley) using ZAP-CDNA synthesis kit
(Stratagene) and Superscript II RT (Life Technologies).
Note: this is a NIH_MGC Library."
                                                                                                                                                                                                                                                                   /organism="Momo sapiens"
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Fornage: a insert size 1.75 kb. Library constructed by Life
Technologies "
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 908)
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Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ATC

CDNA Library Preparation: Ling Hong/Rubin Laboratory

CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Incyte Genomics, Inc.

Clone distribution: MGC clone distribution information can be

found through the I.M.A.G.E. Consortium/LLNL at: image.llnl.gov

Plate: LLCM969 row: k column: 18

High quality sequence stop: 602.
Clone distribution: WGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov
Plate: //image.llnl.gov
Plate: LLAM13456 row: o column: 13
High quality sequence stop: 669.
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National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished
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8 a 302 c 1247 g 211 t 3 others
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Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ATCC
CDNA Library Preparation: Rubin Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
http://image.lln.gov
Plate: LLCM2780 row: j column: 14
High quality sequence stop: 734.
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11 (bases 1 to 932)
NH-MGC http://mgc.ncl.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
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                                                                  ch 72.4%; Score 21; DB 10; Length 908; 1 Similarity 82.8%; Pred. No. 5.6e+02; 24; Conservative 0; Mismatches 5; Indels
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Search completed: October 27, 2003, 11:54:52 Job time: 2577 secs

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GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
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11 US-09-844 653-32

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9 US-09-987-190-7

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13 US-10-156-761-1

13 US-10-027-632-5351

14 US-10-027-632-97-1499

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Perfect score:
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Sequence 54, Appl
Sequence 607, App
Sequence 1, Appli
Sequence 3, Appli
 31331, A
5, Appli
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                      Sequence 16455, A
Sequence 141845,
Sequence 7, Appli
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1 US-09-992-313-5
2 US-10-265-313-5
3 US-10-265-313-5
3 US-09-864-761-16455
3 US-09-938-842A-607
0 US-09-771-161A-54
0 US-09-771-161A-53
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0 US-09-814-353-31634
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ALIGNMENTS

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Sequence 5, Application US/10043418
Fublication No. US20020184662A1
Fublication No. US20020184662A1
Fublication No. US20020184662A1
Fublication No. US20020184662A1
Fublication No. US20020184662A1
FILE REPERENCE Clark, Suzanne E.
FILE REPERENCE: 960296.97486
CURRENT APPLICATION NUMBER: US/10/043,418
FILE REPERENCE: 960296.97486
CURRENT APPLICATION NUMBER: 60/260,787
FRIOR FILING DATE: 2001-01.10
NUMBER OF SEQ ID NOS: 7
SOFTWARE: PALENTIN Ver. 2.1
SEQ ID NO 5
LENGTH: 29
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US-10-027-632-174961
; Sequence 174961, Application US/10027632
Sequence Invokmarion:
; APPLICANT: Wang, David G.
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ORGANISM: Artificial Sequence
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APPLICANT: Brown, Joseph P.
APPLICANT: Burmer, Glenna C.
APPLICANT: Burmer, Glenna C.
APPLICANT: Roush, Christine L.
TITLE OF INVENTION: ANTIGENIC PEPTIDES AND ANTIBODIES FOR G PROTEIN-COUPLED RECEPT-FILE REFERENCE: 1920-4-4
CURRENT APPLICATION NUMBER: 105/10/225,567A
CURRENT FILING DATE: 2001-12-19
PRIOR APPLICATION NUMBER: 60/257,144
PRIOR FILING DATE: 2000-12-19
WINNBER OF SEC ID NOS: 2292
SOFTWARE: Patentin version 3.1
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Patent No. US20020058293A1
GENERAL INFORMATION:
APPLICANT: TAKESAKO, Kazutoh
APPLICANT: MIZUTANI, Shigetoshi
APPLICANT: ENDO, Masahiro
APPLICANT: KATO, Ikunoshin
TITLE OF INVENTION: FUNGAL ANTIGENS AND PROCESS FOR PRODUCING THE SAME
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                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 5659;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME/KEY: misc_feature; NAME/KEY: misc_feature; LOCATION: (2067)...(2067)... OTHER INFORMATION: N at this positiion can be a, c, t, or US-09-944-653-32
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     5; Indels
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Fublication No. US20030054347A1
GENERAL INFORMATION:
TITLE OF INVENTION:
TITLE OF INVENTION: Detecting and Treating Bye Disease
CURRENT APPLICATION NUMBER: US/09/844,653
CURRENT APPLICATION NUMBER: US/09/844,653
CURRENT FILING DATE: 2001-04-27
NUMBER: PATENT OF SEQ ID NOS: 173
SOFFWARE: PATENTIN version 3.0
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PRIOR APPLICATION NUMBER: 09/262,856
                      LifeSpan Biosciences
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82.8%;
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Best Local Similarity 82.8
Matches 24; Conservative
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; ORGANISM: Homo sapiens
US-10-225-567A-521
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ORGANISM: Homo sapiens
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US-09-844-653-32/c
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LENGTH: 48841
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LENGTH: 5659
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TITLE OF INVENTION: Identification and Mapping of Single Nuclectide
FILE REFERENCE: 108827.129
CURRENT APPLICATION NUMBER: US/10/027,632
CURRENT APPLICATION NUMBER: US/10/027,632
PRIOR APPLICATION NUMBER: US 60/18,006
PRIOR PELING DATE: 2000-07-12
PRIOR APPLICATION NUMBER: US 60/198,676
PRIOR FILING DATE: 2000-07-12
PRIOR PELING DATE: 2000-07-12
PRIOR APPLICATION NUMBER: US 60/193,483
PRIOR APPLICATION NUMBER: US 60/193,483
PRIOR PILING DATE: 2000-02-24
PRIOR PILING DATE: 1000-02-24
PRIOR PELING DATE: 1999-11-23
PRIOR PELING DATE: 1999-11-23
PRIOR PELING DATE: 1999-11-23
PRIOR PELING DATE: 1999-10-23
PRIOR PELING DATE: 1999-00-09
PRIOR PILING DATE: 1999-00-09
PRIOR PILING DATE: 1999-09-09-09
NUMBER OF SEQ ID NOS: 328700
SOFTWARE: FastSEQ for Windows Version 4.0
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Publication No. US20030054347A1
GENERAL INFORMATION:
APPLICANT: Richards, Julia
APPLICANT: Rozsa, Frank
TITLE OF INVENTION: Detecting and Treating Eye Disease
FILE REFERENCE: UM-06105
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Pred. No. 15;
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CURRENT FILING DATE: 2001-04-27
NUMBER OF SEQ ID NOS: 173
SOFTWARE: PatentIn version 3.0
SEQ ID NO 44
LENGTH: 215
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ) LOCATION: (1)...(3186778)
; OTHER INFORMATION: n = A,T,C or G
US-10-027-632-174961
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85.7%;
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Best Local Similarity 85.77
Thes 24; Conservative
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NAME/KEY: misc feature
LOCATION: (1)...(31867)
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ORGANISM: Homo sapiens
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ORGANISM: Human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               3186778
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Gaps

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Sequence 5351, Application US/10027632

GENERAL INFORMATION:
APPLICANT: Wang, David G.
TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
TITLE OF INVENTION: Polymorphisms in the Human Genome
TITLE OF INVENTION: Polymorphisms in the Human Genome
FILE REFERENCE: 108827.129
CURRENT APPLICATION NUMBER: US/10/027,632
CURRENT APPLICATION NUMBER: US 60/218,006
PRIOR FILING DATE: 2000-07-12
PRIOR FILING DATE: 2000-04-20
PRIOR FILING DATE: 2000-04-20
PRIOR FILING DATE: 2000-03-29
PRIOR FILING DATE: 2000-03-29
PRIOR PILING DATE: 2000-03-29
PRIOR PILING DATE: 2000-03-29
PRIOR PILING DATE: 1200-02-24
PRIOR PILING DATE: 1999-11-33
PRIOR PLING DATE: 1999-09-28
PRIOR PILING DATE: 1999-09-28
PRIOR PILING DATE: 1999-09-28
PRIOR PILING DATE: 1999-09-28
PRIOR PILING DATE: 1999-09-28
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     Indels
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                                                                                                                                                                                                                                                                            APPLICANT: OMURA, SATOSHI
APPLICANT: IKEDA, HARUO
APPLICANT: IKEDA, HARUO
APPLICANT: ISHIKAMA, JUN
APPLICANT: BISHRAMA, JUN
APPLICANT: SHIBA, TADAYOSHI
APPLICANT: SAKAKI, YOSHITUKI
APPLICANT: SAKAKI, YOSHITUKI
APPLICANT: HATTORI, MASAHIRA
TILE REFERENCE: 249-262
CURRENT APPLICATION NUMBER: US/10/156,761
CURRENT FILING DATE: 2001-05-29
FRIOR APPLICATION NUMBER: JP 2001-204089
FRIOR APPLICATION NUMBER: JP 2001-272697
FRIOR FILING DATE: 2001-08-02
NUMBER: OF SEQ ID NOS: 15109
     Mismatches
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                                                  2 GGTGAAGTTGACAGGATCCAAGGTGAAG 29
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PRIOR APPLICATION NUMBER: US 60/146,002
PRIOR FILING DATE: 1999-08-09
NUMBER OF SEQ ID NOS: 325720
SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: DNA ORGANISM: Streptomyces avermitilis
                                                                                                                                                                                                           ; Sequence 1, Application US/10156761; Publication No. US20030119018A1; GENERAL INFORMATION:
     ..
  23; Conservative
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US-10-027-632-5351/c
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LENGTH: 9025608
     Matches
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Publication No. US20030180953A1
GENERAL INFORMATION:
APPLICANT: Howard, Bussey
APPLICANT: Charles, Boone
APPLICANT: Howard, Bussey
ITILE OF INVENTION: Gene Disruption Methodologies for Drug Target Discovery
FILE REFERENCE: 10182-005-999
CURRENT APPLICATION UNWERR: US/10/032,585
CURRENT FILING DATE: 2001-12-20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 7, Application US/09987190

Patent No. US200200582931

GENERAL INFORMATION:

APPLICANT: TAKESAKO, Kazutch

APPLICANT: TAKESAKO, Kazutch

APPLICANT: ENDO, Masahiro

TITLE OF INVENTION: FUNGAL ANTIGENS AND PROCESS FOR PRODUCING THE SAME

TITLE FEFERENCE: 1422-0502P

CURRENT FILING DATE: 2001-11-13

PRIOR APPLICATION NUMBER: 09/262,856

PRIOR PILING DATE: 1999-04

NUMBER OF SEQ ID NOS: 15

SOFTWARE: Patentin Ver: 2.0

SEC ID NO 7
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69.0%; Score 20; DB 12; Length 1476;
Best Local Similarity 82.1%; Pred. No. 48;
Matches 23; Conservative 0; Mismatches 5; Indels
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Pred. No. 48;
                                                                                                                                                                                                                     DB 9; Length 944;
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                                                                                                                                                                                                                                                               0; Mismatches
                                                                                                                                                                                                                     Score 20; DE
Pred. No. 47;
                                                                                                                                                                                                                                                                                                                                             697 GGTGAAGTGGTCAAGATCGAAGTTGAAG 724
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SEQ ID NO 6687
LENGTH: 1476
                                                                                                                                                                                                                Query Match
Best Local Similarity 82.1%;
Matches 23; Conservative
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82.1%;
PRIOR FILING DATE: 1999-03-04
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; ORGANISM: Candida albicans
US-10-032-585-6687
                    NUMBER OF SEQ ID NOS: 15
SOFTWARE: PatentIn Ver. 2.0
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                                                                                                                   TYPE: DNA; ORGANISM: Candida albicans
US-09-987-190-13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                              US-10-032-585-6687
                                                                   SEQ ID NO 13
LENGTH: 944
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Gaps

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Best Local Similarity
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US-10-128-714-7
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Publication No. US20030096264A1

Publication No. US20030096264A1

Publication No. US20030096264A1

Publication No. US20030096264A1

APPLICANT: Broams, Jeffrey

APPLICANT: Hook, Derek

APPLICANT: Klimczak, Leszek

APPLICANT: Rajan, Prink

APPLICANT: Rajan, Prink

APPLICANT: Rajan, Prink

APPLICANT: Rajan, Prink

APPLICANT: Rajan, Prink

APPLICANT: Rajan, Prink

APPLICANT: Rajan, Prink

APPLICANT: Bajan, Prink

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APPLICANT: Bajan, Prink

APPLICANT: Rajan, Prink

APPLICANT: Rajan, Prink

APPLICANT: Rajan, Prink

APPLICANT: Rajan, Prink

APPLICANT: Rajan, Prink

PRIOR APPLICATION NUMBER: US 60/299,151

PRIOR PILING DATE: 2001-09-07

PRIOR FILING DATE: 2001-09-07

PRIOR FILING DATE: 2001-09-25

PRIOR FILING DATE: 2001-09-25

PRIOR FILING DATE: 2001-109-25

PRIOR FILING DATE: 2001-11-14
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                                                                                                                                                                 Length 526;
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; Sequence 1499, Application US/09918995
; Publication No. US2003007362341
; GENERAL INPORMATION:
    APPLICANT: Hyseq, Inc.
; TITLE OF INVENTION: NOVEL NUCLEIC ACID SEQUENCES OBTAINED
    TITLE OF INVENTION: NOVEL NUCLEIC ACID SEQUENCES
; FILE REFERENCE: 20411-756
; CURRENT APPLICATION NUMBER: US/09/918,995
; CURRENT FILING DATE: 2001-07-30
; PRIOR APPLICATION NUMBER: US/09/235,076
; PRIOR PLILING DATE: 1999-01-20
; NUMBER CF SEQ ID NOS: 38054
; SOFTHARE: PSEASEQ for Windows Version 3.0
; SEQ ID NO 1499
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 65.5%; Score 19; DB 11; Length 487; Best Local Similarity 81.5%; Pred. No. 1.2e+02; Matches 22; Conservative 0; Mismatches 5; Indels
                                                                                                                                                            Query Match 66.2%; Score 19.2; DB 13; Best Local Similarity 87.5%; Pred. No. 1e+02; Matches 21; Conservative 0; Mismatches 3;
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// OTHER INFORMATION: n = A,T,C or G
US-09-918-995-1499
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: DNA ORGANISM: Homo sapiens
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LOCATION: (1)...(487)
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                           LENGTH: 526
TYPE: DNA
ORGANISM: Human
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                                                                                                             US-10-027-632-5351
; SEQ ID NO 5351
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APPLICANT: Jiang, Mandia, Mendia, Mendia, Mendia, Mendia, Mendia, Mendia, Mendia, Carlos
APPLICANT: Tishkoff, Daniel
APPLICANT: Tishkoff, Daniel
APPLICANT: Excentin, Alexey M
APPLICANT: Excentin, Alexey M
APPLICANT: Lemieux, Sebastien M
TITLE OF INVENTION: Methods of Use
TITLE OF INVENTION: Methods of Use
FILE REFERENCE: 10182-018-999
CURRENT APPLICATION NUMBER: US 60/285,697
PRICR FILING DATE: 2001-04-23
PRICR FILING DATE: 2001-04-23
PRICR FILING DATE: 2001-04-23
PRICR FILING DATE: 2001-06-05
PRICR FILING DATE: 2001-06-05
PRICR FILING DATE: 2001-07-09
PRICR FILING DATE: 2001-07-09
PRICR FILING DATE: 2001-07-09
PRICR FILING DATE: 2001-07-09
PRICR FILING DATE: 2001-07-09
PRICR FILING DATE: 2001-08-31
NUMBER: US 60/316,362
PRICR FILING DATE: 2001-08-31
SOFTWARE PATENTIN VETSION 3.1
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Pred. No. 1.6e+02;
0; Mismatches 5; Indels 0;
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PRIOR APPLICATION NUMBER: US 60/349,936
PRIOR FILING DATE: 2002-01-18
PRIOR APPLICATION NUMBER: US 60/361,834
PRIOR FILING DATE: 2002-03-04
NUMBER OF SEQ ID NOS: 197
SOFTWARE: Patentin version 3.1
SEQ ID NO 97
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                                                                                                                                                                                                                      ; TYPE: DNA; ORGANISM: Mus musculus domesticus US-10-175-523-97
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ; Sequence 7, Application US/10128714; Publication No. US20030119013A1; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CONGANISM: Aspergillus fumigatus US-10-128-714-7
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APPLICANT: Jiang, Bo
APPLICANT: Tishkoff,
APPLICANT: Tishkoff,
APPLICANT: Zamudio, Carlos
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  20; Conservative
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APPLICANT: Eroshkin, Alexey M
APPLICANT: Lemieux, Sebastien M
TITLE OF INVENTION: Identification of Essential Genes in Aspergillus fumigatus and
TITLE OF INVENTION: Methods of Use
TITLE OF INVENTION: Methods of Use
FILE REFERENCE: 1018-018-99
CURRENT APPLICATION NUMBER: US/10/128,714
CURRENT APPLICATION NUMBER: US 60/285,697
PRIOR APPLICATION NUMBER: US 60/285,697
PRIOR PELING DATE: 2001-04-23
PRIOR PELING DATE: 2001-04-23
PRIOR APPLICATION NUMBER: US 60/295,890
PRIOR PELING DATE: 2001-06-05
PRIOR APPLICATION NUMBER: US 60/303,899
PRIOR PELING DATE: 2001-06-05
PRIOR PELING DATE: 2001-06-05
PRIOR PELING DATE: 2001-08-31
NUMBER OF SEQ ID NOS: 8603
SOFTWARE: PatentIn version 3.1
SEQ ID NO 5007
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APPLICANT: Restelli, Luca
APPLICANT: Gould-Rothberg, Bonnie
APPLICANT: Gould-Rothberg, Bonnie
APPLICANT: Murphey, Ryan
TITLE OF INVENTION: Complex Associated Disorders
TITLE OF INVENTION: Complex Associated Disorders
FILE REFERENCE: 21402-042
CURRENT APPLICATION NUMBER: US/10/016,253
PRIOR PAPLICATION NUMBER: 60/254,268
PRIOR PILING DATE: 2000-12-08
NUMBER OF SEQ ID NOS: 25
SOFTWARE PATENTIN Ver: 2.1
SEQ ID NO 13
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64.8%; Score 18.8; DB 14; Length 2807;

Best Local Similarity 90.9%; Pred. No. 1.6e+02;

Matches 20; Conservative 0; Mismatches 2; Indels 0;
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US-10-016-253-13/c
'Sequence 13, Application US/10016253
'Publication No. US20030124534A1
'GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; ORGANISM: Aspergillus fumigatus US-10-128-714-5007
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: DNA
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity
Matches 21, Conservat
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                         sequence 1057, Apple sequence 13, Appl sequence 13, Appl sequence 9, Appli sequence 9, Appli sequence 9, Appli sequence 170, Appl sequence 70, Appl sequence 35, Appl sequence 35, Appl sequence 35, Appl sequence 35, Appl sequence 117, Appl sequence 117, Appl sequence 117, Appl sequence 117, Appl sequence 117, Appl sequence 117, Appl sequence 117, Appl sequence 117, Appl sequence 117, Appl sequence 117, Appl sequence 117, Appl sequence 117, Appl sequence 117, Appl sequence 117, Appl sequence 117, Appl sequence 117, Appl sequence 117, Appl sequence 117, Appl sequence 117, Appl sequence 117, Appl sequence 117, Appl sequence 117, Appl sequence 117, Appl sequence 117, Appl sequence 117, Appl sequence 117, Appl sequence 117, Appl sequence 117, Appl sequence 117, Appl sequence 117, Appl sequence 117, Appl sequence 117, Appl sequence 117, Appl sequence 117, Appl sequence 117, Appl sequence 117, Appl sequence 117, Appl sequence 117, Appl sequence 117, Appl sequence 117, Appl sequence 117, Appl sequence 117, Appl sequence 117, Appl sequence 117, Appl sequence 117, Appl sequence 117, Appl sequence 117, Appl sequence 117, Appl sequence 117, Appl sequence 117, Appl sequence 117, Appl sequence 117, Appl sequence 117, Appl sequence 117, Appl sequence 117, Appl sequence 117, Appl sequence 117, Appl sequence 117, Appl sequence 117, Appl sequence 117, Appl sequence 117, Appl sequence 117, Appl sequence 117, Appl sequence 117, Appl sequence 117, Appl sequence 117, Appl sequence 117, Appl sequence 117, Appl sequence 117, Appl sequence 117, Appl sequence 117, Appl sequence 117, Appl sequence 117, Appl sequence 117, Appl sequence 117, Appl sequence 117, Appl sequence 117, Appl sequence 117, Appl sequence 117, Appl sequence 117, Appl sequence 117, Appl sequence 117, Appl sequence 117, Appl sequence 117, Appl sequence 117, Appl sequence 117, Appl sequence 117, Appl sequence 117, Appl sequence 117, Appl sequence 117, Appl sequence 117, Appl sequence 117, Appl sequence 117, Appl sequence 117, Appl sequence 117, Appl sequence 117, Appl se
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Patent No. 5763252
GENERAL INFORMATION:
APPLICANT: Skadsen, Ronald W
APPLICANT: Tibbot, Brian K
TITLE OF INVENTION:
CORRESPONDENCE ADDRESS:
ADDRESSEE: Quarles & Brady
STREET: 1 South Pinckney Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/430,925A
1 CGGTGAAGTTGACAGGATCCAAGGTGAAG 29
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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ETLING DATE:
CLASSIFICATION: 435
ATTORNEY/AGBNT INFORMATION:
NAME: Seay, Nicholas J
REGISTRATION NUMBER: 27,386
REFERENCE/DOCKET NUMBER: 96029
TELECOMMUNICATION INFORMATION:
TELEPHONE: 608-251-5000
TELEPHONE: 608-251-9166
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELEFAX: 608-251-9166
INFORMATION FOR SEQ ID NO: 3
SEQUENCE CHARACTERISTICS:
LENGTH: 2752 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Ouery Match
Best Local Similarity 93.19
Matches 27; Conservative
                           1902
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4403765
4411529
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STRANDEDNESS: double
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         as
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COUNTRY: US
ZIP: 53703
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              US-08-430-925A-3
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Sequence 1, Appli
Sequence 346, Ap
Sequence 3, Appli
Sequence 5, Appli
Sequence 5, Appli
Sequence 2, Appli
Sequence 2, Appli
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Sequence 57, Appl
Sequence 13, Appli
Sequence 7, Appli
Sequence 1, Appli
Sequence 1, Appli
Sequence 1, Appli
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206.453 Million cell updates/sec
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                                                                                                                                     October 27, 2003, 10:20:36; Search time 62 Seconds
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2: /cgn2_6/ptodata/2/ina/5B_COMB.seq:*
3: /cgn2_6/ptodata/2/ina/6A_COMB.seq:*
4: /cgn2_6/ptodata/2/ina/6B_COMB.seq:*
5: /cgn2_6/ptodata/2/ina/PCTUS_COMB.seq:*
6: /cgn2_6/ptodata/2/ina/PCTUS_COMB.seq:*
                         GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
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US-08-445-640-5
US-08-445-640-5
US-08-447-314-5
US-08-447-314-5
US-08-286-305A-2
US-08-441-104A-2
US-08-440-816A-2
US-08-447-314-1
US-08-445-640-1
US-08-445-589-1
US-08-445-314-1
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US-09-262-537-57
US-09-262-856A-13
US-09-518-914-1
US-09-518-914-3
US-09-518-914-3
US-08-947-884-1
4 US-09-643-990A-1
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US-07-938-154-9
                                                                                                                                                                                                                                                                                                                                                      569978 seqs, 220691566 residues
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                                                 OM nucleic - nucleic search, using sw model
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Maximum DB seq length: 2000000000
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29
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Match Length DB
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5610
944
1750
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1541
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APPLICANT: KATO, Ikunoshin
TITLE OF INVENTION: FUNGAL ANTIGENS AND PROCESS FOR PRODUCING THE SAME
TITLE REPREBRICE: 1422-372P
CURRENT APPLICATION WHBER: US/09/262,856A
CURRENT FILING DATE: 1999-03-04
NUMBER OF SEQ ID NOS: 15
SOFTWARE: PATENTIN Ver. 2.0
SEQ ID NO 7
LENGTH: 1750
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 1, Application US/09518914

Patent No. 6413731

GENERAL INFORMATION:
APPLICANT: BOTOWSKY, Beth E.
APPLICANT: Ogozalek, Kristine L.
APPLICANT: Adham, Nika
ITLE OF INVENTION: DNA ENCODING SNORF36a AND SNORF36b RECEPTORS
FILE REPRENCE: 59138-A/JPW
CURRENT APPLICATION NUMBER: US/09/518,914

CURRENT FILING DATE: 2000-03-03
BARLIER PELLOR DATE: 1999-05-03

NUMBER OF SEQ ID NOS: 44

SOFTWARE: PatentIn Ver. 2.1
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Sequence 3, Application US/09518914

Patent No. 6413731

Sequence 3, Application US/09518914

Patent No. 6413731

Sequence 3, Application US/09518914

APPLICANT: Ogozalek, Kristine L.

APPLICANT: Lakhlani, Parul P.

APPLICANT: Lakhlani, Parul P.

APPLICANT: Lakhlani, Parul P.

TITLE OF INVENTION: DNA ENCODING SNORF36a AND SNORF36b RECEPTORS

FILE REPERENCE: 59138-A/JPW

CURRENT APPLICATION NUMBER: US/09/518,914

CURRENT PILING DATE: 2000-03-03

EARLIER APPLICATION NUMBER: US 09/303,593

EARLIER APPLICATION NUMBER: US 09/303,593

SOFTWARE: PatentIn Ver. 2.1
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                                                                                                                                                                                                                                                                                                                                TYPE: DNA ORGANISM: Candida albicans
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Best Local Similarity 78.6
Matches 22; Conservative
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ORGANISM: Homo Bapiens
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US-09-518-914-1/C
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LENGTH: 1541
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APPLICANT: TAKESAKO, Kazutoh
APPLICANT: MIZUTANI, Shigetoshi
APPLICANT: MIZUTANI, Shigetoshi
APPLICANT: MIZUTANI, Shigetoshi
TITLE OF INVENTION: FUNGAL ANTIGENS AND PROCESS FOR PRODUCING THE SAME
FILE REFRERENCE: 1422-37P
CURRENT APPLICATION NUMBER: US/09/262,856A
CURRENT FILING DATE: 1999-03-04
NUMBER OF SEQ ID NOS: 15
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 13
LENGTH: 944
TYPE: DNA
TYPE: DNA
ORGANISM: Candida albicans
US-09-262-856A-13
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                                                                                                                                                                                                                                                                           FILE OF INVENTION: Lectomedin Materials and Methods FILE REFERENCE: 27866/3307 CURRENT APPLICATION WUMBER: US/09/262,537 CURRENT FILIGN DATE: 1999-03-04 EARLIER FILING DATE: 1999-03-04 SARLIER FILING DATE: 1998-03-04 SARLIER FILING DATE: 1998-03-04 SARLIER FILING DATE: 1998-03-04 SEQ ID NO S: 64 SEQ ID NO S: 64 SEQ ID NO S: 6500 SEQ ID NO S: 6500 SEQ ID NO S: 6500 SEQ ID NO S: 6500 SEQ ID NO S: 6500 SEQ ID NO S: 6500 SEQ ID NO S: 6500 SEQ ID NO S: 6500 SEQ ID NO S: 6500 SEQ ID NO S: 6500 SEQ ID NO S: 6500 SEQ ID NO S: 6500 SEQ ID NO S: 6500 SEQ ID NO S: 6500 SEQ ID NO S: 6500 SEQ ID NO S: 6500 SEQ ID NO S: 6500 SEQ ID NO S: 6500 SEQ ID NO S: 6500 SEQ ID NO S: 6500 SEQ ID NO S: 6500 SEQ ID NO S: 6500 SEQ ID NO S: 6500 SEQ ID NO S: 6500 SEQ ID NO S: 6500 SEQ ID NO S: 6500 SEQ ID NO S: 6500 SEQ ID NO S: 6500 SEQ ID NO S: 6500 SEQ ID NO S: 6500 SEQ ID NO S: 6500 SEQ ID NO S: 6500 SEQ ID NO S: 6500 SEQ ID NO S: 6500 SEQ ID NO S: 6500 SEQ ID NO S: 6500 SEQ ID NO S: 6500 SEQ ID NO S: 6500 SEQ ID NO S: 6500 SEQ ID NO S: 6500 SEQ ID NO S: 6500 SEQ ID NO S: 6500 SEQ ID NO S: 6500 SEQ ID NO S: 6500 SEQ ID NO S: 6500 SEQ ID NO S: 6500 SEQ ID NO S: 6500 SEQ ID NO S: 6500 SEQ ID NO S: 6500 SEQ ID NO S: 6500 SEQ ID NO S: 6500 SEQ ID NO S: 6500 SEQ ID NO S: 6500 SEQ ID NO S: 6500 SEQ ID NO S: 6500 SEQ ID NO S: 6500 SEQ ID NO S: 6500 SEQ ID NO S: 6500 SEQ ID NO S: 6500 SEQ ID NO S: 6500 SEQ ID NO S: 6500 SEQ ID NO S: 6500 SEQ ID NO S: 6500 SEQ ID NO S: 6500 SEQ ID NO S: 6500 SEQ ID NO S: 6500 SEQ ID NO S: 6500 SEQ ID NO S: 6500 SEQ ID NO S: 6500 SEQ ID NO S: 6500 SEQ ID NO S: 6500 SEQ ID NO S: 6500 SEQ ID NO S: 6500 SEQ ID NO S: 6500 SEQ ID NO S: 6500 SEQ ID NO S: 6500 SEQ ID NO S: 6500 SEQ ID NO S: 6500 SEQ ID NO S: 6500 SEQ ID NO S: 6500 SEQ ID NO S: 6500 SEQ ID NO S: 6500 SEQ ID NO S: 6500 SEQ ID NO S: 6500 SEQ ID NO S: 6500 SEQ ID NO S: 6500 SEQ ID NO S: 6500 SEQ ID NO S: 6500 SEQ ID NO S: 6500 SEQ ID NO S: 6500 SEQ ID NO S: 6500 SEQ ID NO S: 6500 SEQ ID NO S: 6500 SEQ ID NO S: 6500 SEQ ID NO S: 6500 SEQ ID NO S: 6500 SEQ I
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1062 CGGIGAAGTIGACACGGICCAAGGIGAAG 1034
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GENERAL INFORMATION:
                                                                                                                                                                                 Sequence 57, Application US/09262537
Patent No. 6479256
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Patent No. 6333164
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MIZUTANI, Shigetoshi
ENDO, Masahiro
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: TAKESAKO, Kazutoh
APPLICANT: MIZUTANI, Shigetos
APPLICANT: ENDO, Masahiro
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Best Local Similarity 82.1
Matches 23; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             , NAME/KEY: CDS
; LOCATION: (281)..(4687)
US-09-262-537-57
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: DNA
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GENERAL INFORMATION:
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                                                                                                         RESULT 2
US-09-262-537-57/c
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RESULT 4

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US-09-643-990A-1/C
       US-09-557-884-1/c
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APPLICANT: Williamson, Valerie M.
APPLICANT: Williamson, Valerie M.
APPLICANT: Waloshian, Isgouhi
APPLICANT: Yaghoobi, Jafar
APPLICANT: Bodeau, John
APPLICANT: Brodeau, John
TITLE OF INVENTION: Procedures and Materials for Conferring
TITLE OF INVENTION: Pest Resistance in Plants
NUMBER OF SEQUENCES:
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
                                                                           Length 1541;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 18; DB 3; Length 51952;
Pred. No. 1.2e+02;
0; Mismatches 5; Indels
                                                                                                                              6; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COUNTRY: USA

ZIP: 9411-3834

COUNTRY: USA

ZIP: 9411-3834

COMPUTER READABLE FORM:
MEDIUW TYPE: Floppy disk
COMPUTER: IBM FC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN RC-BOS/MS-DOS
SOFTWARE: PATENTIN RC-BOS/MS-DOS
SOFTWARE: PATENTIN NUMBER: US/08/947,823
FILING DATE: 09-OCT-1997
CLASSIFICATION NUMBER: PCT/US97/18802
FILING DATE: 09-OCT-1997
PRIOR APPLICATION NUMBER: US/08/191
FILING DATE: 09-OCT-1997
PRIOR APPLICATION NUMBER: US/0CT-1997
FILING DATE: 09-OCT-1997
PRIOR APPLICATION NUMBER: US/OCT-1997
APPLICATION NUMBER: US/OCT-1997
FILING DATE: 01-OCT-1996
ATLOND DATE: 10-OCT-1996
                                                                             DB 4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ADDRESSEE: Townsend and Townsend and Crew LLP STREET: Two Enbarcadero Center, Eighth Floor TTT: San Francisco STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ALOUADE SASTIAN, KEVIN L.
REGISTRATION NUMBER: 34,774
REPERENEE/COCKET NUMBER: 32070-070210US
TELEPHONE: (415) 576-0200
TELEPHONE: (415) 576-0300
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 51952 base pairs
                                                                           63.4%; Score 18.4; D
78.6%; Pred. No. 47;
live 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0; Mismatches
                                                                                                                                                                                                                         429 GGTGAAGAGAGAGGGGCCTGGGTGAAG 402
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                                                                                                                                                                             2 GGTGAAGTTGACAGGATCCAAGGTGAAG 29
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Patent No. 6114605
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80.8%;
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                                                                     Query Match
Best Local Similarity 78.61
Matches 22, Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity 80.8°
Matches 21; Conservative
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EDNESS: single
ORGANISM: Homo sapiens
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                                                                                                                                                                                                                                                                                                 RESULT 7
US-08-947-823-1/c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TOPOLOGY:
       ; ORGANISM: Hc
US-09-518-914-3
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HAMPON O. SMITH
J. Craig Venter
TITLE OF INVENTION: The Nucleotide sequence of
the Hamphilus influenzae Rd Genome, Fragments
Thereof, and Uses Thereof
Sequence 1, Application US/09557884

Patent No. 6506581

GENERAL INFORMATION:

APPLICANT: Fleischmann et al.

TITLE OF INVENTION: The Nucleotide sequence of the Haemophilus influenzae Rd Genome, Fragments Thereof, and Uses Thereof
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
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                                                                                                                                                                            NUMBER OF SEQUENCES: 1
CORRESPONDENCE ADDRESS:
ADDRESSE: Human Genome Sciences, Inc.
STREET: 9410 Key West Avenue
CITY: Rockville
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ADDRESSEE: Human Genome Sciences, Inc. STREET: 9410 Key West Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SOFTWARE: AGCII Text
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/557,884
FILING DATE: 25-Apr-2000
CLASSIPICATION: «Unknown»
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/476,102
PILING DATE: JUN-5-1995
ATTORNEY AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                    ZIP: 20850
COMPUTER READABLE FORM:
MEDIUM TYPE: 3 1/2 inch diskette
COMPUTER: Dell Pentium
OPERATING SYSTEM: MS DOS v6.22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME: Michelle S. Marks
REGISTRATION NUMBER: 41,971
REFERENCE/DOCKET NUMBER: PB186P3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  16163 rgaagrrgaaargaccaarggaag 16138
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Mark D. Adams
Owen White
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LENGTH: 1830121 base pairs
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 1, Application US/09643990A Patent No. 6528289 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELEPHONE: 301-309-8504
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELEFAX: 301-309-8439
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: nucleic acid
STRANDEDNESS: double
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CORRESPONDENCE ADDRESS:
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STATE: MD
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Query Match 61.4%; Score 17.8; DB 1; Length 2742; Best Local Similarity 75.9%; Pred. No. 94; Matches 22; Conservative 0; Mismatches 7; Indels 0;
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                 APPLICATION NUMBER: 08/157563
FILING DATE: 23-NOV-1993
ATTORNEY/AGENT INFORMATION:
NAME: Lee, Wendy M.
REGISTRATION NUMBER: 00,000
REFERENCE/COCKET VINBER: 854C1P1
TELECHONE: 415/225-1994
TELECHONE: 415/225-9881
TELEFAX: 415/952-9881
TELEFAX: 415/952-9881
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TELEFAX: 415/952-9881
                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-286-305A-2
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Patent No. 5766863

GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Mark, Melanie R.
APPLICANT: Sadick, Michael D.
APPLICANT: Mong, Wai Lee Tan
ITLE OF INVENTION: KINASE RECEPTOR ACTIVATION ASSAY
NUMBER OF SEQUENCES: 11
CORRESCONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ZIP: 94080

COMPUTER READABLE FORM:
MEDIUM TYPE: 5.25 inch, 360 Kb floppy disk COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: patin (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/286,305A
FILING DATE: 05-AUG-1994
CLASSIFCATION 1435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/170558
FILING DATE: 20-DEC-1993
                 ZUGNICATION OF STATEMENT OF STATEMENT OF STATEMENT OF STATEMENT OF STATEMENT OF STATEMENT OF SOFTWARE. DATEMENT OF SOFTWARE. DATEMENT OF SOFTWARE. DATEMENT OF SOFTWARE. DATEMENT APPLICATION DATA.

APPLICATION NUMBER: US/08/445,461
FILING DATE: 22-MAY-1995
CLASSIFICATION DATA.

APPLICATION NUMBER: 08/17658
FILING DATE: 20-DEC-1993
PRIOR APPLICATION DATA.

APPLICATION NUMBER: 08/17658
FILING DATE: 20-DEC-1993
PRIOR APPLICATION DATA.

APPLICATION NUMBER: 08/15763
FILING DATE: 23-NOV-1993
ATTORNEY/AGENT INFORMATION:
NAME: HASSA, Janet E.

REGISTRATION NUMBER: 28,616
REFERENCE/DOCKET NUMBER: 28,616
REFERENCE/DOCKET NUMBER: 854C3
TELECHMUNICATION INFORMATION:
TELEPHONE: 415/252-19881
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
61.4%; Score 17.8; E
Best Local Similarity 75.9%; Pred. No. 82;
Matches 22; Conservative 0; Mismatches
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STREET: 460 Point San Bruno Blvd
CITY: South San Francisco
STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELEX: 910/371-7168
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 1164 bases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TOPOLOGY: linear
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COUNTRY:
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                                                                                                                          October 27, 2003, 10:20:33 ; Search time 281 Seconds (without alignments) 278.590 Million cell updates/sec
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GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
                                                                                                                                                                                                                                                              29
                                                                                                                                                                                                                                                                                                                                                                                                           Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                     2552756 seqs, 1349719017 residues
                                                                                                                                                                                                                 US-10-043-418-5
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                                                                                            This cDNA sequence encodes a novel barley alpha-glucosidase protein. Recombinant alpha-glucosidase can be used to increase the rate of starch grain hydrolysis when used together with alpha-amylase or can supplement glucoamylase in industrial starch hydrolysis systems. Useful DNA sequence characteristics from this enzyme can be identified which can be used as hybridisation probes for identifying germplasm with high levels of efficient hydrolytic enzymes.
                                                                                                                                                                                                               Gaps
                                     DNA encoding barley alpha-glucosidase protein - useful for producing recombinant protein to increase rate of starch grain hydrolysis when used with alpha amylase
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                                                                                                                                                                                          89.0%; Score 25.8; DB 19; Length 2752; 93.1%; Pred. No. 0.17; 2.1 indels 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human; lectomedin; seven transmembrane receptor protein; antiatherosclerotic; vasotropic; cytostatic; gene therapy; atherosclerosis; restenosis; vascular disease; peripheral neuropathy; cancer; nerve regeneration; renal cystic epithelium; uterine implantation; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Isolated human seven transmembrane receptor lectomedin polypeptide or its fragment, useful for identifying agents which can treat atherosclerosis, restenosis or vascular disease -
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                                                                                                                                                                                                                                                                                       106 cccccaaarrracaccarccaaacrcaac 78
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Example 1; Page 196-200; 241pp; English.
                                                                                                                                                                                                                                                           1 CGGTGAAGTTGACAGGATCCAAGGTGAAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human lectomedin-2 cDNA clone 2.4.
                                                                                                                                                                                                                                                                                                                                                                 AAA96040 standard; cDNA; 3642
                                                                                                                                                                                                72.4%;
82.8%;
           990S-0160989
990S-0161404
990S-0161406
990S-0161359
990S-0161359
990S-0161360
990S-0161361
990S-0161992
990S-0161993
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        99US-0262537
                                                                                                                                                                                                                                                                                                                                                                                                                             26-JAN-2001 (first entry)
                                                                                                                                                                                                              1 Similarity 82.8
24; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Hayflick JS, Fox RD,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WPI; 2000-579274/54.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WO200052039-A2
            22-OCT-1999;
25-OCT-1999;
25-OCT-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        04-MAR-1999;
                                                         25-OCT-1999;
26-OCT-1999;
26-OCT-1999;
26-OCT-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Homo sapiens
                                                                                                                                    28-OCT-1999;
28-OCT-1999;
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                                                                                                                       28-OCT-1999;
                                                                                                                                                                                              Query Match
Best Local S
Matches 24
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The present cDNA sequence was obtained and used in a procedure for the isolation of human seven transmembrane receptor lectomedin polypeptides. The polypeptides have a characteristic extracellular structure including lectin-binding, olfactomedin-like and mucin-like domains. Modulator compounds that inhibit the binding of lectomedin to a binding partner (galectin-3) may be used to treat conditions such as atheroscierosis, restenosis, vascular disease, peripheral neuropathy, carcer, nerve regeneration, and pathologies of the renal cystic epithelia and uterine implantation. Nucleotide sequences encoding the lectomedin polypeptides are useful in gene therapy. The lectomedin polynucleotides and polypeptides may be used to identify lectomedin binding partner compounds. The polynucleotides are useful for detecting lectomedin compounds. The polynucleotides are useful for detecting lectomedin ectomedin genes. Antisense lectomedin nucleic acids are able to inhibit expression of lectomedin genes.
                                                                                                                                                               o,
expression in cells and for identifying genetic mutations in the lectomedin genes. Antisense lectomedin nucleic acids are able to inhibit expression of lectomedin genes.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Isolated human seven transmembrane receptor lectomedin polypeptide or
its fragment, useful for identifying agents which can treat
atherosclerosis, restenosis or vascular disease -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human, lectomedin, seven transmembrane receptor protein, antiatherosclerotic; vasotropic; cytostatic; gene therapy; atherosclerosis; restenosis; vascular disease; peripheral neuropathy; cancer; nerve regeneration; renal cystic epithelium; uterine implantation; ss.
                                                                                                                                                               Gaps
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0
                                                                                                                    72.4%; Score 21; DB 21; Length 3642; 82.8%; Pred. No. 22; Aztive 0; Mismatches 5; Indels (
                                                                                  Seguence 3642 BP; 689 A; 1194 C; 1065 G; 694 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 4091 BP; 770 A; 1370 C; 1192 G; 759 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Puri KD
                                                                                                                                                                                                                                 662 CGGTGAAGATGACAGGGTCCATGAGGAAG 634
                                                                                                                                                                                                    1 CGGTGAAGTTGACAGGATCCAAGGTGAAG 29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Example 1; Page 189-193; 241pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Douangpanya J,
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human lectomedin-2 cDNA clone 2.1.
                                                                                                                                                                                                                                                                                                                                        AAA96039 standard; cDNA; 4091
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                                                                                                                                                             24; Conservative
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                                                                                                                                             Similarity
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Best Local S
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The invention provides G protein (quanine nucleotide binding protein) -conjugated receptor proteins (AAY7727-29) expressed in brain tissue and nucleic acids (AAZ87683-685) expressed in brain tissue polypeptides and the methods are useful for identifying compounds which are agonists or antagonists to the binding of the receptor to its ligand, for use as drugs. DNA encoding all or part of the polypeptides is used for the diagnosis of diseases and in gene therapy, and for the production of transgenic animals for use as disease models. Antibodies recognizing the receptor proteins or their fragments are also useful for disease diagnosis. The present sequence represents a DNA encoding the G
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 New G protein conjugated receptor protein expressed in brain tissue for screening potential agonists and antagonists of its binding to ligands
                 Gaps
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                                                                                                                                                                                                                                                                                        protein; guanine nucleotide binding protein; human; brain; protein-conjugated receptor; gene therapy; HK02631; ds.
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                                                                                                                                                                                                                                                           Human G protein-conjugated receptor HK02631 encoding DNA.
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                  Indels
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                                                                            2630 cegreaagareacaeegrecareaceaag 2602
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Pred. No. 23;
0; Mismatches
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                                               1 CGGTGAAGTTGACAGGATCCAAGGTGAAG 29
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 82.8%; Pred. No.
                                                                                                                                                              BP
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                                                                                                                                                              AAZ87685 standard; DNA; 4422
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98JP-0284328.
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(KAZU-) KAZUSA DNA RES INST.
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                                                                                                                                                                                                                             (first entry)
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Matches 24; Conservative
                 24; Conservative
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 Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       for use as drugs
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                                                                                                                                                                                                                                                                                                                                           Homo sapiens.
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06-OCT-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                       22-JUL-1999;
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AAZ28008/c

Length 4091;

72.4%; Score 21; DB 21;

Query Match

RESULT 6

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lectomedin; seven transmembrane receptor protein;
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                                                       uterine implantation; ss
                                                                                                                                                                                                                                     Fox RD,
                                                                                                                                                                                                                                                            WPI; 2000-579274/54.
P-PSDB; AAB15735.
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Best Local Similarity
                                                                                                                                                                                                           (ICOS-) ICOS CORP.
                                                                                                       WO200052039-A2
                                                                                Homo sapiens
                                                                                                                                                                                  04-MAR-1999;
                                                                                                                                                                                                                                     Hayflick JS,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        26-JAN-2001
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                                                                                                                                08-SEP-2000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      g
                                                                                                                                                                                                                                                                                                                                                                                                                                   The invention provides purified and isolated human 7-transmembrane receptor lectomedin polypeptide or its fragments. The lectomedin polypeptide or its fragments. The lectomedin polypeptide comprises extracellular lectin-binding, olfactomedin-like polypeptide can be produced by standard recombinant methodology. The polypeptide can be produced by standard recombinant methodology. The polypeptide is involved in cellular adhesion and qytoplasmic metabolic pathways that are modulared by extracellular signaling. Specific binding to lectomedin-l expressed on smooth muscle cells may be required for probletaration of these cells in atherosclerosis. The polypeptide is used to raise specific antibodies, and to identify specific binding agents that modulare (increase or of probes and primers, and of therapeutic antisense, ribozyme or triplexforming agents, and in gene therapy to restore deficient lectomedin forming agents, and in gene therapy to restore deficient lectomedin cativity. Specific binding agents of lectomedin are are used for treating diseases that involve lectomedin activity, e.g. vascular diseases such as the present sequence represents the DNA encoding human.
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                                                                                                                                                                                                                                                                                                                                                                          human lectomedin receptor polypeptide, used to identify specific
ling partners for treating e.g. vascular disease
                                                                                                   Human; 7-transmembrane receptor; lectomedin; lectin-binding; mucin;
olfactomedin; cellular adhesion; atherosclerosis; gene therapy;
vascular disease; lectomedin-2; ss.
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Pred. No. 24;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Originally determined sequence of human lectomedin-2 cDNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            5; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 CGGTGAAGTTGACAGGATCCAAGGTGAAG 29
                                                                                                                                                                                                                                                                                                                                                                                                              Claim 11; Page 148-155; 166pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAA96035 standard; cDNA; 5610 BP
AAZ28008 standard; DNA; 5610 BP
                                                                           Human lectomedin-2 encoding DNA
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Local Similarity 82.8%;
nes 24; Conservative (
                                                                                                                                                                                                                                    99WO-US04676
                                                                                                                                                                                                                                                            98US-0076782
                                                  05-JAN-2000 (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                        binding partners for
                                                                                                                                                                                                                                                                                                                                    WPI; 1999-571596/48
                                                                                                                                                                                                                                                                                    (ICOS-) ICOS CORP.
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                                                                                                                                                       Homo sapiens
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                                                                                                                                                                                                                                                            04-MAR-1998;
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Matches
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AAA96035/c
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isolation of human seven transmembrane receptor lectomedin polypeptides. The polypeptides have a characteristic extracellular structure including lectin-binding, olfactomedin-like and mucin-like domains. Modulator compounds that inhibit the binding of lectomedin to a binding partner (galectin-3) may be used to treat conditions such as atherosclerosis, restenosis, vascular disease, peripheral neuropathy, cancer, nerve regeneration, and pathologies of the renal cystic epithelia and uterine implantation. Nucleotide sequences encoding the lectomedin polypeptides are useful in gene therapy. The lectomedin polymucleotides and polypeptides may be used to identify lectomedin binding partner compounds. The polymucleotides are useful for detecting lectomedin compounds. The lactomedin for identifying genetic mutations in the lectomedin genes. Antisense lectomedin nucleic acids are able to inhibit expression of lectomedin genes.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Isolated human seven transmembrane receptor lectomedin polypeptide or its fragment, useful for identifying agents which can treat atherosclerosis, restenosis or vascular disease -
antiatherosclerotic; vasotropic; cytostatic; gene therapy; atherosclerosis; restenosis; vascular disease; peripheral neuropathy; cancer; nerve regeneration; renal cystic epithelium;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human; lectomedin; seven transmembrane receptor protein; antiatherosclerotic; vasotropic; cytostatic; gene therapy; atherosclerosis; restenosis; vascular disease; peripheral neuropathy; cancer; nerve regeneration; renal cystic epithelium; uterine implantation; ss.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Puri KD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2630 CGGTGAAGATGACAGGGTCCATGAGGAAG 2602
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Example 1; Page 174-180; 241pp; English
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The present cDNA sequence was obtained and used in a procedure for the isolation of human seven transmembrane receptor lectomedin polypeptides. The polypeptides have a characteristic extracellular structure including lectin-binding, olfactomedin-like and mucin-like domains. Modulator compounds that inhibit the binding of lectomedin to a binding partner (galectin-a) may be used to treat conditions such as atheroscierosis, restenosis, vascular disease, peripheral neuropathy, cancer, nerve regeneration, and pathologies of the renal cystic epithelia and ucerine implantation. Nucleotide sequences encoding the lectomedin polypeptides or useful in gene therapy. The lectomedin binding partner compounds. The polynucleotides are useful for detecting lectomedin compounds. The polynucleotides are useful for detecting lectomedin extreme compounds. The polynucleotides are useful for detecting lectomedin certomedin genes. Antisense lectomedin nucleic acids are able to inhibit expression of lectomedin genes.
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Pred. No. 24;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      G protein; guanine nucleotide binding protein; human; brain; G protein-conjugated receptor; gene therapy; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 5610 BP; 1057 A; 1893 C; 1656 G; 1004 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Human G protein-conjugated receptor related DNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               5; Indels
                                                                                                                                                                               Puri KD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2630 CGGTGAAGATGACAGGGTCCATGAGGAAG 2602
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 CGGTGAAGTTGACAGGATCCAAGGTGAAG 29
                                                                                                                                                                               Douangpanya J,
                                                                                                                                                                                                                                                                                                                       Claim 4; Page 203-210; 241pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               72.4%;
82.8%;
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98JP-0225060.
98JP-0284328.
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                                                                                03-MAR-2000; 2000WO-US05934
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                                                                                                                99US-0262537
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Best Local Similarity 82.0v
Best Local Similarity
The 24; Conservative
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                                                                                                                                                                             FOX RD,
                                                                                                                                                                                                            WPI; 2000-579274/54.
P-PSDB; AAB15741.
                                                                                                                                              (ICOS-) ICOS CORP.
                  WO200052039-A2
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07-AUG-1998;
06-OCT-1998;
                                                                                                              04-MAR-1999;
                                                                                                                                                                             Hayflick JS,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    22-JUL-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAZ87686;
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The invention provides G protein (guanine nucleotide binding protein) conjugated receptor proteins (AAY7727-29) expressed in brain tissue and nucleic acids (AAZ87683-685) encoding the polypeptides. The polypeptides and the methods are useful for identifying compounds which are agonists or antagonists to the binding of the receptor to its ligand, for use as drugs. DNA encoding all or part of the polypeptides is used for the diagnosis of diseases and in gene therapy, and for the production of transgenic animals for use as disease models. Antibodies recognizing the receptor proteins or their fragments are also useful for disease diagnosis. The present sequence represents a DNA related to the G
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       G protein-coupled receptor; GFCR; antigenic peptide; gene therapy; G protein-coupled receptor modulator; antibody; immune-related disease; growth-related disease; cell regeneration-related disease; AIDS; cancer; immunological-related cell proliferative disease; autoimmune disease; Alzheimer's disease; atherosclerosis; infection; osteoarthritis; allergy; osteoporosis; cardiomyopathy; inflammation; Crohn's disease; diabetes; graft versus host disease; Parkinson's disease; multiple sclerosis; pain; psoriasis; anxiety; depression; schizophrenia; dementia; memory loss; mental retardation; epilepsy; asthma; tuberculosis; obesity; nausea; hypertension; hypotension; renal disorder; rheumatoid arthritis; trauma; ulcer; gene; ds.
                                                                                                                                                                            New G protein conjugated receptor protein expressed in brain tissue for screening potential agonists and antagonists of its binding to ligands
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                               Hinuma S, Fujii R, Kitahara O;
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0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  72.4%; Score 21; DB 21; Length 5659; 82.8%; Pred. No. 24;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 5659 BP; 1077 A; 1896 C; 1664 G; 1022 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          5; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human latrophilin-1 nucleotide SEQ ID NO:521.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2663 CGGTGAAGATGACAGGTCCATGAGGAAG 2635
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0; Mismatches
                                                                                                                                                                                                                                                              Disclosure, Fig 21 to 24; 123pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 CGGTGAAGTTGACAGGATCCAAGGTGAAG 29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    protein-conjugated receptor DNAs.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (LIFE-) LIFESPAN BIOSCIENCES INC.
                                                                           Ohara O, Nagase T, Nomura N,
Mogi S;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Burmer GC, Roush ČL, Brown JP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ABZ42867 standard; DNA; 5659
              (TAKE ) TAKEDA CHEM IND LTD.
(KAZU-) KAZUSA DNA RES INST.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              19-DEC-2000; 2000US-257144P.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Local Similarity 82.8
nes 24; Conservative
                                                                                                                                        WPI; 2000-182652/16.
                                                                                                                                                                                                                        for use as drugs
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
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WPI; 2003-046718/04.

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Seguence 5659 BP; 1077 A; 1896 C; 1664 G; 1022 T; 0 other;
   P-PSDB, ABP82017
                                                                                                                       40200123604-A2
                                                                                       AAH01294/c
                                                                         Matches
                                                                                     RESULT 11
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The present invention describes antigenic peptides (1) comprising:

(a) any one of 1601 sequences (see ABP82019 to ABP88619) of 12-24 amino acids. Also described: (1) an assay for the detection of a particular of protein-coupled receptor (GPCR) or a candidate polypeptide in a sample, and (2) an isolated antibody having high specificity and high affinity or avidity for a particular GPCR. (1) can be used as GPCR modulators and in gene therapy. The antigenic peptides for GPCRs are useful in detecting an antibody against a particular GPCR, and in the production of specific antibodies. The peptides and antibodies are also useful for detecting the greence or absence of corresponding GPCRs. The antigenic peptides for GPCRs and antibodies are useful for diagnosing and designing drugs for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ostecarthritis, osteoporosis, cancer, cardiomyopathy, chronic and acute inflammation, allergies, Crohn's disease, diabetes, graft versus host disease. Parkinson's disease, multiple sclerosis, pain, psoriasis, anxiety, depression, schizophrenia, dementia, mental retardation, memory
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          loss, epilepsy, asthma, tuberculosis, obesity, massea, hypertension, hypotension, renal disorders, rheumatoid arthritis, trauma, ulcers, or any other disorder in which GPCRs are involved. The antibodies may be used in immunoassays and immunodiagnosis. ABZ42523 to ABZ42869 encode GPCR proteins given in ABP81675 to ABP82018, which are used in the exemplification of the present invention.
New isolated antigenic peptides e.g., for G protein-coupled receptors (GPCR), useful for diagnosing and designing drugs for treating conditions in which GPCRs are involved, e.g. AIDS, Alzheimer's disease,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     treating immune-related diseases, growth-related diseases, cell regeneration-related disease, immunological-related deal probliferative diseases, or autoimmune diseases, e.g. AIDS, Alzheimer's disease, atherosclerosis, bacterial, fungal, protozoan or viral infections,
                                                                                                                                                                                                                                                                                                                      Disclosure; Fig 1; 523pp; English.
                                                                                                                                                                                        cancer or autoimmune diseases
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Gaps ; 0 72.4%; Score 21; DB 25; Length 5659; 82.8%; Pred. No. 24; Indels .. 2663 CGGTGAAGATGACAGGTCCATGAGGAAG 2635 Pred. No. 24; 0; Mismatches 1 CGGTGAAGTTGACAGGATCCAAGGTGAAG 29 24; Conservative Similarity Query Match Local

0

Aspergillus nidulans nucleotide sequence SEQ ID NO:1285. AAHC1294 standard; DNA; 764 BP (first entry) 24-JUL-2001 AAH01294;

Species specific; genue specific; family specific; probe; detection; identification; algal; archaeal; bacterial; fungal; parasitical; microorganism; diagnosis; translation elongation factor 1u; toxin; translation elongation factor G; RecA recombinace; resistance; catalytic subunit of proton-translocating ATPase; antimicrobial; vaccine; primer; ds

Aspergillus nidulans.

05-APR-2001

28-SEP-2000; 2000WO-CA01150.

The present invention describes a method for generating a repertory of nucleic acids of tuf, fus, atpD and/or recA genes from which probes and/or primers are derived. The method comprises amplifying the nucleic acids of determined algal, archaeal, bacterial, fungal and parasitical species with a combination of defined primers for detecting one or more used for producing probes and/or primers for detecting one or more related microorganisms e.g. algae, archaeal, bacterial, fungal and parasites, for universal detection and for specific and ubiquitous detection and identification of an algal, archaeal, bacterial, fungal and parasitical species, genus, family and group. A nucleic acid (I) obtained using the method of the invention can be used for the universal detection of any bacterium, fungus or parasite in a sample and for the detection of at least one antimicrobial agent resistance gene or at least one toxin gene. haxA nucleic acids are used for the specific and ubiquitous detection and for identification of Streptococcus pneumoniae. (I) can be used to design a therapeutic agent which is effective against microorganisms. Microbial species or genus or family or phylum or group which can be detected include Abiotrophia adiacens, Bordetella sp., Corynebacterium sp., Enterobacteriaceae group, Escherichia coli, Mycobacteriaceae family, Resudomands group, Streptococus sp., Neisseria gonorrhoeae and Staphylococus sp., Using DNA based tests provides faster results than substrate specificity tests as results can be determined in an hour and improved accuracy is also achieved. AAH00010 to AAH002304 represent nucleotide sequences and primers/probes Nucleic acid sequences are used to generate universal probes and primers which can be used to identify and detect the presence of algal, archaeal, bacterial, fungal and parasitical species in a test sample -Gaps Ouellette M; which are given in the exemplification of the present invention. .; 0 Sequence 764 BP; 159 A; 260 C; 184 G; 160 T; 1 other; Boissinot M, Huletsky A, Menard C, Claim 24; Page 1102-1103; 1580pp; English. (INFE-) INFECTIO DIAGNOSTIC (IDI) INC. 19-MAY-2000; 2000CA-2307010 Bergeron MG, Boles WPI; 2001-245006/25 Query Match Best Local Similarity 23; Matches

69.0%; Score 20; DB 22; Length 764; larity 82.1%; Pred. No. 48; Conservative 0; Mismatches

.. 0

Candida albicans fungal antigen partial encoding cDNA SEQ ID NO:13. (first entry) 30-JUL-1998 AAV20827;

AAV20827 standard; cDNA to mRNA; 944 BP

RESULT 12 AAV20827

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Candida albicans, vaccine; allergen; antigenic protein; fungal antigen; immune response; infection; insoluble; ss.

Candida albicans.

WO9809990-A1

12-MAR-1998

97WO-JP03041 29-AUG-1997;

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                                                                                                                                                                                                                                                        The present sequence represents a partial CDNA sequence from an example of the present invention, which partially encodes an active vaccine component or allargen derived from Candida albicans. The present invention describes fungal antigens, comprising the insoluble fraction of fungal cells having completely/partially removed cell walls. Also described are nucleic acids encoding the antigens and a method for producing the antigens. The antigens can be used for preparing therapeutic compositions for stimulating immune response, e.g. as a vaccine. They can be used for treatment of fungal infections, treatment and prevention of allergies and diagnosis of fungal infections in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Constructing strains for identifying gene products as effective targets
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Fungus; yeast; tetracyclin; promoter; GRACE strain; biosynthesis;
signal transduction; DNA replication; cell division; growth;
proliferation; Candida albicans; fungicide; antifungal; gene; ss.
                                                                                                                                                           Fungal antigens comprising insoluble fraction of fungal cells useful for, e.g. stimulating immune response and treatment and diagnosis of fungal infection(s)
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                                                                                                                                                                                                                                                                                                                                                                                                                       vertebrates. The vaccines are not live, and have low toxicity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    69.0%; Score 20; DB 19; Length 944; ilarity 82.1%; Pred. No. 49; Conservative 0; Mismatches 5; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Candida albicans essential gene SEQ ID NO 6687
                                                                                              Takesako K;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             697 GGTGAAGTGGTCAAGATCGAAGTTGAAG 724
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2 GGTGAAGTTGACAGGATCCAAGGTGAAG
                                                                                                                                                                                                                           Example 27; Page 84; 108pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ABZ32400 standard; DNA; 1476 BP
                                                                                            Endo M, Kato I, Mizutani S,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Boone C,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        20-FEB-2001; 2001US-0792024. 22-AUG-2001; 2001US-314050P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         26-DEC-2001; 2001WO-US49486.
             97JP-0099775
96JP-0255400
                                                              (TAKI ) TAKARA SHUZO CO LTD
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                                                                                                                             WPI; 1998-193553/17.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WPI; 2002-566694/60.
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               31-MAR-1997;
                              04-SEP-1996;
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cells in which both alleles of a gene are modified, comprising modifying one allele by insertion or replacement by a cassette having an expressible selectable marker and modifying other allele by comprising modifying or expressible selectable marker and modifying other allele by recombination, of a promoter replacement fragment with a heterologous promoter. (M.) is useful for constructing a strain of diploid fungal cells in which both alleles modified are useful for identifying a gene that cells in which both alleles modified are useful for identifying a gene that contributes to the virulence and/or pathogenicity of a fungus, a gene that contributes to the virulence and/or pathogenicity of a fungus a gene to that contributes to the resistance of a diploid fungus to an antifungal agent, an antifungal agent for itentifying a characterity of a fungus to an antifungal agent, an inhibits the growth of a diploid fungus of agent, an antifungal agent for itentment of a mammalian disease. (MI) is useful for identifying a compound which modulates the activity of a gene product, preferably enzymatic activity, carbon compound catabolism, biosynthetic, transporter, transcriptional, transporter, preferably enzymatic activity. The method is useful for identifying a compound having the activity. The method is useful for identifying a compound having the continity to inhibit growth or proliferation of C. albicans. The present sequence is that of an essential Candida albicans gene used in the method of the invention.

Conservation but is based on seminere information supplied to Derwent by
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Candida albicans; vaccine; allergen; antigenic protein; fungal antigen; immune response; infection; insoluble; ds.
for therapeutic intervention, by inactivating in the strain one allele of a gene and placing other allele of the gene under conditional expression -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Candida albicans fungal antigen - allergen encoding cDNA SEQ ID NO:7.
                                                                                                                                 The invention relates to constructing (M1) a strain of diploid fungal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
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                                                                                     Claim 37; SEQ ID NO 6687; 167pp + Sequence Listing; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 69.0%; Score 20; DB Best Local Similarity 82.1%; Pred. No. 53; Matches 23; Conservative 0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      805 GGTGAAGTGGTCAAGATCGAAGTTGAAG 832
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2 GGTGAAGTTGACAGGATCCAAGGTGAAG 29
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       97JP-0099775
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   the European Patent Office.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Candida albicans.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WO9809990-A1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         30-JUL-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    12-MAR-1998,
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AAV20821
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(UYFU-) UNIV FUDAN.
(SHAN-) SHANGHAI BIO DOOR GENE TECHNOLOGY LTD.
                                                                                WO200149736-A1.
 Endo M,
                                                       RESULT 15
                                                         AAH73409
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                                                  d:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The present sequence encodes an active vaccine component or aliergen derived from Candida albicans, which is an antigenic protein. The present invention describes fungal antigens, comprising the insoluble fraction of fungal cells having completely/partially removed cell walls. Also described are nucleic acids encoding the antigens and a method for producing the antigens. The antigens can be used for preparing producing the antigens for stimulating immune response, e.g. as a vaccine. They can be used for treatment of fungal infections, treatment and prevention of allergies and diagnosis of fungal infections in vertebrates. The vaccines are not live, and have low toxicity.
                                                                                                                                                                                                           Fungal antigens comprising insoluble fraction of fungal cells useful for, e.g. stimulating immune response and treatment and diagnosis of fungal infection(8)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 1750 BP; 578 A; 315 C; 354 G; 503 T; 0 other;
Takesako K;
                                                                                                                                                                                                                                                                                                                                                                                                        Claim 24; Page 80-81; 108pp; Japanese.
Kato I, Mizutani S,
                                                                                     WPI; 1998-193553/17.
                                                                                                                                    P-PSDB; AAW53251
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
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Gaps
                                      .;
0
69.0%; Score 20; DB 19; Length 1750; 82.1%; Pred. No. 54; ive 0; Mismatches 5; Indels C
                                                                                             2 GGTGAAGTTGACAGGATCCAAGGTGAAG 29
                   Best Local Similarity 82.1
Matches 23; Conservative
```

AAH73409 standard; DNA; 41 BP. 25-SEP-2001 (first entry) AAH73409;

Human RS3 protein coding sequence probe #1

Human; RS3 protein; cancer; haemopathy; immunological disease; inflammation; HIV infection; gene therapy; probe; ss.

Homo sapiens

12-JUL-2001.

25-DEC-2000; 2000WO-CN00662

29-DEC-1999; 99CN-C127231

Mao Y, Xie Y;

WPI; 2001-441855/47

Human RS3 protein and encoded polynucleotide, applicable in diagnosis and treatment of malignant neoplasm, haemopathy, human immunodeficiency virus infection, immunological diseases and inflammation

Example 7; Page 20; 34pp; Chinese.

The present invention provides the protein and coding sequences of human RS3 protein. The sequences can be used in the treatment of cancer, haemopathy, HIV infection, immunological diseases and inflammation. The

present sequence is a probe for the coding sequence of the invention. Gaps .; 0 Length 41; 5; Indels 65.5%; Score 19; DB 22; 81.5%; Pred. No. 83; tive 0; Mismatches 5; Sequence 41 BP; 10 A; 16 C; 7 G; 8 T; 0 other; 2 GGTGAAGTTGACAGGATCCAAGGTGAA 28 36 dereaagregagaagereceagereaa 10 1 Similarity 81.5 22; Conservative Query Match Best Local S Matches SXS ò dC

; 0

Search completed: October 27, 2003, 10:25:34 Job time: 284 secs

OM nucleic - nucleic search, using sw model Run on:

October 27, 2003, 10:20:33; Search time 2677 Seconds (without alignments) 443:175 Million cell updates/sec

US-10-043-418-5 29 Title: Perfect score:

1 cggtgaagttgacaggatccaaggtgaag Sequence:

IDENTITY NUC Gapox 1.0

Scoring table:

Searched:

29

5777422 Total number of hits satisfying chosen parameters:

2888711 segs, 20454813386 residues

Minimum DB Maximum DB

length: C length: 2000000000 Sed Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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em_hum:* em_in:* em_pat:.. em_ph:.. em_pl:.. em_om:* em_or:* em_ov:* em_mu:*

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em_htg_hum:*
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em_htg_other:* htg_pln:* mus:*

htgo hum: * htgo_mus:* vrt:* em_htg_mam:*

the number of results predicted by chance to have a . 1. Pred. No.

em_htgo_other:*

score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Homo sapi Homo sapi Homo sapi AF118226 Hordeum v Homo sapi Homo sapi U22450 Hordeum vul AR012240 Sequence AC109448 | AC090646 | SUMMARIES DB Length Query Score о С Result

Human DNA

E41270 Novel G pro AR233254 Sequence BD138014 Lectomedi AF307079 Homo sapi AX549236 Sequence AB020628 Homo sapi AX549236 Sequence AB02028 Homo sapi AX645219 Homo sapi AL162819 Homo sapi AL162459 Arabidops AC069114 Homo sapi AC162981 Homo sapi AC102803 Homo sapi AC102803 Homo sapi AE011893 Xanthomon Continuation (4 of AC137901 Mus muscu AC113472 Mus muscu Rattus no Arabidops Arabidops Oryza sat Oryza sat Mus muscu Mus muscu Rattus no Rattus no Rattus no Homo sapi Arabidops AC125044 Mus muscu AL929604 Trypanoso AE016783 Pseudomon AC102605 Mus muscu AC111421 Rattus no AC102605 Mus muscu AC113540 Mus muscu AL772426 C AC073668 N AC087138 N AC090884 AL353741 AC120269 AC128316 AC112537 AC114059 BT002222 BC007587 BF014806 AE011893 AC118787_3 AC102803 AC022098 TBBCHR1A2 AE016783 AC102605 AC113540 AC069114 OSJN00182 AC109448 AC090646 AC090884 AL353741 AC120269 AC1128316 AC112537 AC114059 AX549236 AB020628 AX646721 AB065919 ATT22P22 AC073668 AC087138 AF307079 10 89.0 2738 89.0 7115 89.0 7115 89.0 7115 89.0 7115 89.0 7115 89.0 7115 89.0 7115 89.0 7115 89.0 7115 89.0 7115 89.0 7115 89.0 7115 89.0 7115 89.0 7115 89.0 7115 89.0 7115 89.0 7115 89.0 7115 89.0 7115 89.0 7115 89.0 7115 89.0 7115 89.0 7115 89.0 7115 89.0 7115 89.0 7115 89.0 7115 89.0 7115 89.0 7115 89.0 7115 89.0 7115 89.0 7115 89.0 7115 89.0 7115 89.0 7115 89.0 7115 89.0 7115 89.0 7115 89.0 7115 89.0 7115 89.0 7115 89.0 7115 89.0 7115 89.0 7115 89.0 7115 89.0 7115 89.0 7115 89.0 7115 89.0 7115 89.0 7115 89.0 7115 89.0 7115 89.0 7115 89.0 7115 89.0 7115 89.0 7115 89.0 7115 89.0 7115 89.0 7115 89.0 7115 89.0 7115 89.0 7115 89.0 7115 89.0 7115 89.0 7115 89.0 7115 89.0 7115 89.0 7115 89.0 7115 89.0 7115 89.0 7115 89.0 7115 89.0 7115 89.0 7115 89.0 7115 89.0 7115 89.0 7115 89.0 7115 89.0 7115 89.0 7115 89.0 7115 89.0 7115 89.0 7115 89.0 7115 89.0 7115 89.0 7115 89.0 7115 89.0 7115 89.0 7115 89.0 7115 89.0 7115 89.0 7115 89.0 7115 89.0 7115 89.0 7115 89.0 7115 89.0 7115 89.0 7115 89.0 7115 89.0 7115 89.0 7115 89.0 7115 89.0 7115 89.0 7115 89.0 7115 89.0 7115 89.0 7115 89.0 7115 89.0 7115 89.0 7115 89.0 7115 89.0 7115 89.0 7115 89.0 7115 89.0 7115 89.0 7115 89.0 7115 89.0 7115 89.0 7115 89.0 7115 89.0 7115 89.0 7115 89.0 7115 89.0 7115 89.0 7115 89.0 7115 89.0 7115 89.0 7115 89.0 7115 89.0 7115 89.0 7115 89.0 7115 89.0 7115 89.0 7115 89.0 7115 89.0 7115 89.0 7115 89.0 7115 89.0 7115 89.0 7115 89.0 7115 89.0 7115 89.0 7115 89.0 7115 89.0 7115 89.0 7115 89.0 7115 89.0 7115 89.0 7115 89.0 7115 89.0 7115 89.0 7115 89.0 7115 89.0 7115 89.0 7115 89.0 7115 89.0 7115 89.0 7115 89.0 7115 89.0 7115 89.0 7115 89.0 7115 89.0 7115 89.0 7115 89.0 7115 89.0 7115 89.0 7115 89.0 7115 89.0 7115 89.0 7115 89.0 7115 89.0 7115 89.0 7115 89.0 7115 89.0 7115 89.0 7115 89.0 7115 89.0 7115 89.0 7115 89.0 7115 89.0 7115 89.0 7115 89.0 7115 89.0 7115 89.0 7115

AL I GNMENTS

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HVU22450 2738 bp mRNA linear P Hordeum vulgare alpha-glucosidase mRNA, complete cds. U22450 U22450.1 GI:944900 RESULT 1 HVU22450/c LOCUS DEFINITION ACCESSION VERSION

PLN 27-JUN-1996

KEYWORDS SOURCE ORGANISM

REFERENCE AUTHORS TITLE

Hordeum vulgare subsp. vulgare
Bukaryota, Virighjantae, Streptophyta; Embryophyta; Tracheophyta;
Bukaryota, Virighjantae, Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Pooideae; Triticeae; Hordeum.
1 (bases I to 2738)
Tibbot, B.K. and Skadsen, R.W.
Molecular cloning and characterization of a gibberellin-inducible,

.. 0

Gaps

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AP118226 7113 bp DNA linear PLN 15-JUN-2000
Hordeum vulgare high pl alpha-glucosidase (AGL97) gene, complete
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PRYNALDDPPYRINNDGTGRPINKYFYPASAVTYGGYTEXABHULFGLEARAFHRAL
ERDTGRREPVLSRETVEGGRFYTAHTGDNAATWGDLRYSINTMLSFGLFGWPWIGAD
I CGFNGNTTEELCGRWIQLGAFYPPSRDHSAIFTVRRELYLWPSVAAGARKALGIRYD
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SYPEYMDYRPEGTAHGVLLLSSNGWDVLYGGSYVTYKVIGGYLDFYFFRADNPLAVVD
GYTQLIGRPAPMPYWSFGFHQCRYGYLNVSDLERVYAGYAKARIPLEVWMTDIDYMDG
FKOFTLDRYNFTAABLRPFYDRLHRAAQKYVLJLDPGIRIDATYGTFVRGMQDDFLK
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VDAYPPAGRWYSLYDYSLAVATRTGRHVTLPAPADTVNVHVAGGTILPLQQSALTTSR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Hordeum vulgare subsp. vulgare
Hordeum vulgare subsp. vulgare
Hordeum vulgare subsp. vulgare
Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnollophyta; Liliopsida; Poales; Poaceae;
Pooldeae; Triticeae; Hordeum.
1 (bases 1 to 7113)
Frandsen, T.P., Lok, F., Mirgorodskaya, E., Roepstorff, P. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Purification, enzymatic characterization, and nucleotide sequence of a high-isoelectric-point alpha-glucosidase from barley malt Plant Physiol. 123 (1), 275-286 (2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Submitted (66-JAN-1999) Carlsberg Laboratory, Carlsberg Research
Center, Gl. Carlsbergvej 10, Valby 2500, Denmark
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      join(1. .218,4505. .5166,5268. .5498,5585. .7113)
gene="AGL97"
                                                                                                                                                                                                                                                                                                                                  Query Match 89.0%; Score 25.8; DB 6; Length 2752; Best Local Similarity 93.1%; Pred. No. 0.53; Matches 27; Conservative 0; Mismatches 2; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1. .7113
/organism="Hordeum vulgare subsp. vulgare"
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/cultivar="Igri"
/db xref="taxon:112509"
   1 (bases 1 to 2752)
Skadesn,R.W. and Tibbot,B.K.
Cloned .alpha. glucosidase from barley
Patent: US 5763252-A 3 09-UUN-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1062 CGGTGAAGTTGACACGGTCCAAGGTGAAG 1034
                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 CGGTGAAGTTGACAGGATCCAAGGTGAAG 29
                                                                                                                                    Location/Qualifiers
                                                                                                                                                                                                     /organism="unknown"
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AF118226.1 GI:8547061
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SOURCE
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WONTTEELCCRWIQLGAFYPPSRDHADIFTVRRELYLWPSVAAGGRAALGLRYQLLP
YPYILMYEALWTGAPIARPLEPSYPHDVATYVUNGFLIGRGVLVSPVLEPGFTTVDA
YFPAGRWYRLYDYSLAVATRTGGHVRLPAPADTVNVHLYGGTILPLQOSALTTSRARR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /translation="MATVGVLLLCLCLEAPRLCSSKEEGPLAARTVLAVAVTMEGA
LRAEAATGGRSSTGDVQRLAYYASLETDSRLRVRITDADHPRWEVPQDIIPRPAPGDV
LRAEAATGGRSSTGDVQRVLSPAGSDLVLTVHASPPRFTVSRRSTGOTLFOTAPGLVFRDK
YLEVISALPAGRASLYGLGHTKSSFRLRNDSFTLWNADIGASYVDVNLYGSHPFYN
DVRAPQTAHGVLLSSNGMDVLYGGSYVTYKVJGGVLDPFYFRQBNDLAVVDOYTQLIARPAPMPANTDIDYMDGFKJFTLANADIDYMDGFKJFTL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DRVNFTAAELRPFVDRLHRNAQKYVLILDPGIRVDPIDATYGTFVRGNQQDIFLKRNG
TNFVGNVWPGDVYFPDFMHPAAAEFWAREISLFRRTIPVDGLWIDMNEISNFYNPEPX
NALDDPPYRINNDGTGRPINNKTVRPLAVHYGGVTEYEEHNLFGLLEARATGRGVLRD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TAFHLLVALAEDGTASGYLFLDDGESPEYGRRSDWSWVRFNYKI PNNKGAI KVKSEVV
HNSYAQSRTLVISKVVLMGHRSPAAPKKLTVHVNSAEVEASSSAGTRYQNAGGLGGYA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /tissue_type="aleurone"
/dev_stage="aleurones from deembryonated half-seeds from
matured seeds"
                                                                                                                                                                                          Direct Submission
Submitted (10-MAR-1995) Brian K. Tibbot, Agronomy, University of
Wisconsin, 501 N. Walnut St., Madison, WI 53705, USA
Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                       /organism="Hordeum vulgare subsp. vulgare"
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/cultivar="Morex"
/db xref="taxon:112509"
/chromosome="1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 linear
putative alpha-glucosidase gene from barley
Plant Mol. Biol. 30 (2), 229-241 (1996)
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/note="encodes catalytic region"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  42. .2675
/EC_number="3.2.1.20"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /product="alpha-glucosidase"
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Sequence 3 from patent US 5763252.
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974 c 845 g 44
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /map="near Amy2"
/clone="pAGL.2737"
/haplotype="2n"
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27; Conservative (
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Tibbot, B.K.
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Matches 27; Conserv
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SOURCE
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AUTHORS
TITLE
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Complement (35763. .35869)

/note="GRAIL 2 excellent exon, frame 2"
complement (38408. .38595)

/rpt family="MER7"
42337. .42605

/rpt family="Alu"
42852. .42935
/note="GRAIL 2 excellent exon, frame 2"
45174. .45245
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complement (57923. .58284)
/rpt family="THE1"
58788. .59006
                                                                                                                                                                                                                                          /rpt_family="MLT1"
16149. 16433
complement(20408. .20538)
/note="GRAIL 2 excellent ex
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/note="CRAIL 2 excellent e
complement (47409. .47554)
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48205. .48559
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complement (30190, .30464)
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0905. .51188
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complement (4807. .4926)
/rpt_family="MER42"
complement (7052. .7666)
/rpt_family="L1"
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11316. .11369
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55782 .5606
/rpt_family="Alu"
56049 .56070
/note="(A)22"
                                                                             osey. .8676
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15358. .45379
'note="(T)22"
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34356. .34401
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3050. .53359
rpt_family="Alu"
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62501. .62774
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rpt_unit=AC
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rpt_unit=T
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5039. .25369
                                                                                                                        659. .869ī
note="(A)33"
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Homo sapiens chromosome 5, PAC clone 53Ll7 (LBNL H152), complete
ARRTAFHLLVALAEDGTASGDLFLDDGESPEMGGRSDWSMVRFSCEMGSDGAIKVKSE
              VVHNSYAQSRILVISKYVLMGHRSPAAPKKLTVHVNSAEVEASSSAGTRYQNAGGLGG
VAHIGGLSLVVGEEFELKVAMSY"
1935 c 1716 g 1753 t
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I (bases 1 to 119298)
Church, D.M., Yang, J., Bocian, M., Shiang, R. and Wasmuth, J.J.
A high-resolution physical and transcript map of the Cri du chat region of human chromosome 5p
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2 (bases 1 to 119298)
Kimmerly, W., Bondoc, W., Cheng, J., Connolly, K.S., Gunning, K.M.,
Kadmer, K., Miguel, T., Miller, C., Pitluck, S., Pollard, M.,
Kojeski, H., Subramanian, S. and Martin, C.H.
Sequencing of human chromosome 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Ricke, D.O.
Large Scale Sequence Analysis and Annotation with the Sequence
Comparison Analysis (SCAN) System
Unpublished
                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Submitted (04-SEP-1998) Human Genome Center, DOE Joint Genome Institute, Lawrence Berkeley National Laboratory, MS 74-157, Berkeley, CA 94720, U.S.A.
Sequence submitted by:
DOE Joint Genome Institute.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Kimmerly,W., Bondoc,M., Cheng,J., Connolly,K.S., Gunning,K.M.
Radner,K., Miguel,T., Miller,C., Pitluck,S., Pollard,M.,
Rojeski,H., Subramanian,S. and Martin,C.H.
                                                                                                                                         .
                                                                                                        Length 7113;
                                                                                                                                       2; Indels
                                                                                                   Score 25.8; DB 8;
Pred. No. 0.58;
0; Mismatches 2;
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                                                                                                                                                                         1 CGGTGAAGTTGACAGGATCCAAGGTGAAG 29
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/note="(T) 22"

/rpt_type=tandem

/rpt_unit=T

complement (995. .1179)

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/rpt_family="Alu"

/rpt_family="Alu"

complement (1398. .1478)
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/chromosome="5"
                                                  1716 g
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/note="LBNL H152"
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                                                                                                    Query Match
Best Local Similarity 93.1%;
Matches 27; Conservative
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PRI 21-FEB-2002

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163817 bp DNA linear PRI 13-MAR-2002
AC109448
AC109448.3 GI:19387596
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1 (State State State Stanford Human Genome Center.)

1 (Direct Submission Stanford Human Genome Center.)

2 (Dases I to 148288)

2 (Dases I to 148288)

3 (Dases I to 148288)

4 (25-37M-2002) Production Sequencing Facility, DOE Joint Genome Institute, 2800 Mitchell Drive, Malnut Creek, CA 94598, USA DOE Joint Genome Institute and Stanford Human Genome Center.)

5 (Dases I to 148288)

6 (Dases I to 148288)

7 (Dases I to 148288)

8 (Dases I to 148288)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Submitted (1-FBB-2002) DOB Joint Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA
On Feb 21, 2002 this sequence version replaced gi:18369967.

On Feb 21, 2002 this sequence version replaced gi:18369967.

Draft Sequence Produced by DOE Joint Genome Institute

www.jgi.doe.gov

www.fgi.doe.gov

www.spi.completed at Stanford Human Genome Center

www.spic.stanford.edu

Quality: Phrap Quality >=40 99.9% of Sequence;

Estimated Total Number of Errors is 0.1.

Location/Qualifiers

1. 148288

//Crganism="Homo sapiens"
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DOE Joint Genome Institute and Stanford Human Genome Center. Direct Submission
                                                                                                                                                                                                                                                                                                               Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                          AC108121 148288 bp DNA linear PRI 21-FEE
Homo sapiens chromosome 5 clone RP11-553D6, complete sequence.
AC108121
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       ed. No. 19;
Mismatches
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46985 a 27260 c 26231 g 47812
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/db xref="taxon:9606"
/chromcsome="5"
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complement(104144. .104288)

/rpt_family="MER25"

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/rpt_family="LI"

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/rpt_unit=GT
region complement(114907. 115187)
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39136 a 21117 c 21142 g 37903 t
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complement(76841. .77077)

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7249. .76175

/rpt_family="11"

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85132. .85433
                        /rpt_family="Alu"
59558. .69617
                                                         / \text{rpt}_{\epsilon} = \frac{\text{family} = \text{"Ll"}}{69659}. .69945
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72107. .72247
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Direct Submission

Direct Submission

Direct Submission

Direct Submission

Direct Submission

Submitted (06-MAR-2001) Human Genomic Center, Institute of Generics Chinese Academy of Sciences, Datum Road, Beijing, Beijing 100101, P. R.China

Sabo,J., Bao,Q., Bao,W., Bian,X., Cao,T., Chen,C., Chen,J., Ding,H., Dong,W., Fan,H., Feng,X., Gong,J., Guan,Q., Gu,X., Guo,D., Guo,Z., Li,F., Li,J., Li,J., Li,J., Li,J., Li,J., Li,J., Li,J., Li,J., Li,J., Li,J., Li,J., Li,J., Li,J., Li,J., Li,J., Li,J., Li,J., Li,J., Li,J., Li,J., Li,J., Li,J., Li,J., Li,J., Li,J., Li,J., Li,J., Li,J., Li,J., Li,J., Li,J., Li,J., Li,J., Li,J., Li,J., Li,J., Li,J., Li,J., Li,J., Li,J., Li,J., Li,J., Li,J., Li,J., Li,J., Li,J., Li,J., Li,J., Li,J., Li,J., Li,J., Li,J., Li,J., Li,J., Li,J., Li,J., Li,J., Li,J., Li,J., Li,J., Li,J., Li,J., Li,J., Li,J., Li,J., Li,J., Li,J., Li,J., Li,J., Li,J., Li,J., Li,J., Li,J., Li,J., Li,J., Li,J., Li,J., Li,J., Li,J., Li,J., Li,J., Li,J., Li,J., Li,J., Li,J., Li,J., Li,J., Li,J., Li,J., Li,J., Li,J., Li,J., Li,J., Li,J., Li,J., Li,J., Li,J., Li,J., Li,J., Li,J., Li,J., Li,J., Li,J., Li,J., Li,J., Li,J., Li,J., Li,J., Li,J., Li,J., Li,J., Li,J., Li,J., Li,J., Li,J., Li,J., Li,J., Li,J., Li,J., Li,J., Li,J., Li,J., Li,J., Li,J., Li,J., Li,J., Li,J., Li,J., Li,J., Li,J., Li,J., Li,J., Li,J., Li,J., Li,J., Li,J., Li,J., Li,J., Li,J., Li,J., Li,J., Li,J., Li,J., Li,J., Li,J., Li,J., Li,J., Li,J., Li,J., Li,J., Li,J., Li,J., Li,J., Li,J., Li,J., Li,J., Li,J., Li,J., Li,J., Li,J., Li,J., Li,J., Li,J., Li,J., Li,J., Li,J., Li,J., Li,J., Li,J., Li,J., Li,J., Li,J., Li,J., Li,J., Li,J., Li,J., Li,J., Li,J., Li,J., Li,J., Li,J., Li,J., Li,J., Li,J., Li,J., Li,J., Li,J., Li,J., Li,J., Li,J., Li,J., Li,J., Li,J., Li,J., Li,J., Li,J., Li,J., Li,J., Li,J., Li,J., Li,J., Li,J., Li,J., Li,J., Li,J., Li,J., Li,J., Li,J., Li,J., Li,J., Li,J., Li,J., Li,J., Li,J., Li,J., Li,J., Li,J., Li,J., Li,J., Li,J., Li,J., Li,J., Li,J., Li,J., Li,J., Li,J., Li,J., Li,J., Li,J., Li,J., Li,J., Li,J., Li,J., Li,J., Li,J., Li,J., Li,J., Li,
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Quality coverage: 1.77x in Q20 bases;sum-of-contigs
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Chemistry: Dye-terminator: ET 55% of reads
Chemistry: Dye-terminator: ET 55% of reads
Chemistry: Dye-terminator: By Dye; 45% of reads
Assembly program: Phrap; version 0.990229
Consensus quality; 433 bases at least Q40
Consensus quality: 643 bases at least Q20
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Website:http://hgc.igtp.ac.cn
http://www.genomics.org.cn
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1 (bases 1 to 16581)

5 Lou,C., Bao,J., Bao,W., Bian,X., Cao,T., Chen,C., Chen,J., Ding,H., Dong,W., Fan,H., Feng,X., Gong,J., Guan,Q., Gux,, Guo,D., Guo,Z., He,L., Hu,S., Huang,F., Jin,X., Kang,N., Li,C., Li,C., Li,C., Li,C., Li,C., Li,C., Li,C., Li,C., Li,C., Li,C., Li,C., Li,C., Li,C., Li,C., Li,C., Li,C., Li,C., Li,C., Li,C., Li,C., Li,C., Li,C., Li,C., Li,C., Li,C., Li,C., Li,C., Li,C., Li,C., Li,C., Li,C., Li,C., Li,C., Li,C., Li,C., Li,C., Li,C., Li,C., Li,C., Li,C., Li,C., Li,C., Li,C., Li,C., Li,C., Li,C., Li,C., Li,C., Li,C., Li,C., Li,C., Li,C., Li,C., Li,C., Li,C., Li,C., Li,C., Li,C., Li,C., Li,C., Li,C., Li,C., Li,C., Li,C., Li,C., Li,C., Li,C., Li,C., Li,C., Li,C., Li,C., Li,C., Li,C., Li,C., Li,C., Li,C., Li,C., Li,C., Li,C., Li,C., Li,C., Li,C., Li,C., Li,C., Li,C., Li,C., Li,C., Li,C., Li,C., Li,C., Li,C., Li,C., Li,C., Li,C., Li,C., Li,C., Li,C., Li,C., Li,C., Li,C., Li,C., Li,C., Li,C., Li,C., Li,C., Li,C., Li,C., Li,C., Li,C., Li,C., Li,C., Li,C., Li,C., Li,C., Li,C., Li,C., Li,C., Li,C., Li,C., Li,C., Li,C., Li,C., Li,C., Li,C., Li,C., Li,C., Li,C., Li,C., Li,C., Li,C., Li,C., Li,C., Li,C., Li,C., Li,C., Li,C., Li,C., Li,C., Li,C., Li,C., Li,C., Li,C., Li,C., Li,C., Li,C., Li,C., Li,C., Li,C., Li,C., Li,C., Li,C., Li,C., Li,C., Li,C., Li,C., Li,C., Li,C., Li,C., Li,C., Li,C., Li,C., Li,C., Li,C., Li,C., Li,C., Li,C., Li,C., Li,C., Li,C., Li,C., Li,C., Li,C., Li,C., Li,C., Li,C., Li,C., Li,C., Li,C., Li,C., Li,C., Li,C., Li,C., Li,C., Li,C., Li,C., Li,C., Li,C., Li,C., Li,C., Li,C., Li,C., Li,C., Li,C., Li,C., Li,C., Li,C., Li,C., Li,C., Li,C., Li,C., Li,C., Li,C., Li,C., Li,C., Li,C., Li,C., Li,C., Li,C., Li,C., Li,C., Li,C., Li,C., Li,C., Li,C., Li,C., Li,C., Li,C., Li,C., Li,C., Li,C., Li,C., Li,C., Li,C., Li,C., Li,C., Li,C., Li,C., Li,C., Li,C., Li,C., Li,C., Li,C., Li,C., Li,C., Li,C., Li,C., Li,C., Li,C., Li,C., Li,C., Li,C., Li,C., Li,C., Li,C., Li,C., Li,C., 
                                                                                                                                                                                                                                                                                                                                                                                               Direct Submission

Submitted (07-MAR-2002) Production Sequencing Facility, DOE Joint Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA 4 (Dases 1 to 163817)

DoE Joint Genome Institute and Stanford Human Genome Center.

Direct Submission

Direct Submission

Direct Submission

Direct Submission

Drive, Walnut Creek, CA 94598, USA

On Mar 13, 2002 this sequence version replaced gi:1924890.

Drive, Walnut Creek, CA 94598, USA

On Mar 13, 2002 this sequence version replaced gi:1924890.

Prinching Completed at Stanford Human Genome Center

www-1941.doe.gov

Finishing Completed at Stanford Human Genome Center

www-1940-stanford-ded

Quality: Phrap Quality >=40 100% of Sequence;

Estimated Total Number of Errors is 0.
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Luo,C., Bao,J., Bao,R., Bian,X., Cao,T., Chen,C., Chen,J.,
Luo,C., Bao,J., Bao,R., Feng,X., Gong,A., Guan,Q., Gu,X., Guo,D.,
Guo,Z., He,L., Hu,S., Hunng,F., Jin,Y., Kang,N., Li,C., Li,C.,
Li,F., Li,G., Li,J., Li,L., Li,S., Li,T., Liu,Y., Liu,N., Liu,B.,
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Homo sapiens chromosome 3 clone RPI1-690A6 map 3p, complete
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Submitted (04-FEB-2002) Production Sequencing Facility, I Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 3 (bases 1 to 163817)
DOE Joint Genome Institute.
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                                                                                            2 (bases 1 to 163817)
DOE Joint Genome Institute.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Bukaryota; Metazoa; Chordata; Craniata; Verrebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 16691)

1 (bases 1 to 16691)

2 Song, L., Bao, J., Bao, W., Bian, X., Cao, T., Chen, J., Ding, H., Dong, W., Pan, H., Feng, X., Gong, J., Guan, Q., Gu, X., Guo, D., Guo, Z., He, L., Hu, S., Huang, F., Jin, Y., Kang, N., Li, C., Li, C., Li, C., Li, C., Li, C., Li, C., Li, C., Li, C., Li, C., Li, C., Li, C., Li, C., Li, C., Li, C., Li, C., Li, C., Li, C., Li, C., Li, C., Li, C., Li, C., Li, C., Li, C., Li, C., Li, C., Li, C., Li, C., Li, C., Li, C., Li, C., Li, C., Li, C., Li, C., Li, C., Li, C., Li, C., Li, C., Li, C., Li, C., Li, C., Li, C., Li, C., Li, C., Li, C., Li, C., Li, C., Li, C., Li, C., Li, C., Li, C., Li, C., Li, C., Li, C., Li, C., Li, C., Li, C., Li, C., Li, C., Li, C., Li, C., Li, C., Li, C., Li, C., Li, C., Li, C., Li, C., Li, C., Li, C., Li, C., Li, C., Li, C., Li, C., Li, C., Li, C., Li, C., Li, C., Li, C., Li, C., Li, C., Li, C., Li, C., Li, C., Li, C., Li, C., Li, C., Li, C., Li, C., Li, C., Li, C., Li, C., Li, C., Li, C., Li, C., Li, C., Li, C., Li, C., Li, C., Li, C., Li, C., Li, C., Li, C., Li, C., Li, C., Li, C., Li, C., Li, C., Li, C., Li, C., Li, C., Li, C., Li, C., Li, C., Li, C., Li, C., Li, C., Li, C., Li, C., Li, C., Li, C., Li, C., Li, C., Li, C., Li, C., Li, C., Li, C., Li, C., Li, C., Li, C., Li, C., Li, C., Li, C., Li, C., Li, C., Li, C., Li, C., Li, C., Li, C., Li, C., Li, C., Li, C., Li, C., Li, C., Li, C., Li, C., Li, C., Li, C., Li, C., Li, C., Li, C., Li, C., Li, C., Li, C., Li, C., Li, C., Li, C., Li, C., Li, C., Li, C., Li, C., Li, C., Li, C., Li, C., Li, C., Li, C., Li, C., Li, C., Li, C., Li, C., Li, C., Li, C., Li, C., Li, C., Li, C., Li, C., Li, C., Li, C., Li, C., Li, C., Li, C., Li, C., Li, C., Li, C., Li, C., Li, C., Li, C., Li, C., Li, C., Li, C., Li, C., Li, C., Li, C., Li, C., Li, C., Li, C., Li, C., Li, C., Li, C., Li, C., Li, C., Li, C., Li, C., Li, C., Li, C., Li, C., Li, C., Li, C., Li, C., Li, C., Li, C., Li, C., Li, C.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRI 16-MAR-2001
                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ACO90884 1inear PRI 16-P
Homo sapiens chromosome 3 clone RP11-165B2 map 3p, complete
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                On Mar 16, 2001 this sequence version replaced gi:9966194
                               Score 21.6; DB 9; Length 165681;
Pred. No. 71;
0; Mismatches 4; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1.44x in Q20 bases; sum-of-contigs
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Chemistry: Dye-terminator: ET 55% of reads
Chemistry: Dye-terminator: ET 55% of reads
Chemistry: Dye-terminator Big Dye; 45% of reads
Assembly program: Phrap; version 0.990329
Consensus quality: 173 bases at least Q40
Consensus quality: 419 bases at least Q30
Consensus quality: 482 bases at least Q20
Insert size: 490; sum-of-contigs
                                                                                                                                                                                                                                                                                                                                           92763 GGTGAAGTTGAGAGTTCAAGGAAAAG 92736
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Center project name:1% project
Center clone name: RPII-165B2
                                                                                                                                                                                                                                                 2 GGTGAAGTTGACAGGATCCAAGGTGAAG 29
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http://www.genomics.org.cn
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AC090884.1 GI:13357222
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                                          Query Match
Best Local Similarity 85.7%;
Matches 24; Conservative (
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LOCUS
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AUTHORS
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JOURNAL
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KEYWORDS
SOURCE
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Direct Submission

Submitted (28-JAM-2001) Sanger Centre, Hinxton, Cambridgeshire,
CB10 1SA, UK. E-mail enquiries: humquery@sanger.ac.uk Clone
crqueets: clonerquest@sanger.ac.uk
on Jan 28, 2001 this sequence version replaced gi:12580980.

During sequence assembly data is compared from overlapping clones.
Where differences are found these are annotated as variations
together with a note of the overlapping clone name. Note that the
variation annotation may not be found in the sequence submission
corresponding to the overlapping clone, as we submit sequence with
only a small overlap as described above.

This sequence has been finished according to sequence map criteria
as follows. An attempt is made to resolve all sequencing problems,
such as compressions and repeats, but not necessarily within known
annotated repeat sequence elements. Where the sequence is
ambiguous, there is an annotation using the 'unsure' feature key.
The following abbreviations are used to associate primary accession
numbers given in the feature table with their source databases:
Em: EMBL; Sww; SWISSPROT; Tr:, TREMBL; Wp:, WORMPEP; Information
on the WORMPEP database can be found at
http://www.sanger.ac.uk/Projects/C elegans/wormpep This sequence
dromosome 9, constructed by the Sanger centre Chromosome 9 Mapping
Group.
Further information can be found at
http://www.sanger.ac.uk/HGP/Chr9
RPI1-575C20 is from the library RPCI-11.2 constructed by the group
of Pieter de Jong. Four further details see
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AL353741 199517 bp DNA linear PRI 28-JAN-2001 Human DNA sequence from clone RP11-575C20 on chromosome 9, complete
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ..
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 199517)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           This sequence is the entire insert of clone RPI1-575C20 The true left end of clone RPI1-279E1 is at 116738 in this sequence. The true right end of clone RPI1-218I7 is at 84470 in this sequence. Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                 DB 9; Length 166991;
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0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        4; Indels
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VECTOR: pBACe3.6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                 Score 21.6; | Pred. No. 71;
                                                                                                                                                                                                                                                                                   42168 a 41024 c 39989 g 43810
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            53
                                     L. .166991
'organism="Homo sapiens"
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/chromosome="9"
                                                                                                  /mol_type="genomic_DN/db_xref="taxon:9606"
/chromosome="3"
Location/Qualifiers
                                                                                                                                                                                                                                                         /clone="RP11-165B2"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AL353741.16 GI:12584694
                                                                                                                                                                                                                                                                                                                                                                                             74.5%;
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Best Local Similarity 85.7%
Matches 24, Conservative
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/note="wgs_end_extension
clone_end:Sp6"
                                                                                                                                                                                                                                                                                                            2 (bases 1 to 174728)
Worley, K.C.
                                                                                                                                                                                                                                                                                       Unpublished
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TITLE
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Allen, C., Allen, H. Alsbrooks, S., Amin, A., Angutano, D., Allen, C., Allen, H., Alsbrooks, S., Amin, A., Angutano, D., Allen, C., Allen, H., Alsbrooks, S., Amin, A., Angutano, D., Anyelebech, V., Anoyagi, A., Anoyed, M., Baca, E., Baden, H., Baldwin, D., Bandaranaike, D., Barber, M., Baca, E., Baden, H., Baldwin, D., Bandaranaike, D., Barber, M., Baca, E., Baden, H., Baldwin, D., Bandaranaike, D., Barrell, K., Calderon, E., Chen, G., Chen, G., Chen, G., Chen, G., Chen, G., Chen, Y., Chen, Z., Chen, G., Chen, G., Chen, Y., Chen, Z., Chen, G., Chen, G., Chen, Y., Chen, Z., Chen, G., Chen, R., Caderon, E., Davy-Carroll, L., De Anda C., Deberich, D., Delqado, O., Denson, S., Deramo, C., Loyle, M., Cree, A., D'Souza, L., Dedaria, M., Escotto, M., Elgen, A., Escotto, M., Elgen, C., Falls, T., Fan, G., Fernandez, S., Finley, M., Flagg, N., Forbes, L., Foster, M., Gebregeorgis, E., Geer, K., Gill, R., Grady, M., Guevara, W., Gebregeorgis, E., Geer, K., Gill, R., Grady, M., Guevara, W., Gebregeorgis, E., Geer, K., Gill, R., Grady, M., Guevara, W., Gebregeorgis, E., Geer, K., Gill, R., Grady, M., Guevara, W., Guevara, W., Harvajak, P., Hawes, A., S.L., Hodgson, A., Hogues, M., Jackson, L., Jackson, L., Jang, H., Johnson, B., Johnson, R., Johnson, R., Johnson, R., Johnson, R., Johnson, R., Johnson, R., Johnson, R., Johnson, R., Johnson, R., Johnson, R., Johnson, R., Johnson, R., Mander, M., Mahling, S., Kally, K., Khay, L., Koya, C., Kraft, C.L., Loulseged, H., Loran, C., Khay, L., Lu, W., Mahindaruch, M., Mahlingas, M., Martin, R., Mahlingas, M., Martin, R., Martin, R., Mahlingas, R., Mahlingas, R., Martin, R., Mahlingas, R., Martin, R., Martin, R., Mahlingas, R., Martin, R., Martin, R., Martin, R., Martin, R., Martin, R., Martin, R., Martin, R., Martin, R., Martin, R., Martin, R., Martin, R., Martin, R., Martin, R., Martin, R., Martin, R., Martin, R., Martin, R., Martin, R., Martin, R., Martin, R., Martin, R., Martin, R., Martin, R., Martin, R., Martin, R., Martin, R., Martin, R., Martin, 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ACI20269 174728 bp DNA linear HTG 12-OCT-2002
Rattus norvegicus clone CH230-482D3, WORKING DRAFT SEQUENCE.
ACI20269
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Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae,
                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                             159090. 159136
/note="Single clone region. Assembly confirmed by restriction digest data."
159357. 159427
/note="Single clone region. Assembly confirmed by restriction digest data."
a 40153 c 38840 g 59481 t
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0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   HTG; HTGS_PHASE2; HTGS_DRAFT; HTGS_FULLTOP.
Rattus norvegicus (Norway rat)
Rattus norvegicus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    51485 GCTGAAGTTGAAAGGATGCAAGGTGTAG 51458
                                                                                                                                                                                                                                                                                                                                                                               0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                   2 GGTGAAGTTGACAGGATCCAAGGTGAAG 29
                     /clone_lib="RPCI-11.2"
159090. 159136
/clone="RP11-575C20"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AC120269.3 GI:23908187
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                                                                                                                                                                                                                                                                                                                      74.5%;
85.7%;
                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity 85.7%
---nhes 24; Conservative
                                                                                                                                                                                                                                61043
                                                         misc_feature
                                                                                                                                              misc_feature
                                                                                                                                                                                                                                BASE COUNT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DEFINITION
ACCESSION
VERSION
KEYWORDS
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AC120269
LOCUS
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SOURCE

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Direct Submission

AL Submitted (05-MAY-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA

(Dases I to 174728)

Rs demone Sequencing Consortium.

Direct Submission

Submitted (12-OCT-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA

On Oct 12, 2002 this sequence version replaced gi:21747363.

The Sequence in this sassembly is a combination of BAC based reads and whole genome shorgun sequencing reads assembled using Atlas (http://www.hgsc.bcm.tmc.edu/projects/rat/). Each contig described in the Atlas assembly (a 'contig-scaffold'). Within each contig scaffold, individual sequence contigs are ordered and oriented, and separated by sized gaps filled with Ns to the estimated state. The sequence contigs within a contig-scaffold that consist entirely of whole genome shorgun sequence reads. Both end sequences and whole genome shorgun sequence reads. Both end sequences and whole genome shorgun sequence reads. Both end sequences and whole genome shorgun sequence reads.
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* (see http://www.hgsc.bcm.tmc.edu/docs/Genbank draft_data.html).

* NOTE: This is a "working draft' sequence. It currently

* consists of I contigs. Gaps between the contigs

* are represented as runs of N. The order of the pieces
Steimle, M., Strong, R., Sutton, A., Svatek, A., Tabor, P., Taylor, C., Taylor, T. Thomas, S., Tingey, A., Trejos, Z., Usmani, K., Valas, R., Vera, V., Villasana, D., Waldron, L., Walker, B., Wang, J., Wang, Q., Warge, S., Warren, J., Waldron, L., White, F., Williams, G., Willians, K., Willians, K., Willians, G., Willians, R., Willians, Y., Worley, K., Wright, D., Wright, R., Wu, J., Yakub, S., Yen, J., Yoon, U., Yu, F., Zhang, J., Zhou, X., Zhao, S., Dunn, D., von Wilderhausern, A., Weiss, R., Smith, D.R., Wolt, R., Smith, H.O., Weinstock, G. and Gibbs, R.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          is believed to be correct as given, however the sizes of the gaps between them are based on estimates that have provided by the submittor.
This sequence will be replaced
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     by the finished sequence as soon as it is available and the accession number will be preserved.

1 174728: contig of 174728 bp in length.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Web site: http://www.hgsc.bcm.tmc.edu/
Contact: hgsc-help@bcm.tmc.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Center: Baylor College of Medicine Center code: BCM
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2 (bases 1 to 196393)
Worley, K.C.
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Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ACI28316 196393 bp DNA linear HTG 19-NOV-Rattus norvegicus clone CH230-333G1, WORKING DRAFT SEQUENCE, 2 unordered pieces.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match 73.1%; Score 21.2; DB 2; Length 174728; Best Local Similarity 88.5%; Pred. No. 1.18+02; Matches 23; Conservative 0; Mismatches 3; Indels 0;
                                                                                                                                                                                                                                                                           ature 17353. 174728
//note="wed-extension clone end:T7"
44465 a 28574 c 29392 g 44439 t 27858 others
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AC128316.3 GI:25085897
HTGS_PHASE1; HTGS_DRAFT; HTGS_FULLTOP.
Rattus norvegicus (Norway rat)
Rattus norvegicus
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                             'note="clone_boundary
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Nuzny, D.Marie., Metzker, M.Lee., Abramzon, S., Adams, C., Alder, J., Alabbrooke, S., Amin, A., Angulano, D., Allen, H., Alabbrooke, S., Amin, A., Angulano, D., Anyalebechi, V. Aoyagi, A., Apodeji, M., Baca, E., Baden, H. Balakenburg, E., Baden, H. Barnstead, M., Benahmed, F., Baldwin, D., Bandaranaike, D., Barber, M., Barnstead, M., Benahmed, F., Baldwin, D., Bandaronaike, D., Burchl, K., Blyth, P., Brown, M., Bryant, N., Enhay, C., Burch, P., Burrell, K., Calderon, E., Cardenas, V., Carter, K., Cavazos, I., Ceasar, H., Center, A., Chavez, D., Chen, G., Chen, G., Chen, R., Chen, Y., Chen, Z., Chu, J., Clackon, E., Davila, M. L., Davis, C., Davy-Carroll, L., De Anda, C., Dederich, D. Devila, M. L., Davis, C., Davy-Carroll, L., De Anda, C., Dederich, D. Deraper, H., Duyan-Rocha, S., Dunn, A., Durbin, K., Duval, B., Eaves, K., Egan, A., Escotto, M., Eugene, C., Rans, C.A., Falls, T., Fan, G., Fernandez, S., Finley, M., Flagg, N., Forbes, L., Foster, M., Garza, M., Gabsis, A., Ganta, R., Gardy, M., Guerra, W., Guerra, W., Guerra, W., Harvey, Y., Havlak, P., Hawes, A., Handlen, S., Hamilton, C., Hamilton, K., Harlandez, S., Hawes, A., Handes, C., Lu, S., Lu, W., Karpathy, S., Kelly, S., Khan, Z., King, L., Kovar, C., Liu, J., Liu, W., Liu, W., Liu, W., Liu, W., Liu, W., Liu, W., Liu, W., Liu, W., Liu, W., Liu, W., Liu, W., Liu, W., Liu, W., Liu, W., Liu, W., Liu, W., Liu, W., Liu, W., Liu, W., Liu, W., Liu, W., Liu, W., Liu, W., Liu, W., Liu, W., Liu, W., Liu, W., Liu, W., Mahindartne, W., Mahindartne, W., Mahindartne, W., Martin, R., Liu, W., Mangum, B., Mapua, P., Mattin, R., Martin, R., Martin, R., Martin, R., Martin, R., Martin, R., Martin, R., Martin, R., Martin, R., Martin, R., Martin, R., Martin, R., Martin, R., Martin, R., Martin, R., Martin, R., Martin, R., Martin, R., Martin, R., Martin, R., Martin, R., Martin, R., Martin, R., Martin, R., Martin, R., Martin, R., Martin, R., Martin, R., Martin, R., Martin, R., Martin, R., Martin, R., Martin, R., Martin, R., Martin, R., Martin, R
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Rattus norvegicus clone CH230-40P13, *** SEQUENCING IN PROGRESS
AF*, 2 unordered pieces.
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 73.1%; Score 21.2; DB 2; Length 196393; Best Local Similarity 88.5%; Pred. No. 1.1e+02; Matches 23; Conservative 0; Mismatches 3; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     40837 a 37304 c 38177 g 41134 t 38941 others
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HTG, HTGS PHASB1, HTGS DRAFT, HTGS_ENRICHED.
Rattus norvegicus (Norway rat)
Rattus norvegicus
organism="Rattus norvegicus"
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                                                                                                                                                                                                      clone_end:Sp6
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                                                                                                                                     misc feature
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ORIGIN
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AC112537/c
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KEYWORDS
SOURCE
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Microsalisation, Caracata and Manchana and Warpey, Mores S., Markeris S., Manichas M. Morris K. Morris S. Manichas M. Murphy, M. Mirl. L., Mankeris S. Manichas M. Murphy, M. Mirl. L., Mankerinsk, S. Pall, M. Percz A. Percz L., Falmucch, C. L., Plager S. Pall, M. Percz A. Percz J., Falmucch, C. L., Plager S. Pall, M. Percz A. Percz J., Falmucch, C. L., Plager S. Manichasham, O. Manichasham, D. Manichasham, D. Palago, M. Markerinsk, S. Pall, M. Pall, S. Pall, M. Pall, S. Pall, M. Pall, S. Pall, M. Pall, S. Pall, M. Pall, S. Pall, M. Pall, S. Pall, M. Pall, S. Pall, M. Pall, S. Pall, M. Pall, M. Pall, M. Pall, M. Pall, M. Pall, M. Pall, S. Pall, M. Pall, M. Pall, M. Pall, M. Pall, M. Pall, M. Pall, M. Pall, M. Pall, M. Pall, M. Pall, M. Pall, M. Pall, M. Pall, M. Pall, M. Pall, M. Pall, M. Pall, M. Pall, M. Pall, M. Pall, M. Pall, M. Pall, M. Pall, M. Pall, M. Pall, M. Pall, M. Pall, M. Pall, M. Pall, M. Pall, M. Pall, M. Pall, M. Pall, M. Pall, M. Pall, M. Pall, M. Pall, M. Pall, M. Pall, M. Pall, M. Pall, M. Pall, M. Pall, M. Pall, M. Pall, M. Pall, M. Pall, M. Pall, M. Pall, M. Pall, M. Pall, M. Pall, M. Pall, M. Pall, M. Pall, M. Pall, M. Pall, M. Pall, M. Pall, M. Pall, M. Pall, M. Pall, M. Pall, M. Pall, M. Pall, M. Pall, M. Pall, M. Pall, M. Pall, M. Pall, M. Pall, M. Pall, M. Pall, M. Pall, M. Pall, M. Pall, M. Pall, M. Pall, M. Pall, M. Pall, M. Pall, M. Pall, M. Pall, M. Pall, M. Pall, M. Pall, M. Pall, M. Pall, M. Pall, M. Pall, M. Pall, M. Pall, M. Pall, M. Pall, M. Pall, M. Pall, M. Pall, M. Pall, M. Pall, M. Pall, M. Pall, M. Pall, M. Pall, M. Pall, M. Pall, M. Pall, M. Pall, M. Pall, M. Pall, M. Pall, M. Pall, M. Pall, M. Pall, M. Pall, M. Pall, M. Pall, M. Pall, M. Pall, M. Pall, M. Pall, M. Pall, M. Pall, M. Pall, M. Pall, M. Pall, M. Pall, M. Pall, M. Pall, M. Pall, M. Pall, M. Pall, M. Pall, M. Pall, M. Pall, M. Pall, M. Pall, M. Pall, M. Pall, M. Pall, M. Pall, M. Pall, M. Pall, M. Pall, M. Pall, M. Pall, M. Pall, M. Pall, M. Pall, M. Pall, M. Pall, M. Pall, M. Pall, M. Pall, M. Pall, M. Pall,
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REFERENCE
AUTHORS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Z/1434 bp DNA linear HTG 13-MAY-2003
Rattus norvegicus clone CH230-197C21, *** SEQUENCING IN PROGRESS
ACTIVATOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ô
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0; Gaps

    as soon as it is available and the accession number will.
    be preserved.

                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
73.1%; Score 21.2; DB 2; Length 264340;
Best Local Similarity 88.5%; Pred. No. 1.1e+02;
Matches 23; Conservative 0; Mismatches 3; Indels 0;
This record will be updated with the finished sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                /note="wgs_contig"
ature 255872. 257215
/note="wgs_contig"
ature 25830. 260324
/note="wgs_contig"
75767 a 46794 c 45644 g 67385 t 28750 others
                                                                                                260325 260424: conrig of 260324 bp in length 260325 260424: gap of unknown length 260425 264340: conrig of 3916 bp in length. Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AC114059
AC114059.5 GI:30581570
HTG; HTGS_PHASE1; HTGS_DRAFT; HTGS_ENRICHED.
Rattus norvegicus (Norway rat)
Rattus norvegicus

    264340
    organism="Rattus norvegicus"

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                                                                                                                                                                                                                                                                                                           /mol_type="genomic DNA'
/db_xref="taxon:10116"
/clone="CH230-40P13"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2 GGTGAAGTTGACAGGATCCAAGGTGA 27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                          misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 misc_feature
                                                                                                                                                                                                                                                    Bource
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AC114059/c
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ORGANISM
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KEYWORDS
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                                                                                                                                                                                                           FEATURES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ORIGIN
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Nankeria, C., Noria, S., Noria, S., Nuldasa, M., Noria, S., Nanki, L., Nankeochem, O., Okoronia, C., Olaminguagoon, A., Pal, S., Parks, K., Paters, L., Palankoch, C., Paters, L., Palankoch, C., Paters, L., Palankoch, C., Paters, E., Paters, E., Paters, E., Paters, E., Paters, E., Paters, E., Paters, E., Paters, E., Paters, E., Paters, E., Paters, E., Paters, E., Paters, E., Paters, E., Paters, E., Paters, E., Paters, E., Paters, E., Paters, E., Paters, E., Paters, E., Paters, E., Paters, E., Paters, E., Paters, E., Paters, E., Paters, E., Paters, E., Paters, E., Paters, E., Paters, E., Paters, E., Paters, E., Paters, E., Paters, E., Paters, E., Paters, E., Paters, E., Paters, E., Paters, E., Paters, E., Paters, E., Paters, E., Paters, E., Paters, E., Paters, E., Paters, E., Paters, E., Paters, E., Paters, E., Paters, E., Paters, E., Paters, E., Paters, E., Paters, E., Paters, E., Paters, E., Paters, E., Paters, E., Paters, E., Paters, E., Paters, E., Paters, E., Paters, E., Paters, E., Paters, E., Paters, E., Paters, E., Paters, E., Paters, E., Paters, E., Paters, E., Paters, E., Paters, E., Paters, E., Paters, E., Paters, E., Paters, E., Paters, E., Paters, E., Paters, E., Paters, E., Paters, E., Paters, E., Paters, E., Paters, E., Paters, E., Paters, E., Paters, E., Paters, E., Paters, E., Paters, E., Paters, E., Paters, E., Paters, E., Paters, E., Paters, E., Paters, E., Paters, E., Paters, E., Paters, E., Paters, E., Paters, E., Paters, E., Paters, E., Paters, E., Paters, E., Paters, E., Paters, E., Paters, E., Paters, E., Paters, E., Paters, E., Paters, E., Paters, E., Paters, E., Paters, E., Paters, E., Paters, E., Paters, E., Paters, E., Paters, E., Paters, E., Paters, E., Paters, E., Paters, E., Paters, E., Paters, E., Paters, E., Paters, E., Paters, E., Paters, E., Paters, E., Paters, E., Paters, E., Paters, E., Paters, E., Paters, E., Paters, E., Paters, E., Paters, E., Paters, E., Paters, E., Paters, E., Paters, E., Paters, E., Paters, E., Paters, E., Paters, E., Paters, E., Paters, E., Paters, E., P
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FEATURES

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GGVIDLYVFAGESPEMVMQYTELIGRPAPMPYWSFGFHQCRYGYKNYSDLEYVVDGY
AKGAGIPLEWWMTDIDXHGSYADFTLGRPAPMPPEDRAGSFYDTHUNGGYKYLLIDDSIG
VDSSYGTYNGGMEDNYFIKNAFEBYLGEVMPCKVY FPDFLIRPAATFWSNEIRAFOE
LPLDGLWIDMNELSNFITSPLSGSSLDDPPYKINNSGDKRPINNKTVPATSIHFGNI
SYSTABINLYGGLEAKYTHQAVUDITGKFPFILSRSTFVSSGKYTAHWTGDNAKYMEDL
AYSIPGILNYGLEGIPWAGAIVGGFHDTTEELCRRWIOLGAFYPFREDHSGTARG
ELYLMOSVASSARKULGGFHDTTEELCRRWIOLGAFYPFREDHSGTARG
ELYLMOSVASSARKULGGFHDTTEELCRRWIOLGAFYPFREDHSGTARG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SQFLIGKSIMVSPALKQGAVAVDAYFPAGNWFDLFNYSFAVGGDSGKHVRLDTPADHV
NPVPRGSITYNMQGRALTTRDAKTPYQLLVVASRLENISBELFLDDGSBNLRMGAGGG
NDPTLVKFRCYWTGKSVLYPSPSYNNPBYASKHKWSIGKVTFVGFENVENVKTYEVRT
SERLREPRISLIKTVSONDDRRELSVENSKELSLLAVGKKFEMRIRL"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AYOS3414 2769 bp mRNA linear PLN 05-SEP-2001
Arabidopsis thaliana AT5g11720/T22P22_110 mRNA, complete cds.
AYOS3414
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta, Spermatophyta; Magnoliophyta; eudicotyledons, core eudicots, Core eucicots, Cosdae, eurosida II; Brassicales; Brassicaceae, Arabidopsie. (Dases 1 to 2769)
Shinn, P., Chen, H., Cheuk, R., Kim, C.J., Koesema, E., Meyers, M.C., Hayashizaki, Y., Ishida, J., Jang, P.X., Jones, T., Kamiya, A.D., Karlin-Neumann, G., Rawin, J., Dan, B., Lee, J.M., Lin, J., Liu, S.X., Miranda, M., Narusaka, M., Nguyen, M., Onodera, C.S., Palm, C.J., Pham, P.K., Quach, H.L., Sakuwi, Satou, M., Seti, M., Southwick, A., Tang, C.C., Torxiumi, M., Yamada, K., Yamanra, Y., Yu, G., Yu, S., Shinozaki, K., Davis, R.W., Theologis, A. and Ecker, J.R.
       Chang, E., Dale, J.M., Goldsmith, A.D., Jones, T., Karlin-Neumann, G.,
Lam, B., Lee, J.M., Lin, J., Miranda, M., Nguyen, M., Onodera, C.S.,
Palm, C.J., Quach, H.L., Southwick, A., Tang, C.C., Toriumi, M.,
Wu, H.C., Yamada, K., Yamamura, Y., Yu, G., Davis, R.W., Theologis, A.
                                                                                                                                                                                                                                      Cheuk, R. (SSP/Salk) and Seki, M. (RIKEN GSC) contributed equally this work. Shinozaki, K. (RIKEN GSC) and Ecker, J.R. (SSP/Salk) contributed equally to this work as PIs.

Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Indels
                                                                                                                                                                                                                                                                                                                                                                                                                              /organism="Arabidopsis thaliana"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /codon_start=1
/product="At5g11720/T22P22_110"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              51
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /note="This clone is in pUNI
ecotype: Columbia"
1. .2709
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               'note="alpha-glucosidase 1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         733 t
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Arabidopsis thaliana
                                                                                                                                                                                                                                                                                                                                                                                                                                                     /mol_type="mRNA"
/db_xref="taxon:3702"
/chromosome="5"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             663 g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /clone="U13819"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AY053414.1 GI:15450744
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nes 24; Conservative
                                                                                                                                                                    and Ecker, J.R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         729 a
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LOCUS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RIKEN Genomic Sciences Center (GSC) members carried out the collection and clustering of RAFL cDNAs (RAFL cDNA: RIKEN Arabidopsis Full-Length cDNA): Seki,M., Narusaka,M., Ishida,J., Satou,M., Kamiya,A., Sakurai,T., Carninci,P., Kawai,J., Hayashizaki,Y. and Shinozaki,K.
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Arabidopsis thaliana At5g11720/T22P22_110 mRNA, complete cds.
BT002222
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 271434;
269670: contig of 269670 bp in length 269770: gap of unknown length 271434: contig of 1664 bp in length.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /note="wgs_contig"
56784 a 53038 c 51445 g 57872 t 52295 others
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 73.1%; Score 21.2; DB 2; Best Local Similarity 88.5%; Pred. No. 1.1e+02; Matches 23; Conservative 0; Mismatches 3;
                                                                                                         Location/Qualifiers

1. 27434

2. 27434

1. 27434

2. crganism="Rattus norvegicus" /mol_type="genomic DNA" /clone="CH230 197C21" /clone="CH230 197C21" /s3225. .54589 /note="wgs_contig" /note="wgs_contig" /s3040. .74665 /note="wgs_contig" /s0413. .151781
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269771
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BT002222/C
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
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ORIGIN
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TITLE JOURNAL

COMMENT

TITLE JOURNAL REFERENCE AUTHORS

AUTHORS REFERENCE

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Arabidopsis cDNA clones

TITLE

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Uppublished
Shin, P., Cheuk, R., Kim, C.J., Koesema, E., Meyers, M.C.,
Shinn, P., Cheu, H., Carninci, P., Dale, J. M., Goldsmith, A.D.,
Banh, J., Bowser, L., Carninci, P., Dale, J. M., Goldsmith, A.D.,
Hayashizaki, Y., Ishida, J., Jiang, P. X., Jones, T., Kamiya, A.,
Karlin-Neumann, G., Kawai, J., Lam, B., Lee, J. M., Lin, J., Lin, J., Lin, J.,
Miranda, M., Narusaka, M., Buyyen, M., Onodera, C.S., Palm, C.J.,
Pham, P. K., Quach, H. L., Sakurai, T., Satou, M., Seki, M., Southwick, A.,
Tang, C.C., Toriumi, M., Yamada, K., Yamamura, Y., Yu, G., Yu, S.,
Shinozaki, K., Davis, R.W., Theologis, A. and Ecker, J.R.
Direct Submission
L. Submitted (28 AUG-2001) Salk Institute Genomic Analysis Laboratory
Submitted (28 AUG-2001) Salk Institute for
Biological Studies, 10010 N. Torrey Pines Road, La Jolla, CA 92037,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      VI PRACNHSPRRFSTEEDGGNSPENNFLADPSSDLVFTLHNTTPFGFSVSRRSGDLLFDTSPBSSDSNTYFIFKOGPLGLSSALPENRSNLYGIGEHTKRSFRLIPGETMTLWNADIGSNPDNYFGISPFFWRSFRENTIFWNADIGSNPDNYFGSHPFYMONGGSKGREBAGTTHGVLLLNSNGNDVKYEGHRITYNVI GGVI DLLYFYGAPSPENWYMYTHELI BRAPWPYWSFGFHQCRYGYKNVSDLEYVVDGY AKAGI PLEVMMTDIDYMDGYKDFTLDPYMFEDKMQSPTDTLHKNGGKYVLLIDPPGIG VDSSYGTYNRGMEADVFIKRNGBPYLGEVWPGKVYFPDFLNRQRAATFWSNEIKMFQEI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The Salk, Stanford, PGEC (SSP) Consortium members carried out the sequencing and annotation of the RAFL cDNAs: Shinn, P. Chen, H. Cheuk, R., Kim, C.J., Koeseme, E., Meyers, M.C., Banh, J. Bowser, L., Dale, J. M., Goldsmith, A.D., Jiang, P. X., Jones, T., Karlin-Neumann, G., Lam, B., Lee, J. M., Lin, J., Liu, S.X., Miranda, M., Nguyen, M., Ondera, C.S., Palm, C.J., Pham, P.K., Quach, H.L., Southwick, A., Tang, C.C., Toriumi, M., Yamada, K., Yamamura, Y., Yu, G., Yu, S., Davis, R.W., Theologis, A., and Ecker, J.R.
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SEYDAHNLYGLLEAKATHQAVVDITGKRPFILSRSTFVSSGKYTAHWTGDNAAKWEDL
AYSIPGILNFGLFGIPMVGADICGFSHDTTEELCRRWIQLGAFYPFARDHSSLGTARQ
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NVHVREGSIVAMQGEALITRDARKTPYQLLVVASRLENISGELFLDDGENLRMGAGGG
NRDWTLVKFRCYVTGKSVVLRSEVVNPEYASKOKMSIGKVTFVGFENVENVKTYEVRT
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gvdsnrqvltakldlikpssvyapdikslnlhvsletserlriridssqqrweipe"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ELYLWDSVASSARKVLGLRMRLLPHLYTLMYEAHVSGNPIARPLFFSFPQDTKTYEID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Shinn, P. (SSP/Salk) and Seki, M. (RIKEN GSC) contributed equally to this work. Shinozaki, K. (RIKEN GSC) and Ecker, J.R. (SSP/Salk) contributed equally to this work as PIS. Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         collection and clustering of RAFL cDNAs (RAFL cDNA: 'RIKEN Arabidopsis Full-Length cDNA'): Seki,M., Narusaka,M., Ishida,J., Satou,M., Kamiya,A., Sakurai,T., Carninci,P., Kawai,J., Hayasbizaki,Y. and Shinozaki,K.
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Pred. No. 95;
0; Mismatches 5; Indels

    2769
    organism="Arabidopsis thaliana"

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/product="ATS911720/T22222_110"
/protein_id="AAX96644.1"
/db_xref="GI:15450745"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /chromosome="5"
/clone="RAFL09-14-L23(R13819)
/note="ecotype: Columbia"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1. .26
27. .2735
/note="alpha-glucosidase 1"
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Best Local Similarity 82.8%;
Matches 24; Conservative
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Search completed: October 27, 2003, 11:10:33 Job time : 2688 secs